

## NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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## BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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## SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

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Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2*n*-1, wherein *n* is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2*n*, wherein *n* is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

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Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

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In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.



In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a  
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic  
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORFX polypeptide or nucleic  
20 acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

In a another aspect, the invention provides a method of determining the presence of or  
30 predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is  
5 preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

10 In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a  
15 control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which  
20 such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention  
25 belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and  
30 examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

## DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF $n$  according to the invention (wherein  $n$  is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2 $n$ -1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2 $n$ . For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected. Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu/>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of '7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

### **Amylases**

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

### 5      **Amyloid**

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 15 Amyloid deposition is also associated with type II diabetes mellitus.

### **Angiopoeitin**

Members of the angiopoietin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

### 25      **Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

5           **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form  
10 of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

**Colony-stimulating factor-related proteins**

Granulocyte/macrophage colony-stimulating factors are cytokines that act in  
15 hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

**Complement-related proteins**

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a  
20 membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent  
25 cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

### **Cytochrome**

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

### **Kinesins**

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

### **Cytokines, Interferon, Interleukin**

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

### **G-protein coupled receptors**

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

**Thioesterases**

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_rna_bind	DNA/RNA binding protein/factor
	dna_rna_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein



	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase	phosphorylase
	PIR	PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase	polymerase
	potassium_channel	potassium channel protein
	prostaglandin	prostaglandin
	protease	protease
	proteaseinhib	protease inhibitor
	reductase	reductase
10	ribosomalprot	ribosomal associated protein
	RTR	EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
	SIM	similar
15	SPTR	EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
	struct	structural associated protein
	sulfotransferase	sulfotransferase
20	SWP	SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN	SWISS-PROT Update (release 11-NOV-98)
	synthase	synthase
	tgf	transforming growth factor
25	tgfreceptor	transforming growth factor receptor
	thioesterase	thioesterase
	thiolase	thiolase
	tm7	seven transmembrane domain G-protein coupled receptor
30	tnf	necrosis factor receptor
	traffic	tumor necrosis factor
	tnfreceptor	tumor trafficking associated protein
	TRN	EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor	transcription factor
	transferase	transferase
	transport	transport protein
	tubulin	tubulin
	ubiquitin	ubiquitin
40	unclassified	Protein not categorized into one of the aforementioned protein families
	water channel	water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are  
5 useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to  
10 identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

### ORFX Nucleic Acids

15 The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2*n*, wherein *n* = 1 to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, ..., 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

20 In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof, any of whose bases may be changed from the  
25 disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), including fragments, derivatives,

analogues and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as  
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is  
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and  
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic  
20 acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism  
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular  
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2<sup>nd</sup> Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

5 As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect.

10 Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the  
15 nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively,  
20 and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but  
25 differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or  
30 analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified

oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161);  
5 or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be  
10 used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides  
15 exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX  
20 proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

## 25 ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of  
30 the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).



In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at  $T_m$ , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (e.g., 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2*n*-1 (wherein  $n = 1$  to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein  $n = 1$  to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, e.g., Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and  
5 Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A  
10 non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (e.g., as  
15 employed for cross-species hybridizations). See, e.g., Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

#### Conservative mutations

In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in  
20 the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions  
25 leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present  
30 invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely  
5 to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such  
10 ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). Preferably, the protein encoded by the nucleic acid is at least  
15 about 80% homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) can be created by introducing one or more  
20 nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2*n*-1 for the corresponding *n*, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably,  
25 conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine,  
30 tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

#### Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

#### Ribozymes and PNA moieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are

carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

- 5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
- 10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
- 15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

- Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
- 20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

- In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
- 25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
- 30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide



synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24:

3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

### ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX -like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

#### **Determining homology between two or more sequences**

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch* 1970 *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2n-1 (wherein n = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

#### **Chimeric and fusion proteins**

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5           For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10           In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

15           In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

20           In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX  
25           cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of  
30           ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

#### ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one

embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477).

#### Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,



transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

#### Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as  $F_{ab}$  or  $(F_{ab})_2$ , that bind immunospecifically to any of the proteins of the invention.

10 An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in  
15 any of SEQ ID NO:2n (wherein n = 1 to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6  
20 contiguous amino acids of any of SEQ ID NO:2n (wherein n = 1 to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example,  
25 the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as  
30 immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$  and  $F_{(ab)}_2$  fragments, and an  $F_{ab}$  expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein  $n = 1$  to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND  
5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of  $F_{ab}$  expression libraries (see *e.g.*, Huse, *et al.*,  
10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by  
15 techniques known in the art including, but not limited to: (i) an  $F_{(ab)_2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)_2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_v$  fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized  
20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent  
25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J.*  
30 *Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060.

Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and  
5 other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or  
10 derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or  
15 derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly  
20 produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated  
25 by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein,  
30 fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

### ORFX Recombinant Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can  
10 be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are  
15 replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the  
20 invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the  
25 recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation  
30 system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the  
5 nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as  
10 described herein (*e.g.*, ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY:  
15 METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or  
20 non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is  
25 introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and  
30 pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons  
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,  
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,  
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*  
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,  
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant



host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

## 5 Transgenic animals

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences  
10 have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal  
15 includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous  
20 recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding  
25 nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to  
30 the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2n-1 (wherein  $n = 1$  to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2n-1 (wherein  $n = 1$  to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G<sub>0</sub> phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

### Pharmaceutical Compositions

5 The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, 10 antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human 15 serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

20 A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent 25 such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with 30 acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder  
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated  
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible  
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as  
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired  
5 therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of  
10 routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the  
15 complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

## 20 Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and  
25 pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be  
30 used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for



example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5        This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

#### Screening Assays

      The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,  
10        peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

      In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained  
15        using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are  
20        applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

      Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993)  
25        *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

      Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409),  
30        plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^3\text{H}$ , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular  $\text{Ca}^{2+}$ , diacylglycerol,  $\text{IP}_3$ , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton<sup>®</sup> X-100, Triton<sup>®</sup> X-114, Thesit<sup>®</sup>, Isotridecypoly(ethylene glycol ether)<sub>n</sub>, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J Biol Chem* 268:12046-12054; Bartel *et al.* (1993) *Biotechniques* 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

#### Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

### **Predictive Medicine**

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (e.g., blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (e.g., drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (e.g., the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (e.g., drugs, compounds) on the expression or activity of ORFX in clinical trials.

### **Use of Partial ORFX Sequences in Forensic Biology**

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, or semen



found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs: \_\_ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

### Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5           Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

10           Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

          These and other agents are described in further detail in the following sections.

#### **Diagnostic Assays**

15           Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

          An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

20           The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be administered in which an antibody specifically binding the ORFX-like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX nucleic acids of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161) may be used to detect DNA  
5 containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological  
10 sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid  
15 probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

20 An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')<sub>2</sub>) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or  
25 antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as  
30 tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

#### Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for  
5 identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained  
10 from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder  
15 associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample  
20 is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a  
25 proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion  
30 of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, e.g., U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, e.g., Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared.

5 Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ORFX can be identified by hybridizing a  
10 sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through  
15 long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one  
20 complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS*  
25 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

30 Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA

heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that  
5 cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest  
10 mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

15 In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T  
20 mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

25 In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments  
30 of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting



alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers *et al.* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, e.g., Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, e.g., Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, e.g., Gasparini *et al.* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5       The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10       Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

#### **Pharmacogenomics**

15       Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be  
20       considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate  
25       dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30       Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

### Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

#### Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

#### **Determination of the Biological Effect of a Therapeutic**

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

#### **Malignancies**

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (e.g., cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,

but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models, in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

#### 10 Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.



Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein. Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

### Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of  
5 the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

10 Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination);  
15 benign tumors; fibrocystic conditions and tissue hypertrophy (e.g., benign prostatic hypertrophy).

### Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate  
20 (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of  
25 apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

#### Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

#### Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5           A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),  
10       transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein  
15       (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for  
20       example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

          Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be  
25       treated or prevented by administration of a Therapeutic that modulates activity.

#### **Cytokine and Cell Proliferation/Differentiation Activity**

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D,  
5 DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+ ), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing  
10 Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or  
15 thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells  
20 include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons,  
25 Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

30 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immun* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

### Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania species, malaria species and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the

immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the



patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be  
5 capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a  
10 subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression  
15 of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells.  
20 In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on  
25 the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a  
30 B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without  
5 limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981;  
10 Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which  
15 will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins  
20 that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by  
25 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J Exp Med* 172:631-640, 1990.  
30

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

#### **Hematopoiesis Regulating Activity**

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5        Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*  
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,  
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.  
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

#### **Tissue Growth Activity**

A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for  
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation  
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with

5 the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular

10 insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such

15 tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions

20 resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the

25 following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

30 Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

#### Activin/Inhibin Activity

A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*, eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

- 20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for  
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*



45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

#### Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor  
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and  
ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and  
their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell  
interactions and their ligands (including without limitation, cellular adhesion molecules (such as  
selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,  
10 antigen recognition and development of cellular and humoral immune responses). Receptors and  
ligands are also useful for screening of potential peptide or small molecule inhibitors of the  
relevant receptor/ligand interaction. A protein of the present invention (including, without  
limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of  
receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the  
following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:  
CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and  
Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions  
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp.*  
*Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*,  
*J Immunol Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

#### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The  
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the  
inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example,  
cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory  
process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production  
of other factors which more directly inhibit or promote an inflammatory response. Proteins  
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from  
5 over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

### **Tumor Inhibition Activity**

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit  
10 tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote  
15 tumor growth.

### **Other Activities**

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing  
20 or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or  
25 elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other  
30 than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or  
5 entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

## 10 EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular  
15 embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to  
20 those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gii4691395[emb]CAB41562.1] - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	80248081 (3, 4)	Novel Protein sim. GBank gii2829506[sp]P71559[SUCC. MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)]	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264689, 264638, 264587
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264905, 264636, 264691, 264907, 264692, 264629
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264760, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22279002, 264563
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gii4415926[gb]AAD20157] - (AC006282) unknown protein (Arabidopsis thaliana)		UNCLASSIFIED	20281099, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 285008, 264512, 265009, 264910, 264595, 264596, 264758, 264603, 264604, 264760, 264762, 264683, 264768, 264767, 264689, 35695917, 264690, 264692, 264693, 33657109, 264628, 264629, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264486
8	56924278 (15, 16)	Novel Protein sim. GBank gii585562[sp]Q06458[NIRB. KLEPN - NITRITE REDUCTASE (NAD(P)H) LARGE SUBUNIT		reductase	264907
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79558459 (19, 20)			UNCLASSIFIED	264908
11	20414027 (21, 22)			UNCLASSIFIED	264605
12	94141210 (23, 24)	Novel Protein sim. GBank gii3878145[emb]CAA99871] - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264564
14	95105114 (27, 28)	Novel Protein sim. GBank gii2832781[emb]CAA12645] - (AJ225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35696288, 35696052, 264510, 35695917, 264691, 264628, 35696423, 264555, 264558, 264559, 83373044
15	20458307 (29, 30)	Novel Protein sim. GBank gii1710791[sp]Q10234[RT05. SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20292744 (33, 34)	Novel Protein sim. GBank gij1174884[spIP44391]URE1 - HAEIN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	264600	
18	80246804 (35, 36)	Novel Protein sim. GBank gij2281102 (AC002333) - SF16 isolog [Arabidopsis thaliana]		29331827, 264555, 264557, 264638, 264558	
19	80076624 (37, 38)	Novel Protein sim. GBank	UNCLASSIFIED	22278998, 264907, 264600, 264693	
20	20724558 (39, 40)	gij2506112[spIP43672]UUP_ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP	transport	264602	
21	80417554 (41, 42)	Novel Protein sim. GBank gij1730203[spIP50442]GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)	UNCLASSIFIED	22278995, 264906, 265008, 265010, 265011, 264602, 264605, 264768, 264688, 21908784, 264691, 18108376, 264638, 18108387, 264486	
22	11705858 (43, 44)	Novel Protein sim. GBank gij1877329[emb]CAB07077] - (Z92771) fadE25 [Mycobacterium tuberculosis]		264685	
23	80418178 (45, 46)		Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	264488, 264807, 264809, 264600, 264602, 264603, 264605, 264682, 264768, 32833988, 264638, 264488	
24	20291697 (47, 48)			264600	
25	80253774 (49, 50)			264593	
26	80255394 (51, 52)		UNCLASSIFIED	22278998, 56182435, 265018, 264566	
27	80235795 (53, 54)	Novel Protein sim. GBank gij4808369[emb]CAB42783.1] - (AL049841) putative 30S ribosomal protein S14 [Streptomyces coelicolor]	Contains protein domain (PF00253) - Ribosomal protein S14p/S29e	18108370, 35696423, 264635, 264555	
28	76483581 (55, 56)			264638	
29	82448765 (57, 58)	Novel Protein sim. GBank gij3122280[spIO8333]K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)	UNCLASSIFIED	264601, 264762, 264766, 264768, 264638	
30	78199333 (59, 60)		Contains protein domain (PF00365) - Phosphofructokinase		
31	19848158 (61, 62)		UNCLASSIFIED	264908, 265019, 264687, 21906764, 21906766	
32	82449495 (63, 64)	Novel Protein sim. GBank gij3560504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED	264534	
33	79582828 (65, 66)	Novel Protein sim. GBank gij2129003[pir]G64507 - hypothetical protein MJ1685 - Methanococcus jannaschii	UNCLASSIFIED	264905, 264605, 264762, 264766, 264687, 264689	
34	87467657 (67, 68)		UNCLASSIFIED	264687	
35	95005170 (69, 70)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	60432288, 264600, 264602, 264760, 18108357, 264769, 265020, 264691	
36	19642042 (71, 72)	Novel Protein sim. GBank gij3287739[spIP73538]BIOB_SYNY3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)	UNCLASSIFIED	264600, 264687, 264558, 264639	
37	20368215 (73, 74)	Novel Protein sim. GBank gij2313134[spIP4AD07126.1] - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26695]	synthase	264566	
			dehydrogenase	264603	

38	20466334 (75, 76)	Novel Protein sim. GBank gij3805970[embjCAA06231] - (AJ004933) periplasmic nitrate reductase, large subunit [Rhodospirillum rubrum sp.]		reductase	264605	
39	94300715 (77, 78)	Novel Protein sim. GBank gij1929448 (L63543) - endodermin [Xenopus laevis]	Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	264905, 264906, 264907, 66712502, 264908, 264909, 264511, 265009, 264910, 55812038, 264758, 265011, 264762, 264682, 264763, 264764, 264766, 265022, 264893, 264628, 264631, 264634, 264635, 264555, 264638, 18108381, 264558, 18108385, 264482	
40	20635625 (79, 80)			UNCLASSIFIED	264592	
41	80023287 (81, 82)	Novel Protein sim. GBank gij854065[embjCAA58337] - (X83413) U88 [Human herpesvirus 6]			264591, 35695917	
42	20724566 (83, 84)			UNCLASSIFIED	264602	
43	20467069 (85, 86)	Novel Protein sim. GBank gij3820584 (AF086791) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]		synthase	264605	
44	13085297 (87, 88)	Novel Protein sim. GBank gij2494764[spjQ50729]GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)	Contains protein domain (PF00958) - GMP synthase C terminal domain	synthase	264769, 264636	
45	39384711 (89, 90)	Novel Protein sim. GBank gij1881738 (U89888) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]		UNCLASSIFIED	264769, 264510, 264508	
46	95003398 (91, 92)			ngl	264566	
47	11698624 (93, 94)			UNCLASSIFIED	264689	
48	79407218 (95, 96)				18108385, 264635, 264828	
49	21659844 (97, 98)			UNCLASSIFIED	264603	
50	80503896 (99, 100)				264508, 264603, 264769, 264689, 264636, 264558, 264486	
51	80255569 (101, 102)	Novel Protein sim. GBank gij3411177 (AF076240) - MocC [Rhizobium leguminosarum bv. viciae]		UNCLASSIFIED	264593, 18108387	
52	79208528 (103, 104)	Novel Protein sim. GBank gij3914992[spjQ26264]SM41 - HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)		struct	264634	
53	36986970 (105, 106)	Novel Protein sim. GBank gij3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]		UNCLASSIFIED	264782	
54	79570897 (107, 108)			UNCLASSIFIED	264630, 264909, 264766	
55	80202703 (109, 110)	Novel Protein sim. GBank gij1633572 (U52064) - Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]			29331824, 264102, 265018, 18108376	
56	87584008 (111, 112)	Novel Protein sim. GBank gij4321580[gbjAAD15785] - (AF050114) alginate lyase [Pseudomonas sp. W7]			264604	
57	11223386 (113, 114)		Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264557	

58	91227508 (115, 116)	Novel Protein sim. GBank gi 5816074 gb AAD45616.1 AF06194 - (AF061943) protate- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	56182575, 264259, 60432048, 35696052, 68712502, 264909, 265008, 265010, 265011, 264681, 29148784, 35695917, 60170615, 264691, 264692, 264693, 18108374, 35698423, 56182323, 60432113 264600, 264689, 264638
59	80077371 (117, 118)	Novel Protein sim. GBank gi 1172920 sp P45830 RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYLTRANSFERASE	Contains protein domain (PF00953) - Glycosyl transferase	transferase	
60	12958341 (119, 120)				264689
61	80426808 (121, 122)	Novel Protein sim. GBank gi 1710216 (U79260) - unknown [Homo sapiens]		glycoprotein	264768
62	13504966 (123, 124)				264630
63	16474553 (125, 126)			UNCLASSIFIED	265019
64	20724578 (127, 128)	Novel Protein sim. GBank gi 420945 pir A47041 - transposase homolog (insertion element [SAE1] - Alcaligenes eutrophus		UNCLASSIFIED	264602
65	78326308 (129, 130)	Novel Protein sim. GBank gi 3122312 sp O06134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	264563
66	46854384 (131, 132)	Novel Protein sim. GBank gi 3928723 emb CAA22219  - (AL034355) putative ABC transporter [Streptomyces coelicolor]		transport	22278996, 264558
67	78952343 (133, 134)	Novel Protein sim. GBank gi 231985 sp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE (40 KD ANTIGEN)		dehydrogenase	265021
68	78817382 (135, 136)				264909
69	78841764 (137, 138)			UNCLASSIFIED	264908
70	78871329 (139, 140)				264908, 264908
71	65897458 (141, 142)			UNCLASSIFIED	264602, 265021
72	87734977 (143, 144)	Novel Protein sim. GBank gi 4415926 gb AAD20157  - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264758, 87188474, 264682, 264766, 264686, 264689, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 264629, 264631, 264639, 22279000
73	80025241 (145, 146)			UNCLASSIFIED	60424179, 264508, 264908, 265007, 264603, 264687, 264689, 264692, 18108387
74	20377410 (147, 148)			UNCLASSIFIED	264605
75	11818032 (149, 150)	Novel Protein sim. GBank gi 2853098 emb CAA16914  - (AL021787) vacuolar protein sorting [Schizosaccharomyces pombe]		UNCLASSIFIED	264689
76	95105303 (151, 152)	Novel Protein sim. GBank gi 4468811 emb CAB38212  - (AL035601) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	83373044, 264906, 264557
77	10144718 (153, 154)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264563
78	8758258 (155, 156)			UNCLASSIFIED	264604

79	94140190 (157, 158)	Novel Protein sim. GBank gij5889453dbj BAA83010.1  - (AB028981) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	35696286, 22278998, 29331822, 29331824, 29331825, 29331827, 264905, 264906, 264907, 66712502, 264908, 264909, 265008, 265009, 264910, 60170831, 55812038, 33109954, 285017, 265018, 264288, 264768, 56181562, 21906765, 21908769, 29148784, 265020, 264690, 264691, 264692, 264693, 60431528, 35896423, 264631, 264632, 264634, 264636, 264639, 83373044, 264564, 264566, 264567
80	82314840 (159, 160)		UNCLASSIFIED	264769, 264601, 265006, 264910, 264604, 264605, 264634, 264635, 264905, 264762, 264637, 264592, 264628, 264907, 264691, 264908, 264567, 264909, 264766, 264605
81	20467247 (161, 162)	Novel Protein sim. GBank gij1723442 sp Q10258 YD2A_SCHPO - HYPOTHETICAL 89.0 KD PROTEIN C56F8.10 IN CHROMOSOME I	reductase	264567
82	16331388 (163, 164)	Novel Protein sim. GBank gij2895866 (AF045770) - methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]	dehydrogenase	264567
83	94741180 (165, 166)	Novel Protein sim. GBank gij3402673 (AC004697) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264488, 264508, 264509, 264905, 264908, 264909, 264511, 264591, 264593, 264594, 264595, 264596, 264758, 264603, 264760, 264681, 18108351, 264762, 264682, 264764, 264684, 264766, 264686, 264632, 264637, 264557, 264638, 264639, 18108385, 264566
84	80355375 (167, 168)	Novel Protein sim. GBank gij1173364 sp P45380 SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTIPORTER)	transport	264508, 264906, 264907, 264908, 264909, 264910, 264760, 264763, 264764, 264766, 264768, 264769, 35695855, 264638, 264637
85	80499600 (169, 170)	Novel Protein sim. GBank gij2120998 pir J570682 - glycosyltransferase homolog - Bordetella pertussis	transferase	264605, 264762, 264687, 264769, 18108374, 264636, 264486
86	39559043 (171, 172)	Novel Protein sim. GBank gij3256023 emb CAA17228.1  - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]		264910
87	13856808 (173, 174)		UNCLASSIFIED	264093



88	85344718 (175, 176)	Novel Protein sim. GBank gi 559703 dbj BAA07552  - (D38549) ha1025 is new [Homo sapiens]		52644507, 52846365, 18108398, 65274572, 56182575, 56994075, 35696288, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 284259, 29331822, 29331824, 36182181, 66714117, 29331825, 29331826, 80432289, 29331827, 29331828, 35696052, 33656970, 264105, 264508, 264905, 264808, 264907, 264908, 29331830, 66712502, 52844045, 58182435, 265007, 285009, 264910, 60170831, 264592, 80431735, 60433356, 33657402, 264757, 80433438, 55812038, 264758, 21906754, 52646317, 33109954, 52844298, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265019, 264448, 264369, 284288, 264766, 52644229, 21906766, 21908767, 21908768, 21906769, 55811857, 35695917, 265020, 265021, 265022, 60170815, 52644150, 33657023, 65274620, 33657109, 27486261, 27486264, 33657349, 35695763, 264628, 263972, 18108374, 55810764, 35696423, 55811576, 65274791, 35695855, 60431850, 264636, 52644332, 56182323, 60170394, 83373044, 18108385, 18108387, 18108388, 58526486, 87168518, 60432113, 22279000, 22279002, 264482, 264584, 264488, 264600
89	80077389 (177, 178)	Novel Protein sim. GBank gi 1710383 sp P46352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX		
90	82115989 (178, 180)	Novel Protein sim. GBank gi 249881 sp P76403 YEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGRK INTERGENIC REGION	UNCLASSIFIED protease	264760 265006
92	79554871 (183, 184)	Novel Protein sim. GBank gi 3367754 emb CAA20078  - (AL031155) hypothetical protein SC3A7.16c [Streptomyces coelicolor]	UNCLASSIFIED	264691
93	80496778 (185, 186)	Novel Protein sim. GBank gi 2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]	ATPase associated	264907, 264908, 264910, 265009, 264605, 264769
94	78646649 (187, 188)	Novel Protein sim. GBank gi 171919 sp P46920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUA	Contains protein domain (PF00571) - transport CBS domain	264906
95	11090238 (189, 190)			264594

96	94322125 (191, 192)	Novel Protein sim. GBank gi 4589560 dbj BAA78602.1  - (AB023175) KIAA0958 protein [Homo sapiens]	UNCLASSIFIED	22278995, 22278999, 264259, 29331822, 29331826, 35696052, 29146499, 264509, 264906, 264907, 264908, 264909, 265007, 265008, 264910, 265009, 264593, 265010, 265017, 264604, 265019, 18108351, 264288, 264766, 264768, 264769, 21906765, 21906767, 21906769, 265020, 264692, 33657182, 35695763, 264628, 264629, 18108379, 264631, 264636, 18108381, 264559, 18108382, 8337304, 22279002, 264508
97	79605200 (193, 194)	Novel Protein sim. GBank gi 4583559 emb CAB40388.1  - (AJ005255) OxyR [Erwinia chrysanthemi]	UNCLASSIFIED	
98	78427000 (195, 196)	Novel Protein sim. GBank gi 1001693 dbj BAA10430  - (D64002) hypothetical protein [Synecococcus sp.]	UNCLASSIFIED	264909
99	20466524 (197, 198)	Novel Protein sim. GBank gi 1169479 sp P43925 EFG_HAEIN - ELONGATION FACTOR G (EF-G)	UNCLASSIFIED	264605
100	79640113 (199, 200)	Novel Protein sim. GBank gi 480897 pir J S37485 - gene msg1 protein - mouse	UNCLASSIFIED	264693
101	80203298 (201, 202)	Novel Protein sim. GBank gi 2894186 emb CAA11773.1  - (AJ223998) PCZA361.18 [Amycolatopsis orientalis]	UNCLASSIFIED	265020, 264102, 263972
102	20467259 (203, 204)	Novel Protein sim. GBank gi 1731040 sp P54509 YQH_H_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	synthase	264605
103	20466368 (205, 206)	Novel Protein sim. GBank gi 1731040 sp P54509 YQH_H_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	helicase	264605
104	80247572 (207, 208)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	264591, 264595, 264602
105	79605208 (209, 210)	Novel Protein sim. GBank gi 1685117 U70770 - furrowed [Drosophila melanogaster]	complement	264508
106	28382058 (211, 212)	Novel Protein sim. GBank gi 1705505 sp P54729 BS4_MOUSE - BS4 PROTEIN	UNCLASSIFIED	264511, 265009
107	80057791 (213, 214)	Novel Protein sim. GBank gi 4887229 gb AAD3244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	ATPase-associated	29331824, 264591, 21906754, 265019
108	80237936 (215, 216)	Novel Protein sim. GBank gi 2635771 emb CAB15264  - (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]	transport	18108374, 35695917, 22278996, 264113, 264600, 264602, 264603, 265017, 264910, 264906, 264636, 264768
109	95194148 (217, 218)	Novel Protein sim. GBank gi 2330791 emb CAB11265  - (Z98801) carboxypeptidase s precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	264758, 264603, 264630, 264636, 264637
110	79562823 (219, 220)			264687
111	39565458 (221, 222)			264564
112	79565038 (223, 224)		UNCLASSIFIED	264908
113	17959439 (225, 226)		UNCLASSIFIED	265007
114	80502101 (227, 228)		UNCLASSIFIED	264769

115	80251003 (229, 230)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52645156, 52645080, 33656870, 264592, 21908754, 27486284, 18108378, 35698423, 264635, 52644332, 18108382
116	81286688 (231, 232)				264905, 264906, 264907, 264908, 264909, 264910, 264758, 265010, 264763, 284682, 264764, 264766, 264685, 264688, 264788, 264789, 33857023, 264693, 33857109, 264628, 18108374, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 56528486, 264565, 264566
117	79636695 (233, 234)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	264639, 264693
118	80222170 (235, 236)				263974
119	91013071 (237, 238)	Novel Protein sim. GBank gll732526 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 29331824, 60432289, 265007, 60433438, 264603, 264605, 18108351, 264789, 264689, 265020, 264534, 27486281, 264558, 83373044, 18108385, 264584
120	8756481 (239, 240)	Novel Protein sim. GBank gll2131219iprj[S50157 - cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae)]		kinase	264603
121	80026153 (241, 242)				264595
122	20457620 (243, 244)	Novel Protein sim. GBank gll2052147embj[CAB08137] - (Z84752) ksgA [Mycobacterium tuberculosis]	Contains protein domain (PF00398) - Ribosomal RNA adenine dimethylases	transferase	264605
123	8758278 (245, 246)				264604
124	79104017 (247, 248)	Novel Protein sim. GBank gll2833385ipq43134UGST_SORBI - GRANULE-BOUND GLYCOPROTEIN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 265006, 265007, 265008, 265010, 265011, 18108355, 18108379, 18108380, 18108384
125	87797986 (249, 250)	Novel Protein sim. GBank gll475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	264508, 264906, 265009, 264596, 22279002
126	56701283 (251, 252)	Novel Protein sim. GBank gll5102785embj[CAB45200.1] - (AL079308) putative transcriptional regulator [Streptomyces coelicolor]			264511
127	20467267 (253, 254)				264605
128	80248473 (255, 256)	Novel Protein sim. GBank gll130120iprj23620PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED - phosphatase	264907, 264909, 264910, 264600, 264601, 264603, 264605, 18108351, 264693, 264557
129	95290543 (257, 258)	Novel Protein sim. GBank gll2506493iprj38036YGC8_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION [X83413] U88 [Human herpesvirus 6]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35698423, 35695855, 264600, 264602, 264603, 264604, 264605, 264508, 264908, 264584, 264628, 264682, 264565, 264683
130	80085563 (259, 260)	Novel Protein sim. GBank gll8540655embj[CAB458337] - (X83413) U88 [Human herpesvirus 6]			264634
131	94895022 (261, 262)	Novel Protein sim. GBank gll1076038iprj[S54660 - ABC transporter PstC-2 chain - Mycobacterium tuberculosis]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 264769, 29331828, 264689, 22278996, 265021, 264600, 264511, 264601, 264602, 264605, 264905, 264686

132	10887692 (263, 264)	Novel Protein sim. GBank gij1877340 emb CAB07068  - (Z92771) acc-A3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264638 264905, 264669
133	94630883 (265, 266)	Novel Protein sim. GBank gij4585838 emb CAB40932.1  - (AL049630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	264905, 264605, 265021
134	78834660 (267, 268)	Novel Protein sim. GBank gij1460074 emb CAB01049  - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]			264634
135	18885057 (269, 270)	Novel Protein sim. GBank gij2125896 emb CAA73511  - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]		synthase	264508
136	78846083 (271, 272)				
137	78619770 (273, 274)				264683, 264685, 264686, 264691, 264692, 264693
138	78635971 (275, 276)	Novel Protein sim. GBank gij5420387 emb CAB46679.1  - (A243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108374, 18108385, 33657109, 33657182, 265010, 22278998, 265008, 265007, 265008, 265009, 264693
139	86688076 (277, 278)	Novel Protein sim. GBank gij5689912 emb CAB52075.1  - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) - Chorismate mutase	dehydrogenase	22278996, 265007, 264910, 60433356, 265010, 264602, 264605, 264766, 264688, 264769, 264693, 32833986, 18108374, 18108387
140	78825759 (279, 280)			UNCLASSIFIED	264908
141	20700094 (281, 282)	Novel Protein sim. GBank gij3581916 emb CAA20855  - (AL031545) mulS family DNA mismatch repair protein [Schizosaccharomyces pombe]		nuclease	264600 264602, 265017
142	80028104 (283, 284)				
143	11072274 (285, 286)	Novel Protein sim. GBank gij3334127 sp P97303 BAC2, MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)		UNCLASSIFIED	264600 263978, 264600, 264910, 264632, 264508, 264563, 264564, 264591, 264556, 264908, 264629, 264639
144	95009102 (287, 288)	Novel Protein sim. GBank gij3757569 emb CAA21315  - (AL031863) 1-evidence=predicted by content; 1-evidence=genefinder;084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]		UNCLASSIFIED	22278996, 264602
145	80027058 (289, 290)	Novel Protein sim. GBank gij140807 sp P24536 Y121_BURGE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN	Contains protein domain (PF01675) - Transposase		264687
146	13085662 (291, 292)	Novel Protein sim. GBank gij2827608 emb CAA16563  - (AL021846) uvrD2 [Mycobacterium tuberculosis]		helicase	264905, 264906, 264909, 264510, 265009, 60433356, 264600, 264601, 264604, 264605, 264687, 264769, 18108385, 65274791, 18108387
147	94320366 (293, 294)				
148	80248804 (295, 296)	Novel Protein sim. GBank gij2916947 emb CAA17585  - (AL021999) hypothetical protein Rv0986 [Mycobacterium tuberculosis]		transport	265009, 265010, 264600, 264602, 264603, 264604, 264605, 264693, 33657109, 264636

149	80249373 (297, 298)	Novel Protein sim. GBank gi 1723073 sp Q11040 Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01	Contains protein domain (PF00005) - ABC transporter	transport	265010, 264600, 264601, 264603, 264604, 27486285, 264636
150	20294748 (299, 300)	Novel Protein sim. GBank gi 372412 emb CAA11909  - (AJ224340) maltose phosphorylase [Lactobacillus sanfrancisco]			264600
151	20726398 (301, 302)	Novel Protein sim. GBank gi 729312 sp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	264602
152	95002877 (303, 304)	Novel Protein sim. GBank gi 2497952 sp P35667 Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM		peptidase	264602
153	80256665 (305, 306)	Novel Protein sim. GBank gi 3123021 sp Q90508 VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	264593
154	82305968 (307, 308)	Novel Protein sim. GBank gi 419697 pir JUN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	mapolymerase	264910, 264762, 264691, 264634 264605
155	20428658 (309, 310)	Novel Protein sim. GBank gi 628710 pir J541739 - hypothetical protein - Escherichia coli		UNCLASSIFIED	264565
156	39564742 (311, 312)	Novel Protein sim. GBank gi 3695013 (AF052586) - CitA [Pseudomonas aeruginosa]	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/HnfX family	hydrolase	264691
157	10358887 (313, 314)	Novel Protein sim. GBank gi 1073072 pir J55543 - cmaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	264905
158	79761938 (315, 316)	Novel Protein sim. GBank gi 1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	265008 264605
159	78890376 (317, 318)	Novel Protein sim. GBank gi 5304869 emb CAB46028.1  - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00327) - Ribosomal protein L30p/L7e	ribosomal prot	22278986, 264600, 264603, 35695917, 32833986, 35698423, 264636
160	11075119 (319, 320)	Novel Protein sim. GBank gi 2661691 emb CAA15795  - (AL009204) putative protease [Streptomyces coelicolor]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	Interleukin	264112, 264532, 22278002
161	80055007 (321, 322)	Novel Protein sim. GBank gi 4416478 gb AAD20378  - (AF125999) transposase [Mycobacterium avium]		UNCLASSIFIED	264639 264805, 264907, 264600 264691
162	80016371 (323, 324)	Novel Protein sim. GBank gi 76177 pir JQECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli		UNCLASSIFIED	264605, 264486
163	11682308 (325, 326)			UNCLASSIFIED	265010
164	80077902 (327, 328)			UNCLASSIFIED	264600
165	10856067 (329, 330)			UNCLASSIFIED	
166	88095003 (331, 332)			UNCLASSIFIED	
167	16395460 (333, 334)			UNCLASSIFIED	
168	80079362 (335, 336)			UNCLASSIFIED	
169	80238581 (337, 338)				264556, 264557, 264558, 264559

170	79512364 (339, 340)	Novel Protein sim. GBank gi 140888 sp P27847 YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECO.PLDB INTERGENIC REGION (F138)	Contains protein domain (PF01810) - LysE type translocator		264906 264595, 264604
171	95293073 (341, 342)				
172	37787007 (343, 344)	Novel Protein sim. GBank gi 4210905 gb AAD12048.1  - (AF045609) AgIG (Sinorhizobium meliloti)	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264769
173	57529660 (345, 346)	Novel Protein sim. GBank gi 132854 sp P02387 RL2_ECOLI - 50S RIBOSOMAL PROTEIN L2	Contains protein domain (PF00181) - Ribosomal Proteins L2	ribosomal prot	264769
174	95293078 (347, 348)	Novel Protein sim. GBank gi 1881350 dbj BAA10377  - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIBIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]		transport	264510, 264593, 264602, 264603, 264605, 264762, 264693
175	79758270 (349, 350)	Novel Protein sim. GBank gi 2072722 emb CAB08328  - (Z95121) manA [Mycobacterium tuberculosis]		isomerase	264565
176	80066898 (351, 352)	Novel Protein sim. GBank gi 1055198 (U40187) - similar to PIR-A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264907, 264910, 264681, 264558
177	86684852 (353, 354)	Novel Protein sim. GBank gi 2326738 emb CAB10952  - (Z98268) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	264768, 60424179, 264687, 264688, 264769, 29331826, 60432289, 18108376, 264689, 18108387, 32833986, 22278998, 265020, 264600, 264601, 264602, 264603, 264604, 264605, 264635, 264762, 264638, 264908, 264564, 264637, 264638, 264486, 60433356, 264766
178	79559528 (355, 356)	Novel Protein sim. GBank gi 1906596 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	264693, 33657109, 264635
179	20263112 (357, 358)			UNCLASSIFIED	264583
180	80488958 (359, 360)	Novel Protein sim. GBank gi 169367 sp P45256 DNAB_HAEIN - REPLICATIVE DNA HELICASE		helicase	264769
181	79585369 (361, 362)	Novel Protein sim. GBank gi 3170615 (AF059485) - DOC4 [Mus musculus]		UNCLASSIFIED	21806767, 264635, 264639, 18108384
182	80577899 (363, 364)			UNCLASSIFIED	264259, 35696052, 56182435, 264511, 265018, 33657109, 264555, 264568, 264690
183	11614017 (365, 366)	Novel Protein sim. GBank gi 1076627 pir S54172 - inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco		UNCLASSIFIED	
184	10174167 (367, 368)	Novel Protein sim. GBank gi 4371280 gb AAD18138  - (AC006260) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264510

185	21650822 (369, 370)	Novel Protein sim. GBank gij3006178[emb]CAA18398.1] - (AL022304) putative mma transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gij2829802[sp]P94408[YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERA INTERGENIC REGION]		transport	264595
187	80186611 (373, 374)	Novel Protein sim. GBank gij3150260[emb]CAA19179] - (AL023634) cyclin [Schizosaccharomyces pombe]		UNCLASSIFIED	264369
188	20464942 (375, 376)	Novel Protein sim. GBank gij2145853[pr]j[S72938 - hlx protein - Mycobacterium leprae]		kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gij1881244[db]BAA19271] - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE: [Bacillus subtilis]		UNCLASSIFIED	35686052, 264802, 264605, 264762, 264689, 35695917, 18108370, 18108372, 264638, 264565
190	80086821 (379, 380)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]		synthase	264593
191	88095012 (381, 382)	Novel Protein sim. GBank gij4980892[gb]AAD35474.1[AE00171] - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]		isomerase	264508, 264604, 264605, 264769, 264555
192	16333379 (383, 384)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]			264587
193	78910127 (385, 386)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]			264908, 264693
194	20464948 (387, 388)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]			264605
195	13518389 (389, 390)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]		transport	264638
196	95005589 (391, 392)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]		gaba	264600, 264689, 264638
197	80248665 (393, 394)	Novel Protein sim. GBank gij3122305[sp]Q2778[K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)]			
198	79163635 (395, 396)	Novel Protein sim. GBank gij1781203[emb]CAB06110] - (Z83859) gnd [Mycobacterium tuberculosis]		kinase	264602, 264682, 264692, 18108374
199	78890715 (397, 398)	Novel Protein sim. GBank gij2642222 (AF030885) - telomere-associated recQ-like helicase [Ustilago maydis]			264638
200	79413849 (399, 400)	Novel Protein sim. GBank gij2894378[emb]CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]		6-phosphogluconate dehydrogenases	265008
201	86945924 (401, 402)	Novel Protein sim. GBank gij2894378[emb]CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]		UNCLASSIFIED	264595, 264596
				UNCLASSIFIED	29331826, 265007, 264512, 33657402, 264598, 265017, 18108351, 264682, 264683, 264767, 264629, 55810784, 264834, 264635, 58182323, 60432113, 22279000

202	78588046 (403, 404)	Novel Protein sim. GBank gi 231772 sp P30598 CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)	Contains protein domain (PF01644) - synthase Chitin synthase	264600
203	78843927 (405, 406)	Novel Protein sim. GBank gi 1504042 dbj BAA13220  - (D86984) similar to yeast adenylate cyclase (S56776) [Homo sapiens]		22278995, 28331822, 29331825, 29331827, 264908, 21908754, 264683, 21908789, 21908789, 35896423, 264558
204	78855186 (407, 408)	Novel Protein sim. GBank gi 2633808 emb CAB13310  - (Z99111) similar to hypothetical proteins [Bacillus subtilis]	UNCLASSIFIED transport	264809 264808
205	10090583 (409, 410)	Novel Protein sim. GBank gi 213438 l p S60678 - polybrono 1 protein - chicken	UNCLASSIFIED UNCLASSIFIED	264604 264558
206	8758473 (411, 412)	Novel Protein sim. GBank		264605
207	20754522 (413, 414)	Novel Protein sim. GBank		264605, 264689
208	20289261 (415, 416)	Novel Protein sim. GBank		
209	80071069 (417, 418)	Novel Protein sim. GBank		
210	80168800 (419, 420)	Novel Protein sim. GBank		264905, 264907, 264909, 264786, 264687, 264691, 264629, 18108374, 264838 263978
211	80034539 (421, 422)	Novel Protein sim. GBank		
212	82442474 (423, 424)	Novel Protein sim. GBank gi 5031809 ref NP_005536.1 p SLR - immunoglobulin superfamily containing leucine-rich repeat	UNCLASSIFIED	264508, 264905, 264906, 264907, 264908, 264600, 284782, 264534, 264832, 264634, 264635, 264639, 264486
213	80248562 (425, 426)	Novel Protein sim. GBank gi 3122359 sp O33123 LEU2_MYCLE - 3- ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	22278996, 264508, 264600, 264602, 264603, 264605, 33657023, 264565, 264486
214	80079381 (427, 428)	Novel Protein sim. GBank gi 116238 sp P19421 CH60_COXBU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	264600, 264693
215	14973283 (429, 430)	Novel Protein sim. GBank		
216	80177716 (431, 432)	Novel Protein sim. GBank gi 3417297 AC002310  - Unknown gene product [Homo sapiens]	UNCLASSIFIED dna_rna_bind	264829 264448
217	79603634 (433, 434)	Novel Protein sim. GBank gi 2506924 sp P49754 VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)		264508
218	80258475 (435, 436)	Novel Protein sim. GBank gi 173288 sp P38106 RSEA_EC01 - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	tnapolymerase	264594
219	20438797 (437, 438)	Novel Protein sim. GBank gi 1781097 emb CAB06231  - (Z83864) gi B [Mycobacterium tuberculosis]	synthase	264604
220	13489572 (439, 440)	Novel Protein sim. GBank gi 2984703 AF052427  - unknown [Trypanosoma cruzi]	nucleaseinhib	264689
221	11287488 (441, 442)	Novel Protein sim. GBank gi 4587313 dbj BAA76709.1  - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]	UNCLASSIFIED	264555



222	79862802 (443, 444)	Novel Protein sim. GBank gij1877268[emb]CAB07049] - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]	UNCLASSIFIED	264605, 264769, 35696423
223	83053869 (445, 446)		UNCLASSIFIED	264908, 264807, 264603
224	79557920 (447, 448)		UNCLASSIFIED	264684, 264683
225	79559541 (449, 450)	Novel Protein sim. GBank gij2274851[dbj]BA21315] - (D64159) 3-7 gene product [Homo sapiens]	UNCLASSIFIED	264692
226	79172397 (451, 452)	Novel Protein sim. GBank gij868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]	UNCLASSIFIED	22278998, 264112, 33657023, 263981
227	81777198 (453, 454)		UNCLASSIFIED	35695917, 264636, 264807
228	79872285 (455, 456)			264768, 264807, 264908, 264682, 264593, 264639
229	79838268 (457, 458)			264808, 264910
230	11013209 (459, 460)		UNCLASSIFIED	264631
231	20622207 (461, 462)	Novel Protein sim. GBank gij1835114[emb]CAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]		264906, 264800, 264803, 264692
232	80055035 (463, 464)		UNCLASSIFIED	264600, 264603, 264605, 264687, 264768
233	80063054 (465, 466)	Novel Protein sim. GBank gij2642340 (AF032970) - imidazolone propionate hydrolase [Pseudomonas putida]	Contains protein domain (PF00449) - Urease	264604
234	7523398 (467, 468)	Novel Protein sim. GBank gij3510505 (AF030881) - polypeptide [Fugu rubripes]	UNCLASSIFIED	264369
235	80203871 (469, 470)		UNCLASSIFIED	264106
236	78940001 (471, 472)	Novel Protein sim. GBank gij2104609[emb]CAB08805] - (Z95398) PckA [Mycobacterium leprae]	carboxylase	264905
237	11755273 (473, 474)			264681
238	79461401 (475, 476)		UNCLASSIFIED	264639
239	82435180 (477, 478)	Novel Protein sim. GBank gij2495617[sp]Q57252[YDJ_HAEIN - HYPOTHETICAL PROTEIN HJ1183	Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron-sulfur cluster binding domains.	264908, 265010, 264603, 264762, 264682, 264636, 264638, 264486
240	21635575 (479, 480)	Novel Protein sim. GBank gij3183458[sp]P75786[YLIA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA	transport	264259, 264769
241	80377307 (481, 482)	Novel Protein sim. GBank gij3875920[emb]CAB0411] - (Z81503) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264908, 264909, 264764, 264639
242	82148454 (483, 484)		UNCLASSIFIED	264489, 264907, 264908, 264511, 264760, 264764, 264692, 264635, 264637
243	79633207 (485, 486)		UNCLASSIFIED	264908
244	80248682 (487, 488)	Novel Protein sim. GBank gij2624302[emb]CAA15575] - (AL008967) ald [Mycobacterium tuberculosis]	dehydrogenase	264600, 264602, 264605, 264769, 264689
245	79863543 (489, 490)	Novel Protein sim. GBank gij2920625 (AF044499) - vgrE protein [Escherichia coli]	UNCLASSIFIED	264907, 264758
246	79162828 (491, 492)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - NIT-like domain	264637, 18108381, 18108387, 264565

247	79873185 (493, 494)	Novel Protein sim. GBank gij183006[embjCAB06648] - (Z85982) argB [Mycobacterium tuberculosis]		kinase	264908, 264591, 35696423, 18108387
248	80488983 (495, 496)	Novel Protein sim. GBank gij1168574[spP42464]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35696286, 264907, 264511, 264602, 264768, 264688, 265021, 35695855, 18108385
249	78764645 (497, 498)			UNCLASSIFIED	264907, 264910, 265011, 264762, 264638
250	79619980 (498, 500)				21908768, 264692
251	84359489 (501, 502)			UNCLASSIFIED	52645158, 29331822, 29331824, 52644045, 265018, 21906765, 21908768, 265020, 27486261, 27486265, 35695763, 18108376, 264556, 264559, 264565
252	79737758 (503, 504)	Novel Protein sim. GBank gij3327166[dbjBAA31651] - (AB014576) KIAA0676 protein [Homo sapiens]			264685, 264687, 264632
253	20443124 (505, 506)	Novel Protein sim. GBank gij3036880[embjCAA18513] - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	264604
254	80027421 (507, 508)	Novel Protein sim. GBank gij3915488[spP42422]YJ31 - JMB_BACSU - HYPOTHETICAL SYMPTER IN COTT-RAPA INTERGENIC REGION		UNCLASSIFIED	264508, 264806, 264602, 264687, 265021, 264486
255	11398315 (509, 510)	Novel Protein sim. GBank gij1665720[dbjBAA04134] - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank gij465787[spP34422]YJ31 - CAEE - HYPOTHETICAL 86.0 KD PROTEIN F4489.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	284602, 264692
257	20289282 (513, 514)	Novel Protein sim. GBank gij1172039[spP42315]SCOA_BACSU - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	264605
258	20459464 (515, 516)	Novel Protein sim. GBank gij3127836[embjCAA18902] - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	79910152 (517, 518)			collagen	264681, 264686, 264692
260	20379437 (519, 520)			UNCLASSIFIED	264692, 264558
261	20285883 (521, 522)	Novel Protein sim. GBank gij123761[spP24221]HUTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	265017, 264369
263	88095045 (525, 526)	Novel Protein sim. GBank gij3924708[embjCAA84646] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blast score 71); cDNA EST EMBL: T02069 comes from this gene; cDNA EST EMBL: D76135 comes from this gene; cDNA EST EMBL: D73147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 264758, 264596, 264604, 265019, 264605, 264760, 18108351, 264763, 264764, 264288, 264766, 264788, 264769, 264691, 264692, 264693, 264628, 264634, 264635, 264555, 264636, 264638, 264639
264	87370826 (527, 528)	Novel Protein sim. GBank gij3043734[dbjBAA25531] - (AB011177) KIAA0605 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	264259, 264908, 21906754, 265018, 265019, 265020

265	95355646 (528, 530)	Novel Protein sim. GBank gll4589624[db][BAA76934, 1] - (AB023207) KIAA0990 protein [Homo sapiens]	Kinase	264488, 35896286, 29331824, 56182181, 35896052, 284508, 264905, 284908, 264907, 66712502, 264908, 264909, 284511, 284512, 284910, 264592, 284595, 284738, 264598, 55811386, 284600, 285017, 284603, 284604, 264605, 264760, 18108351, 284782, 284881, 284784, 284288, 284786, 264788, 264789, 21908765, 21908767, 21908769, 265020, 284691, 33857023, 33857109, 33857182, 284628, 35896423, 35895855, 284630, 284631, 284632, 284634, 284635, 284638, 284555, 284638, 83373044, 58528488, 87168518, 284564, 284568, 264488, 264600
266	79588075 (531, 532)		UNCLASSIFIED	284828
267	11362222 (533, 534)		UNCLASSIFIED	284887, 264769, 284689
268	79809568 (535, 536)		UNCLASSIFIED	284602
269	80025810 (537, 538)		UNCLASSIFIED	284693
270	84361144 (539, 540)	Novel Protein sim. GBank gll4507367[ref][NP_003182.1]pTARS - ltheonyl-IRNA Synthetase	UNCLASSIFIED	
271	79552301 (541, 542)	Novel Protein sim. GBank gll4980738[gb][AAD35331.1]AE00170 - (AE001707) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]	UNCLASSIFIED	284909, 284693
272	9674778 (543, 544)	Novel Protein sim. GBank gll1168224[sp][P44569]5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR	synthase	284908
273	12840684 (545, 546)	Novel Protein sim. GBank gll1168224[sp][P44569]5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR	UNCLASSIFIED	264688
274	39524246 (547, 548)	Novel Protein sim. GBank gll3253159 (AF005355) - Translation Initiation factor eIF2C [Oryctolagus cuniculus]		264584
275	82787041 (549, 550)	Novel Protein sim. GBank gll134820[sp][P21997]SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	UNCLASSIFIED	284907, 284908, 284909, 284766, 284768, 284691, 284632, 284638
276	86671073 (551, 552)	Novel Protein sim. GBank gll128021[sp][P20984]OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN		265008, 60432229
277	80078735 (553, 554)	Novel Protein sim. GBank gll128021[sp][P20984]OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN	ribosomal prot	264600, 18108387
278	12968947 (555, 556)	Novel Protein sim. GBank gll79839[pir][S03812 - uvrB protein - Micrococcus luteus]	UNCLASSIFIED	264689
279	95282719 (557, 558)		nuclease	264508, 264604, 21906764, 264638, 264557, 264404
280	5603617 (559, 560)			264259
281	80249599 (561, 562)	Novel Protein sim. GBank gll3123180[sp][Q18964]YLN2 CAEL - HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II		18108392, 264634, 264555, 264556, 264557, 264558
282	18598682 (563, 564)		UNCLASSIFIED	265019
283	20814211 (565, 566)		UNCLASSIFIED	264555

284	91212160 (567, 568)	Novel Protein sim. GBank gij2429094 (U56632) - acetyl xylan esterase; AxeA (Thermotoga neapolitana)	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696052, 29331828, 264508, 264905, 264600, 264602, 264605, 264682, 264764, 56181582, 21906764, 16108378, 264638, 264559, 18108387
285	8757940 (569, 570)			UNCLASSIFIED	264603
286	80503235 (571, 572)	Novel Protein sim. GBank gij2072674 (emb) (CAB08305) - (Z95120) rhlE (Mycobacterium tuberculosis)	Contains protein domain (PF00270) - DEAD/DEAH box helicase	ATPase associated	35696052, 264769, 264638
287	12745521 (573, 574)			UNCLASSIFIED	264689
288	20756502 (575, 576)	Novel Protein sim. GBank gij765323 (bbs) (S74439) silk fibroin heavy chain (C-terminal) (Bombyx mori); silkworms. Peptide Partial, 633 aa (Bombyx mori)		collagen	264557
289	80043804 (577, 578)	Novel Protein sim. GBank gij1670009 (emb) (CAB06860) - (Z92539) hypothetical protein Rv1019 (Mycobacterium tuberculosis)	Contains protein domain (PF00440) - Bacterial regulatory proteins, IeIR family	ribosomal prot	264593, 264600
290	80430175 (579, 580)			UNCLASSIFIED	264768
291	20747431 (581, 582)	Novel Protein sim. GBank gij2506684 (sp) (P40120) (YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264601
292	80052555 (583, 584)	Novel Protein sim. GBank gij625182 (L35015) - mitochondrial glutamyl-tRNA synthetase (Saccharomyces cerevisiae)		UNCLASSIFIED	264605
293	80062519 (585, 586)	Novel Protein sim. GBank gij1718065 (sp) (P5328) (UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG		helicase	264909, 264605, 264687, 264689, 264692
294	79830303 (587, 588)	Novel Protein sim. GBank gij117422 (sp) (P10040) (CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696052, 264906, 265011, 264628, 55811576
295	79444180 (589, 590)	Novel Protein sim. GBank gij1181619 (db) (BAA11565) - (D82364) a variant of TSC-22 (Gallus gallus)			52644507, 28331822, 264592, 265020, 264639
296	79607076 (591, 592)	Novel Protein sim. GBank gij3649789 (db) (BAA33403) - (AB012228) SecA (Vibrio alginolyticus)		synthase	264508
297	79631297 (593, 594)	Novel Protein sim. GBank gij5689967 (emb) (CAB52004.1) - (AL109663) putative membrane protein (Streptomyces coelicolor A3(2))		UNCLASSIFIED	264905, 264687, 264638
298	80418698 (595, 596)			UNCLASSIFIED	264905, 264681, 264639, 264766

298	95293298 (597, 598)	Novel Protein sim. GBank gij220637(dj)jBAA014771 - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	264488, 263994, 56994075, 22278997, 22278998, 22278999, 20281099, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264906, 264907, 264908, 5264045, 264909, 264511, 265008, 264910, 264595, 264598, 264758, 33657084, 87168559, 265018, 265019, 264764, 264288, 264768, 264687, 56181582, 264769, 21906765, 21906768, 21908769, 33857023, 264692, 33657109, 27488281, 18108370, 264628, 264629, 55811576, 35695855, 264631, 264634, 264635, 264638, 264639, 83373044, 18108387, 87168518, 22278000, 22279002, 264565, 264566, 264567
300	20711340 (599, 600)	Novel Protein sim. GBank gij145922 (M20981) - iron diclrate transport protein precursor [Escherichia coli]	UNCLASSIFIED	264602
301	13511332 (601, 602)	Novel Protein sim. GBank	transport	264687
302	8873260 (603, 604)	Novel Protein sim. GBank gij1174661[sp]P44594[IGT_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)]		264908
303	79574895 (605, 606)	Novel Protein sim. GBank gij67985[pi]jHJNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus	helicase	264689
304	20711344 (607, 608)	Novel Protein sim. GBank		264602
305	80412520 (609, 610)	Novel Protein sim. GBank gij728867[sp]P40602[APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		264763
306	8515876 (611, 612)	Novel Protein sim. GBank gij7657554[gb]AAB18082.1] - (U73857) hypothetical protein [Escherichia coli]	UNCLASSIFIED	263978
307	80222801 (613, 614)	Novel Protein sim. GBank	UNCLASSIFIED	
308	80064305 (615, 616)	Novel Protein sim. GBank gij1710812[sp]Q10793[RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)]	Contains protein domain (PF01351) - Ribonuclease HII	265010, 21906768, 285020, 18108374, 263977
309	80504138 (617, 618)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		264910, 264600, 264605, 264687, 264689, 264638, 18108387
310	80053616 (619, 620)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]		264769
311	11090659 (621, 622)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]	synthase	264603
312	80054347 (623, 624)	Novel Protein sim. GBank		264602
313	80046168 (625, 626)	Novel Protein sim. GBank	UNCLASSIFIED	264566
				264603, 264567

314	87645112 (627, 628)	Novel Protein sim. GBank gj 3661583 (AF092175) - ikaros [Danio rerio]	Contains protein domain (PF00320) - GATA zinc finger	dna_rna_bind	264259, 60432289, 29331828, 264805, 264906, 264908, 264909, 265008, 264910, 60432228, 33657402, 60433438, 33109954, 265011, 265017, 264603, 265018, 264288, 264766, 264692, 35695783, 264628, 264629, 264639, 60170394, 22279002, 264568
315	82356091 (629, 630)	Novel Protein sim. GBank gj 1552620[dj BAA17540] - (D90907) pyridine nucleotide transhydrogenase beta subunit [Synecocystis sp.]			264508, 264600, 264762, 264687, 264768, 52644228, 264769, 264689, 264635, 264636, 264638, 264488
316	79911071 (631, 632)	Novel Protein sim. GBank		UNCLASSIFIED	264693
317	20466944 (633, 634)	Novel Protein sim. GBank gj 118244[sp P24176]DAPE_ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (SDAP)		UNCLASSIFIED	264805
318	94141636 (635, 636)	Novel Protein sim. GBank gj 4680229[jb AAD27583.1 AF118274] DNB-5 [Homo sapiens]	Contains protein domain (PF00526) - Dictyostellum (slime mold) repeats	transport	264808, 264908, 264910, 264593, 264594, 264760, 264288, 264768, 264769, 21906769, 264691, 264693, 264628, 65274791, 264635, 264638, 264638, 83373044, 22278002, 264568
319	17289360 (637, 638)	Novel Protein sim. GBank gj 1149693[emb CAA60220] - (X86499) rbsC [Clostridium perfringens]		transport	265018
320	13527675 (639, 640)	Novel Protein sim. GBank gj 2811033[sp O05314]GLGC_MYCTU - GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)		synthase	264687
321	94134387 (641, 642)	Novel Protein sim. GBank gj 1680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]		cyto450	264509, 264906, 264907, 264908, 265008, 264596, 264764, 264628, 264634, 264635, 264638, 264639, 83373044, 264567
322	68489053 (643, 644)	Novel Protein sim. GBank gj 1160355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 264691, 60431828, 55810764
323	94653725 (645, 646)			UNCLASSIFIED	264488, 265009, 264593, 264628, 264635
324	79174383 (647, 648)			UNCLASSIFIED	264887
325	79862691 (649, 650)			UNCLASSIFIED	264693
326	28774974 (651, 652)			UNCLASSIFIED	264288, 18108385
327	79776267 (653, 654)	Novel Protein sim. GBank gj 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264488, 264905, 264509, 264910
328	80253202 (655, 656)			UNCLASSIFIED	264592
329	10173821 (657, 658)			UNCLASSIFIED	264510
330	86597767 (659, 660)	Novel Protein sim. GBank gj 4191358 (AF087825) - claudin-7 [Mus musculus]		UNCLASSIFIED	264259, 264908
331	79754688 (661, 662)	Novel Protein sim. GBank gj 80741[pri S20912 - regulatory protein whiB - Streptomyces coelicolor		transcriptfactor	264910, 264687, 264689, 264636, 264567
332	80071440 (663, 664)	Novel Protein sim. GBank gj 114049[sp P19480]AHPEF_SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)		reductase	35696423, 264636, 264638, 264565
333	13009555 (665, 666)				264687

334	80230771 (667, 668)	Novel Protein sim. GBank gij322228[pil]S32227 - glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905, 264600, 264604, 264488
335	80057026 (669, 670)	Novel Protein sim. GBank gij2193938[emb]CAB06602] - (Z98800) glpQ2 [Mycobacterium tuberculosis]		esterase	264907, 264603, 264693, 18108374, 264638, 18108387
336	80414319 (671, 672)			UNCLASSIFIED	264602
337	11090829 (673, 674)				265009, 264766, 264686
338	65413134 (675, 676)	Novel Protein sim. GBank gij5454074[ref]NP_006303.1pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nud_rept	264599, 18108397, 22278998, 29331822, 20281099, 29331824, 56182181, 66714117, 29331825, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87168559, 265017, 265018, 265019, 264760, 55811150, 264981, 264782, 18108351, 264682, 264784, 264766, 264685, 264688, 264768, 52844229, 264892, 264693, 55811957, 35695917, 264892, 264693, 264628, 18108370, 18108374, 55811576, 35698423, 35695855, 264635, 264555, 264638, 264556, 264637, 264557, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87168518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank gij4001713[db]BAA35087.1] - (AB015879) DnaK [Porphyromonas gingivalis]		eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank gij2842699[sp]Q92353]UBPC_SCHPO - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)		ubiquitin	264905, 265019, 264789, 18108374
341	11075198 (681, 682)	Novel Protein sim. GBank gij2688580 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	Contains protein domain (PF00290) - Tryptophan synthase alpha chain	isomerase	264605
342	80054186 (683, 684)	Novel Protein sim. GBank gij1684738[emb]CAA70601] - (Y09452) Yed [hypothetical protein [Pseudomonas syringae]]			264603, 264604
343	20466782 (685, 686)				264605
344	80428870 (687, 688)	Novel Protein sim. GBank gij2117275[emb]CAB09104] - (Z95618) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264600, 264605, 264768, 18108370, 18108374, 35695855
345	80258853 (689, 690)	Novel Protein sim. GBank gij3023317[sp]Q46935]APHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE		histone	264593
346	79831058 (691, 692)	Novel Protein sim. GBank gij4239787[emb]CAA75437] - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905

347	79158185 (693, 694)	Novel Protein sim. GBank gij1731675 sp P38795 YHN4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION		UNCLASSIFIED	265006, 265008, 265010, 265018, 263967, 263981
348	80020208 (685, 686)	Novel Protein sim. GBank gij1073610 p S47672 - ugpB protein - Escherichia coli		transport	264602, 18108351, 18108387
349	17282112 (697, 698)				265007
350	80502370 (699, 700)	Novel Protein sim. GBank gij3261589 emb CAB009171 - (Z77137) hypothetical protein Rv1277 [Mycobacterium tuberculosis]		nuclease	265009, 264769, 264689, 18108370
351	80501805 (701, 702)	Novel Protein sim. GBank gij2959387 emb CAA179211 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	264769, 264905, 264908
352	11611585 (703, 704)	Novel Protein sim. GBank gij4416302 gb AAD203071 - (AF105716) copia-type pol polyprotein [Zea mays]		protease	264595
353	80061653 (705, 706)	Novel Protein sim. GBank gij1174887 sp P42873 URE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
354	56626130 (707, 708)			UNCLASSIFIED	264628
355	80046344 (709, 710)	Novel Protein sim. GBank		UNCLASSIFIED	264909, 264595, 264683, 22279002
356	80043835 (711, 712)	gij115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) - Response regulator receiver domain	transcriptfactor	264909, 264591, 264592
357	80070568 (713, 714)	Novel Protein sim. GBank gij497637 (J03939) - cytochrome oxidase d subunit I [Escherichia coli]		oxidase	264605
358	37032758 (715, 716)	Novel Protein sim. GBank gij2290990 (AF006000) - Btg1 [Bordetella pertussis]		UNCLASSIFIED	264768
359	80501488 (717, 718)			UNCLASSIFIED	264604, 264769
360	80026748 (719, 720)			UNCLASSIFIED	264594
361	80584075 (721, 722)	Novel Protein sim. GBank gij3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 [Rattus norvegicus]		transferase	22278996, 264259, 29331822, 29331824, 264605, 55811957, 265022
362	13089485 (723, 724)	Novel Protein sim. GBank gij113764 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		amylase	264688
363	79750145 (725, 726)				264566
364	82443593 (727, 728)	Novel Protein sim. GBank gij2829816 sp P95171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	Contains protein domain (PF00420) - NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	dehydrogenase	264769, 264602, 264604, 264508, 264762, 264638, 264486



365	88040288 (729, 730)	Novel Protein sim. GBank gij4929268[gbjAA033824.1] - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	264488, 21806768, 21806767, 55811576, 21906769, 29148629, 22278995, 22278996, 265020, 265022, 264634, 284891, 264593, 33857023, 33857402, 264693, 264639, 264594, 29331824, 264758, 18108385, 29331827, 87188559, 265018, 22278000, 265019, 284482, 264761, 264681, 18108351, 265017, 264757
366	81821838 (731, 732)	Novel Protein sim. GBank gij4503843[re]NP_003908.1[pG2AD - UNKNOWN]	Contains protein domain (PF01602) - Adaplin N terminal region	60424178, 65274572, 56182575, 22278994, 56994075, 22278998, 264259, 29331822, 29331824, 56182181, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264905, 264828, 56182435, 265008, 264512, 265008, 264591, 55812038, 55811386, 265010, 87168559, 265017, 265018, 264604, 265019, 55811150, 264448, 264369, 264288, 284866, 264766, 56181592, 21906768, 21906769, 55811857, 35695917, 265022, 60170615, 33857023, 85274620, 18108365, 263967, 33857109, 33857349, 35695763, 264628, 18108376, 55811576, 85274791, 35695855, 56182323, 83373044, 60432113, 264563, 264564, 264567
367	95357471 (733, 734)	Novel Protein sim. GBank gij3913029[sp]P94967[ALR_MYCSM - ALANINE RACEMASE]	UNCLASSIFIED	264509, 264508, 264604, 264605, 264636
370	88090966 (738, 740)	Novel Protein sim. GBank gij3249559 (AF018261) - EH domain binding protein Epsin [Rattus norvegicus]		264905, 264592, 264605, 264766, 264691
371	95292599 (741, 742)	Novel Protein sim. GBank gij2895299[emb]CAA183281 - (AL022268) putative IRNA delta(2)-isopentenylpyrophosphate transferase [Streptomyces coelicolor]	Contains protein domain (PF01715) - transferase IPP transferase	264805, 264908, 264510, 264600, 264601, 264802, 264603, 265018, 264604, 264605, 265021, 264892, 264636, 264564
372	80021107 (743, 744)	Novel Protein sim. GBank gij2506393[sp]P31576[FXX_ECOLI - FERREDOXIN LIKE PROTEIN]		264564
373	79863766 (745, 746)	Novel Protein sim. GBank gij3341640[emb]CAA13164 - (AJ231122) z811 [Vibrio cholerae]	UNCLASSIFIED	264909
374	79847568 (747, 748)	Novel Protein sim. GBank gij5456934[gbj]AAD43716.1 - (AF152322) protocadherin gamma A2 [Homo sapiens]	UNCLASSIFIED	264905, 264906
375	81230181 (749, 750)	Novel Protein sim. GBank gij1805408[dbj]BAA08970 - (D50453) homologues to nitrite hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	cadherin	85274572, 264259, 28331826, 56182435, 60433356, 60433438, 264757, 55812038, 264758, 55811957, 264690, 33857023
376	80505214 (751, 752)		UNCLASSIFIED	264769
377	10339083 (753, 754)			264906

378	80056153 (755, 756)	Novel Protein sim. GBank gij1076013ipirjA49930 - carb protein homolog - Mycobacterium bovis (strain BCG) (fragment)	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	UNCLASSIFIED	265008, 264555
379	80503437 (757, 758)	Novel Protein sim. GBank gij216556jdbjBAA021741 - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - PQQ enzyme repeat	dehydrogenase	264769
380	80060937 (758, 760)				264604
381	11789027 (761, 762)			UNCLASSIFIED	264684
382	80054377 (763, 764)				264592
383	83259025 (765, 766)	Novel Protein sim. GBank gij3327136jdbjBAA316361 - (AB014561) KIAA0661 protein [Homo sapiens]			264595, 265017, 265021, 264638, 87188518, 22279002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264288, 264766, 263987, 65274791, 35695855, 263981, 83373044, 264567, 264692
385	10237678 (769, 770)				264808
386	79633434 (771, 772)	Novel Protein sim. GBank gij1073456jpirjS47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	
387	17960637 (773, 774)	Novel Protein sim. GBank gij1460074jembjCAB010491 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741378 (775, 776)	Novel Protein sim. GBank gij4240169jdbjBAA74863.11 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00846) - F-box domain.	homeobox	35696286, 264905, 66712502, 60432229, 264593, 60433356, 264686, 264688, 21908765, 264691, 22279000, 264482, 18108394, 22278996, 264630, 264556, 22279002
389	79316971 (777, 778)			UNCLASSIFIED	264600
390	80079949 (778, 780)				264482
391	7657302 (781, 782)	Novel Protein sim. GBank gij854055jembjCAA583371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264908
392	79796056 (783, 784)	Novel Protein sim. GBank gij3378523jembjCAA088671 - (AJ009832) cyclomaltodextrinase glucanotransferase [Thermotoga neapolitana]		synthase	264802, 21906764
393	33206031 (785, 786)				
394	10104463 (787, 788)				264693
395	80229010 (789, 790)			UNCLASSIFIED	264508, 264563
396	20436224 (791, 792)	Novel Protein sim. GBank gij2677780 (U70327) - unknown	Contains protein domain (PF00047) - Immunoglobulin domain	- struct	264556
397	80417014 (793, 794)	[Paretropus polyactis] Novel Protein sim. GBank gij4507909jrefjNP_000368.1lpVAS1 - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)			265007, 265009, 264508, 264556, 264629, 264766
398	91230517 (795, 796)	Novel Protein sim. GBank gij1518458 (U45998) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	- transport	18108398, 22278995, 22278996, 56994075, 22278999, 264259, 29331824, 29331826, 264905, 264908, 265007, 265008, 265009, 21906754, 33657084, 265017, 264448, 264288, 264766, 21906765, 21906766, 21906767, 265020, 265021, 33657023, 33657109, 264628, 35696423, 35695855, 264952, 18108380, 264567, 18108391

399	80055278 (797, 798)	Novel Protein sim. GBank gi 3358091 dbj BAA31995  - (AB015974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF000370) - kinases FGY family of carbohydrate kinases	kinase	284582, 284595
400	94117480 (799, 800)	Novel Protein sim. GBank gi 728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII	Contains protein domain (PF00580) - Leucine Rich Repeat	cadherin	18108394, 56182575, 22278995, 22278997, 22278998, 284259, 28331824, 265008, 265007, 265008, 60432229, 33657402, 21908754, 285010, 285017, 285018, 285019, 18108351, 18108357, 21908765, 265021, 265022, 284591, 284682, 33657023, 18108370, 65274781, 284634, 284636, 60170394, 56182323, 284594
401	11397481 (801, 802)	Novel Protein sim. GBank gi 4928292 gb AAD33527.1 AF13211 - (AF132117) FhuA [Staphylococcus aureus]		transport	
402	95420284 (803, 804)	Novel Protein sim. GBank gi 5689487 dbj BAA83027.1  - (AB028998) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	phosphatase	65274572, 56182575, 35696286, 22278996, 22278998, 284093, 284259, 28331822, 28331824, 28331825, 28331826, 60432289, 28331827, 28331828, 264908, 284907, 284908, 285008, 284511, 285007, 265008, 284910, 284591, 33657402, 60433356, 60433438, 284598, 21908754, 52844288, 285010, 285011, 87168559, 265017, 265018, 265019, 284681, 18108351, 284682, 284448, 284288, 284684, 284766, 284767, 284686, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 285020, 265021, 285022, 284690, 284693, 65274620, 35695763, 284628, 18108370, 284629, 18108378, 35696423, 55811576, 284635, 284636, 284557, 284638, 18108385, 22279002, 284583, 284584, 284585, 284586, 284768, 284632, 284639, 284563, 284682, 265009, 284682
403	80438913 (805, 806)			UNCLASSIFIED	
404	11809865 (807, 808)				
405	79471280 (809, 810)	Novel Protein sim. GBank gi 2661649 emb CAA15755  - (AL009198) dnaE2 [Mycobacterium tuberculosis]			
406	78634172 (811, 812)			polymerase	
407	80478229 (813, 814)		Contains protein domain (PF00159) - Pancreatic hormone peptides	UNCLASSIFIED	18108357, 284693
408	80078958 (815, 816)			UNCLASSIFIED	284769
409	5840527 (817, 818)	Novel Protein sim. GBank gi 3047117 (AF058819) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]		UNCLASSIFIED	284600
				helicase	284259

410	95357486 (819, 820)	Novel Protein sim. GBank gij475016[dbj BAA06184] - (D28801) Unknown [Mus musculus]		UNCLASSIFIED	264489, 52846365, 52846842, 56181686, 35696286, 52845080, 29331822, 29331824, 56182181, 29331825, 60424289, 35696052, 33656970, 264508, 264509, 264905, 264906, 264907, 264908, 52844045, 264909, 264510, 265007, 264512, 265008, 264910, 33657402, 264758, 52846317, 55811388, 265010, 265011, 265017, 264604, 265018, 55811150, 264762, 264764, 264768, 264887, 264768, 264769, 52844228, 21906768, 265020, 265021, 264534, 52644150, 264692, 33657023, 65274620, 33657109, 33657182, 27486281, 35695763, 284628, 264628, 60431528, 18108376, 283978, 35698423, 35695855, 264632, 264634, 264635, 264637, 284638, 264558, 264639, 56182323, 264559, 60432113, 22279002, 264563, 264565, 264486
411	80501670 (821, 822)			UNCLASSIFIED	264769
412	80241662 (823, 824)	Novel Protein sim. GBank gij3261784[emb CAB08997] - (Z95558) hlpX [Mycobacterium tuberculosis]		eph	264907, 264910, 263973, 22278002, 264805
413	11076446 (825, 826)	Novel Protein sim. GBank gij129036[sp P20707 ODO1_AZOV1 - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)		dehydrogenase	18108374, 264760, 264769, 264602, 264638, 264603, 264909, 264805
414	82050554 (827, 828)	Novel Protein sim. GBank gij4868350[gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	264908, 87168518
415	84453144 (829, 830)	Novel Protein sim. GBank gij2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium etli]		kinase	264488, 264600, 264602, 264784, 264636
416	80402775 (831, 832)	Novel Protein sim. GBank gij1709171[sp P5231 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M.XORII)]	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		264605
417	20153797 (833, 834)	Novel Protein sim. GBank gij3261658[emb CAB03751] - (Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	264689, 264693
418	94125841 (835, 836)	Novel Protein sim. GBank gij2916942[emb CAA17580] - (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	collagen	264908, 264910, 264764, 264639
419	95314273 (837, 838)			phosphatase	284789
420	37036349 (839, 840)				
421	95292942 (841, 842)	Novel Protein sim. GBank gij231752[sp Q00767 CH61_STRAL - 60 KD CHAPERONIN 1 (PROTEIN CPN60 1) (GROEL PROTEIN 1) (HSP58)]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	phosphatase	264906, 264600, 264601, 264603, 264604, 264760, 264769
422	79471293 (843, 844)			eph	22278996, 264682, 18108376, 18108387
423	79604948 (845, 846)			UNCLASSIFIED	264509

424	78966557 (847, 848)	Novel Protein sim. GBank glj4826814[re]NP_004977.1 pKTN1 - kinesin 1 (kinesin receptor)		struct	265019
425	80431450 (849, 850)	Novel Protein sim. GBank glj1703701[bsb]178462 - KRP5=kinesin-related protein [rats, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - kinesin motor domain	struct	264909, 265007, 55811386, 264768, 55810764
426	80645322 (851, 852)				
427	80057232 (853, 854)	Novel Protein sim. GBank glj231829[sp]P29929 COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	264605, 264559, 264803, 264636
428	79487788 (855, 856)	Novel Protein sim. GBank glj81286[pir]j522697 - extensin - Volvox cartet (fragment)		UNCLASSIFIED	264683
429	80091252 (857, 858)	Novel Protein sim. GBank glj1808154[emb]CAB064511 - (284385) hypothetical protein Rv0688 [Mycobacterium tuberculosis]		UNCLASSIFIED	35686423, 35695763, 35695855, 265017, 264594, 264762
430	80504182 (859, 860)			reductase	264508, 264905, 264509, 264908, 264809, 265008, 264800, 264687, 264769, 264889, 264636, 264638, 18108385, 264488
431	20624249 (861, 862)				264568
432	18525372 (863, 864)				265020
433	81494303 (865, 866)	Novel Protein sim. GBank glj3123352[emb]CAA18609 - KIAA0269 (LUKE) [Homo sapiens]		UNCLASSIFIED	264807, 264908, 264909, 264910, 264582, 264595, 264758, 264604, 264760, 264762, 264763, 264636, 264637, 22279002
434	94326323 (867, 868)	Novel Protein sim. GBank glj2495272[sp]Q99626 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	55812038, 56182181, 56181562, 29331828, 35696052, 55810764, 55811576, 63274791, 35695855, 80432113, 55811150, 264636, 264766
435	80502738 (869, 870)	Novel Protein sim. GBank glj114105[sp]P08532 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		transport	264595, 264769
436	41085953 (871, 872)			UNCLASSIFIED	265020, 22278002
437	11399291 (873, 874)			UNCLASSIFIED	264593
438	11773835 (875, 876)			UNCLASSIFIED	264686
439	80019485 (877, 878)	Novel Protein sim. GBank glj3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			264905, 264600, 264602, 264604
440	78841062 (879, 880)	Novel Protein sim. GBank glj2291232[gb]AAB6535.1.1 - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA). Score=288.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)	ATPase_associated	35696052, 264905, 264908, 264909, 265011, 35696423
441	20396935 (881, 882)	Novel Protein sim. GBank glj5638946[gb]AAD45904.1 AF16132 - (AF161328) histidine kinase CslS [Corynebacterium diphtheriae]			264605
442	85281058 (883, 884)	Novel Protein sim. GBank glj1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
443	82456427 (885, 886)	Novel Protein sim. GBank glj5689893[emb]CAB52056.1 - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35696052, 264508, 264806, 264512, 264604, 264762, 264769, 264689, 264636
444	11395987 (887, 888)	Novel Protein sim. GBank glj1783249[dbj]BAA11726j - (D83026) homologous to citrate-sodium symport (citrate transporters), hypothetical [Bacillus subtilis]		UNCLASSIFIED	264591

445	79552709 (889, 890)	Novel Protein sim. GBank gij5531272[embjCAB50897.1] - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	264693
446	79810937 (891, 892)	Novel Protein sim. GBank gij538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00086) - Zinc finger, C2H2 type		264509
447	80438888 (893, 894)	Novel Protein sim. GBank gij1542814[embjCAB02185] - (Z80108) fnt [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase	transcript factor	264768, 55811576
448	80238110 (895, 896)	Novel Protein sim. GBank gij118794[spjP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		dehydrogenase	264508, 264600, 264603, 264605, 264682, 264769, 18108362, 264634, 18108387
449	20460634 (897, 898)	Novel Protein sim. GBank gij118794[spjP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264605, 264559
450	84631210 (898, 900)	Novel Protein sim. GBank gij458950[embjBAA76775.1] - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C	phosphatase	55274572, 22278998, 29331824, 29331826, 264906, 264910, 264592, 52846317, 265017, 21906767, 55811957, 56528486, 22279002
451	21433609 (901, 902)	Novel Protein sim. GBank gij2650614 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	264486
452	10267276 (903, 904)	Novel Protein sim. GBank gij249300[spjQ09450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		UNCLASSIFIED	264692
453	52560096 (905, 906)	Novel Protein sim. GBank gij249300[spjQ09450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		UNCLASSIFIED	264907, 264600
454	39523922 (907, 908)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]		transferase	264603
455	13089692 (909, 910)	Novel Protein sim. GBank gij446869[embjCAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264687
456	79563081 (911, 912)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]		UNCLASSIFIED	264691
457	79831273 (913, 914)	Novel Protein sim. GBank gij446869[embjCAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264905
458	79581227 (915, 916)	Novel Protein sim. GBank gij4506075[refjNP_002733.1]pPRKC - protein kinase C, mu	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	kinase	55812038, 265010, 265018, 264681
459	80567359 (917, 918)	Novel Protein sim. GBank gij113158[spjP25516]ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	22278997, 264259, 29331826, 265018, 264448, 264369, 21908765, 35696423
460	79245890 (919, 920)	Novel Protein sim. GBank gij113158[spjP25516]ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)		UNCLASSIFIED	264906
461	95287618 (921, 922)	Novel Protein sim. GBank gij1168574[spjP42464]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	264602, 264605, 264768, 264769, 265021, 33657023, 264559

462	79606589 (923, 924)	Novel Protein sim. GBank gi 1346897 sp P45597 PTF1_XANCP - MULTIPHOSPHORYL TRANSFER PROTEIN (MTP) (CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ... (X83413) U88 [Human herpesvirus 8]	Contains protein domain (PF00391) - PEP-utilizing enzymes	UNCLASSIFIED	284807
463	79706417 (925, 926)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	284905, 284906, 284908, 284909, 284910, 284951, 284955, 285011, 284932, 284935, 284936, 284937, 284938, 284939
464	82340151 (927, 928)	Novel Protein sim. GBank gi 5689776 emb CAB52137.1  - (AJ242832) calpain [Homo sapiens]	Contains protein domain (PF00648) - Calpain family cysteine protease	UNCLASSIFIED	284634
465	83005730 (929, 930)	Novel Protein sim. GBank gi 1806175 emb CAB06470  - (Z84395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	UNCLASSIFIED	285017, 21906784, 285020
466	20460645 (931, 932)	Novel Protein sim. GBank gi 5689776 emb CAB52137.1  - (AJ242832) calpain [Homo sapiens]		UNCLASSIFIED	284605, 284559
467	80408035 (933, 934)	Novel Protein sim. GBank gi 548705 sp P36949 IRSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	284764
468	52562208 (935, 936)	Novel Protein sim. GBank gi 2114024 emb CAB08957  - (Z95558) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	284692
469	19520527 (937, 938)	Novel Protein sim. GBank gi 2909459 emb CAA17347  - (AL021929) cobQ [Mycobacterium tuberculosis]		UNCLASSIFIED	284488
470	80502756 (939, 940)	Novel Protein sim. GBank gi 114921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	synthase		284602, 284769
471	17637351 (941, 942)	Novel Protein sim. GBank gi 114921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	transport		285019
472	80047458 (943, 944)	Novel Protein sim. GBank gi 862343 (L10908) - Gcap1 gene product [Mus musculus]		UNCLASSIFIED	284596, 284885, 284557
473	20558793 (945, 946)	Novel Protein sim. GBank gi 862343 (L10908) - Gcap1 gene product [Mus musculus]		UNCLASSIFIED	284369
474	80593365 (947, 948)	Novel Protein sim. GBank gi 5453856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	22278997, 284692, 284288
475	82454665 (949, 950)	Novel Protein sim. GBank gi 5453856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	284907, 284908, 284511, 285009, 284762, 284448, 284638, 284638
476	94143657 (951, 952)	Novel Protein sim. GBank gi 5453856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat		85274572, 60432049, 284259, 284508, 52644045, 55812038, 284758, 285011, 284288, 284686, 52844229, 85274791, 284638, 284566
477	79175833 (953, 954)	Novel Protein sim. GBank gi 5453856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	284936
478	78633483 (955, 956)	Novel Protein sim. GBank gi 5453856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	284690, 284693
479	80189746 (957, 958)	Novel Protein sim. GBank gi 5453856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	collagen		284686, 35695855, 285008, 284631, 284910, 284632, 284638, 285018, 284369, 284909
480	79390729 (959, 960)	Novel Protein sim. GBank gi 1127551 (U18939) - orf2 [Batrachocottus baikalensis]	mapolymerase		284369
481	78624578 (961, 962)	Novel Protein sim. GBank gi 1127551 (U18939) - orf2 [Batrachocottus baikalensis]		UNCLASSIFIED	284693
482	83050611 (963, 964)	Novel Protein sim. GBank gi 4003042 (AF068065) - GP800; mucin-like glycoprotein [Cryptosporidium parvum]		UNCLASSIFIED	284909, 284686, 284768, 284693, 55811576, 56182323, 18108385

483	20293306 (865, 866)	Novel Protein sim. GBank gij2104303jemb[CAB08632] - (Z95387) hypothetical protein Rv2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1		264600
484	11618046 (867, 868)	Novel Protein sim. GBank gij3450883 (AF083334) - fibroin [Antheraea pernyi]		UNCLASSIFIED	264594
485	80191234 (969, 970)	Novel Protein sim. GBank gij5042272jemb[CAB44526.1] - (AL078818) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		UNCLASSIFIED	264369, 21908785, 22279000, 22279002
486	80059042 (971, 972)			dehydrogenase	264604
487	11813339 (973, 974)				264638
488	91222383 (975, 976)	Novel Protein sim. GBank gij5724778jgb[AAC53522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain		264686, 66714117, 264768, 18108385, 55811576, 265008, 265008, 265009, 265019, 22279002, 264259, 18108370, 264907, 264764, 56182323, 264288, 264593
489	10867710 (977, 978)	Novel Protein sim. GBank gij388223jdbj[BAA34471.1] - (AB018294) KIAA0751 protein [Homo sapiens]		kinase	264639
490	95351124 (979, 980)	Novel Protein sim. GBank gij82091jprj[A25494 - hydroxyproline-rich glycoprotein - tomato (fragment)]		collagen	22278996, 29331822, 29331828, 264107, 264909, 264110, 265009, 264592, 264593, 60433356, 264288, 264693, 263974, 263976, 20281071, 60432113
491	80498412 (981, 982)	Novel Protein sim. GBank gij2894206jemb[CAA17072] - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]		UNCLASSIFIED	264769
492	87421264 (983, 984)				264600
493	11632942 (985, 986)			UNCLASSIFIED	264638
494	87726604 (987, 988)	Novel Protein sim. GBank gij5262603jemb[CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 60432289, 29331828, 35696052, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 33657402, 284762, 264764, 264768, 264769, 264688, 21908765, 21908769, 35695917, 265020, 284693, 33657109, 264628, 35696423, 35695855, 264634, 264638
495	80026599 (989, 990)	Novel Protein sim. GBank gij2791517jemb[CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	transport	264602, 264682, 264638
496	7895624 (991, 992)	Novel Protein sim. GBank gij230281jdbj[IR69] - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF01381) - Helix-turn-helix		264601, 265021
497	78949661 (993, 994)	Novel Protein sim. GBank gij129736jprjP28225jPDH, ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PPMP OXIDASE)		oxidase	265006



488	88085488 (895, 986)	Novel Protein sim. GBank gi 1145789 (U41662) - neurologin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	esterase	264259, 28331826, 35698052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264591, 33657402, 264758, 265010, 265011, 264600, 264601, 264605, 264683, 264764, 264768, 264767, 264768, 264687, 264769, 21908767, 33657023, 264693, 264628, 264629, 35696423, 264630, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 18108385, 264553, 264584, 264565, 264566, 264567, 264605
489	20438222 (987, 998)	Novel Protein sim. GBank gi 97480 p S19739 - Integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	264605
500	11076810 (999, 1000)	Novel Protein sim. GBank gi 5708250 emb CAB52363.1 - (AL109747) putative integral membrane protein		UNCLASSIFIED	264688
501	13418034 (1001, 1002)	[Streptomyces coelicolor A3(2)]			
502	80021176 (1003, 1004)	Novel Protein sim. GBank gi 4468678 emb CAB38132.1 - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278996, 265011, 264602, 264605, 264635
503	20264483 (1005, 1006)			UNCLASSIFIED	264564
504	10887321 (1007, 1008)			UNCLASSIFIED	264687
505	85003068 (1009, 1010)			UNCLASSIFIED	264369
506	16454282 (1011, 1012)	Novel Protein sim. GBank gi 4033509 sp P02598 CALM_TETPY - CALMODULIN	Contains protein domain (PF00036) - EF hand	struct	265010
507	20451598 (1013, 1014)	Novel Protein sim. GBank gi 2501069 sp Q46127 SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS)		UNCLASSIFIED	264604
508	79841424 (1015, 1016)	Novel Protein sim. GBank gi 486068 sp P34618 YO82_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III		UNCLASSIFIED	264808
509	11776386 (1017, 1018)				264638
510	83373485 (1019, 1020)			UNCLASSIFIED	264687, 264639
511	16525578 (1021, 1022)				265007
512	20399484 (1023, 1024)	Novel Protein sim. GBank gi 2497419 sp P55635 Y4RB_RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	264565
513	79457404 (1025, 1026)	Novel Protein sim. GBank gi 1276897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - Cyclin	cyclin	264683, 264688, 35696423, 264639
514	79813805 (1027, 1028)	Novel Protein sim. GBank gi 1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
515	79462591 (1029, 1030)				22278999, 264690
516	9862020 (1031, 1032)	Novel Protein sim. GBank gi 2127400 p S65770 - maltotrioglycosyltrehalose trehalohydrolase - Arthrobacter sp. (strain Q36)		amylase	264910

517	95292894 (1033, 1034)	Novel Protein sim. GBank gij2983605 (AE000725) - ribose 5 phosphate isomerase B [Aquifex aeolicus]		isomerase	265018, 264605, 264764, 264766, 264687, 264691, 264565
518	8491831 (1035, 1036)	Novel Protein sim. GBank gij854065[lemb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264487
519	91677888 (1037, 1038)	Novel Protein sim. GBank gij5689365[dbj]BAA83073.1] - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_rna_bind	52644507, 22278997, 22278998, 60432049, 284259, 52645080, 29331824, 66714117, 60424269, 29331826, 35696052, 264905, 29331830, 86712502, 284511, 265007, 264591, 60432229, 33657402, 60433438, 21908754, 33109954, 52644298, 87188474, 87168559, 265017, 265018, 284604, 265019, 264681, 264448, 264369, 264288, 264685, 21908765, 21908766, 21908767, 21906769, 265021, 60170615, 33657023, 264692, 52645129, 33657109, 27486262, 27486264, 35695763, 18108370, 264629, 52644332, 56182323, 284639, 83373044, 18108385, 56526488, 60432113
520	79869188 (1039, 1040)				264769
521	11076821 (1041, 1042)	Novel Protein sim. GBank gij1169126[sp]P46839[CTPA, MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A		transport	264605
522	80435060 (1043, 1044)	Novel Protein sim. GBank gij1172869[sp]P44331[RBKS_HAEIN - RIBOKINASE	Contains protein domain (PF00294) - pfkB family carbohydrate kinase	kinase	264905, 264768
523	18356013 (1045, 1046)	Novel Protein sim. GBank gij2132243[pir]S61028 - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gij4033608[dbj]BAA35136] - (AB012308) B2HC [Anthracis crassispina]		ATPase_associated	264092, 264596, 265011
525	79610046 (1049, 1050)				264907
526	36827630 (1051, 1052)	Novel Protein sim. GBank gij4106610[lemb]CAA21365] - (AL031866) ORF42, len=386 aa, similarity to an aminotransferase, In P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap. Fast scores: opt:468, E(): 8.5e-24, in Q64602 R. norvegicus, (425 aa), 28.6% ident...		UNCLASSIFIED	264758
527	80504728 (1053, 1054)			UNCLASSIFIED	264769
528	65484134 (1055, 1056)			UNCLASSIFIED	56182575, 265017, 265018
529	17936810 (1057, 1058)	Novel Protein sim. GBank gij731088[sp]P24215[JUXUA, ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		hydrolase	265019
530	10887336 (1059, 1060)	Novel Protein sim. GBank gij42144[lemb]CAA25200] - (X00513) NusA protein (nusA) [Escherichia coli]		UNCLASSIFIED	264687
531	80226576 (1061, 1062)				
532	90933444 (1063, 1064)	Novel Protein sim. GBank gij5262640[lemb]CAB45758.1] - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264555, 264558, 264557, 264558, 18108385, 264488, 264480, 264259, 264592, 264760, 265021, 264690, 263976, 264558

533	87761531 (1085, 1086)	Novel Protein sim. GBank gi4883636 gb AAD31593.1 AF11229 Integral inner nuclear membrane protein MAN1 [Homo sapiens]				264907, 264908, 264768, 35685917, 264630, 264555
534	82388284 (1087, 1088)	Novel Protein sim. GBank gi2995352 emb CAA04606.1  - (AJ001206) pep1 [Streptomyces coelicolor]	UNCLASSIFIED			264905, 265011, 264601, 264602, 264605, 264782, 264788, 265020, 264893, 264836
535	79641850 (1089, 1070)	Novel Protein sim. GBank gi3878636 emb CAA88953  - (Z49128) similar to CAMP-dependant protein kinase; cDNA EST EMBL:700719 comes from this gene; cDNA EST YK465d8.3 comes from this gene; cDNA EST YK465d8.5 comes from this gene; cDNA EST YK49214.3 comes from this gene; cDNA EST Y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	ATPase-associated		264906
536	79907207 (1071, 1072)	Novel Protein sim. GBank gi2495628 sp P55757 YOH1_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5 REGION	reductase			18108376, 264805, 264908, 264807, 264809
537	84147448 (1073, 1074)					265008, 264605, 65274781
538	87821863 (1075, 1076)	Novel Protein sim. GBank gi134920 sp P21897 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	collagen			26331822, 29331824, 29331825, 29331826, 29331827, 264908, 52644045, 33657402, 265017, 264782, 264883, 264288, 264685, 21908785, 35895783, 264558, 60170394, 264559, 22279002
539	28386288 (1077, 1078)	Novel Protein sim. GBank gi2498433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE	histone			264602, 265019
540	79637077 (1078, 1080)					264893
541	87762268 (1081, 1082)	Novel Protein sim. GBank gi3882241 db BAA34480.1  - (AB018303) KIAA0760 protein [Homo sapiens]	transcript factor			18108394, 22278997, 22278998, 264259, 264112, 265009, 33657402, 55612038, 52648317, 265017, 21908785, 264693, 55811578, 264635, 56526488, 264569
542	85285838 (1083, 1084)	Novel Protein sim. GBank gi5042272 emb CAB44526.1  - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase			264910, 265018, 264689, 264638, 264488
543	78796280 (1085, 1086)					264602, 264908
544	20437191 (1087, 1088)	Novel Protein sim. GBank gi2781398 emb CAA15994  - (AL021184) hypothetical protein Rv1484 [Mycobacterium tuberculosis]	UNCLASSIFIED			264605
545	80434504 (1089, 1090)					264768, 264634, 264907, 264592, 264908
546	80249018 (1091, 1092)	Novel Protein sim. GBank gi4887211 gb AAD32237.1 AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]				264600, 264602, 21908785
547	11077563 (1093, 1094)	Novel Protein sim. GBank gi1350855 sp P18176 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)	mapolymerase			264604
548	82114938 (1095, 1096)	Novel Protein sim. GBank gi2330021 (AF019250) - Kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]	UNCLASSIFIED			264488, 264905, 264910, 264760, 264693, 264839, 264563, 264564

548	95421904 (1097, 1098)	Novel Protein sim. GBank gij4337460[jb]AADI8133] - (AF058195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108398, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 29331828, 35896052, 265007, 265008, 264910, 264592, 33857402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264764, 264389, 264288, 264766, 264686, 264688, 21906765, 21906766, 21908787, 21908789, 265020, 264681, 33837023, 264692, 264693, 65274620, 52845129, 33857109, 27486261, 27486262, 27486264, 33857349, 55811576, 18108387, 60432113, 22279002
550	10886816 (1099, 1100)				264688
551	80439980 (1101, 1102)	Novel Protein sim. GBank gij3122893[jsp]P94985[SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)]		UNCLASSIFIED	264908, 264909, 264768
552	94672870 (1103, 1104)				
553	80106002 (1105, 1106)	Novel Protein sim. GBank gij552087 (M33753) - crumbs protein [Drosophila melanogaster]	Contains protein domain (PF000008) - EGF-like domain	UNCLASSIFIED	264689, 264639, 264563 55811957, 264628
554	78618378 (1107, 1108)	Novel Protein sim. GBank gij5019771[jb]AAD37857.1[AF13326 - (AF133263) histidine protein kinase-response regulator hybrid protein CvgSY [Pseudomonas syringae pv. syringae]		kinase	264906
555	78986347 (1109, 1110)	Novel Protein sim. GBank gij13151[jsp]P02808[PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)]	Contains protein domain (PF00358) - phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	transport	264762
556	20457127 (1111, 1112)	Novel Protein sim. GBank gij3914014[jsp]P66380[MFD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)]		transcriptfactor	264508, 264605, 264559
557	18523405 (1113, 1114)	Novel Protein sim. GBank gij5042273[embj]CAB44527.1 - (AL078818) nuoE, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	264488
558	20724429 (1115, 1116)	Novel Protein sim. GBank gij1170933[jsp]P45331[METE_HAEIN - 5-METHYL TETRAHYDROPTEROYL TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)]		UNCLASSIFIED	264602
559	80084353 (1117, 1118)	Novel Protein sim. GBank gij4980567[jb]AAD35173.1[AE001694] Iron(III) ABC transporter, permease protein [Thermotoga maritima]		UNCLASSIFIED	264634

560	80066533 (1119, 1120)	Novel Protein sim. GBank glj2492595[sp]Q53183[Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF00005) - ABC transporter	transport	18103386, 264908, 264602, 264604, 18108374
561	20293187 (1121, 1122)				
562	11698161 (1123, 1124)				
563	79761420 (1125, 1126)	Novel Protein sim. GBank glj4104925 (AF042276) - poly(hydroxycarboxylate) granule associated protein GA2 [Pseudomonas putida]			
564	56716390 (1127, 1128)	Novel Protein sim. GBank glj2792310 (AF040370) - unknown [Amycolatopsis mediterranei]		dehydrogenase	264592
565	56465618 (1129, 1130)	Novel Protein sim. GBank glj3449294[dbj]BAA32462] - (AB011532) MEGF8 [Rattus norvegicus]	Contains protein domain (PF00008) - EGF-like domain	synthase	265010
566	94323888 (1131, 1132)	Novel Protein sim. GBank glj4539568[emb]CAB38487.1] - (AL035836) putative helicase [Streptomyces coelicolor]		helicase	264909, 264510, 265008, 264910, 264758, 264600, 264602, 264604, 264805, 264788, 264887, 264889, 35895917, 264893, 65274620, 264486
567	79560955 (1133, 1134)	Novel Protein sim. GBank glj100508[pir]SJ17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria trinervia (fragment)	Contains protein domain (PF00390) - Malic enzyme	UNCLASSIFIED dehydrogenase	264681, 264691, 264593 264689
568	39506887 (1137, 1138)	Novel Protein sim. GBank glj3915843[sp]O31212[RS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00318) - Ribosomal protein S2	ribosomalprot	264565
570	78375927 (1139, 1140)				
571	78793961 (1141, 1142)	Novel Protein sim. GBank glj115122[sp]P21627[BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		UNCLASSIFIED transport	18108378, 18108387, 264585 264907, 264908
572	36998838 (1143, 1144)				
573	20715521 (1145, 1146)	Novel Protein sim. GBank glj4539223[emb]CAB39881.1] - (AL049497) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED UNCLASSIFIED	264782 265007, 264601
574	13521592 (1147, 1148)				
575	13076416 (1149, 1150)	Novel Protein sim. GBank glj118794[sp]P10443[DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264638 264687
576	20482246 (1151, 1152)	Novel Protein sim. GBank glj5457625[emb]CAB49116.1] - (AJ248283) PAB2227 [Pyrococcus abyssi]			264805
577	66727102 (1153, 1154)	Novel Protein sim. GBank glj5042274[emb]CAB44528.1] - (AL078618) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	dehydrogenase	35898052, 264636
578	11804477 (1155, 1156)				
579	11794723 (1157, 1158)	Novel Protein sim. GBank glj1723081[sp]Q11046[Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.08		transport	264638 264682, 264556

580	80059417 (1159, 1160)					22278999, 35696052, 264555, 264556, 264558
581	79230833 (1161, 1162)				UNCLASSIFIED	265008, 264564
582	80049617 (1163, 1164)			Contains protein domain (PF00047) - titin	- striat	265021, 264555, 264557
583	79321392 (1165, 1166)			[Drosophila melanogaster]	transport	264594
584	79845024 (1167, 1168)			Novel Protein sim. GBank gij2501162spj7726jYAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION		
585	79561454 (1169, 1170)			Novel Protein sim. GBank gij3882221dbj BAA34470.1  - (AB018293) KIAA0750 protein [Homo sapiens]	UNCLASSIFIED	264488, 264906, 264766, 284687, 35696423
586	38277486 (1171, 1172)			Novel Protein sim. GBank gij4467250jemb CAB37575  - (AL035569) probable Glu-tRNA Cln amidotransferase subunit [Streptomyces coelicolor]	UNCLASSIFIED	265018, 284684, 21806789
587	80497359 (1173, 1174)			Novel Protein sim. GBank gij5689519dbj BAA83043.1  - (AB029014) KIAA1091 protein [Homo sapiens]	UNCLASSIFIED	264908, 265007
588	79557239 (1175, 1176)				hydrolase	264600, 264602, 264605, 264769, 264690, 264557
589	79805828 (1177, 1178)				UNCLASSIFIED	265020, 264692
590	79815629 (1179, 1180)				UNCLASSIFIED	22278996, 264907, 264909, 264510, 265008, 265010, 264687, 284769, 35695917, 18108376, 264634, 264638, 264638
591	10313540 (1181, 1182)			Novel Protein sim. GBank gij2143293jemb CAB09390  - (Z95972) rpoB [Mycobacterium tuberculosis]	UNCLASSIFIED	284908, 264909
592	13889767 (1183, 1184)			Novel Protein sim. GBank gij4511983jg AAD21543.1  - (AF088896) electrotransfer ubiquinone oxidoreductase [Zymomonas mobilis]	mapolymerase	264691
593	82348699 (1185, 1186)			Novel Protein sim. GBank gij1272368 (U51896) - LigE [Vibrio parahaemolyticus]	MHC	263972
594	20212392 (1187, 1188)			Novel Protein sim. GBank gij1272368 (U51896) - LigE [Vibrio parahaemolyticus]	dehydrogenase	264511, 264762, 264769, 264486
595	10064064 (1189, 1190)			Novel Protein sim. GBank gij131490spj20966jPTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU)	UNCLASSIFIED	264605
				(FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EI-FRU)		264769
596	13085170 (1191, 1192)				UNCLASSIFIED	264636
597	80259003 (1193, 1194)				UNCLASSIFIED	264592
598	94140216 (1195, 1196)				UNCLASSIFIED	264758, 55810764, 264555, 264558, 264837, 83373044
599	20385137 (1197, 1198)			Novel Protein sim. GBank gij125329spjP04951 KDSB_ECOLI - 3-DEOXY-MANNO-OCTULONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULONIC ACID SYNTHETASE) (CKS)	UNCLASSIFIED	264603
600	10357663 (1199, 1200)					
601	79610404 (1201, 1202)			Novel Protein sim. GBank gij2127414jprj S60064 - hypothetical protein 2 - Corynebacterium glutamicum	UNCLASSIFIED	264906
						264510

602	79250602 (1203, 1204)	Novel Protein sim. GBank gij3522961[gibAAC34243.1] - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - Kinase Eukaryotic protein kinase domain	265007
603	11466067 (1205, 1206)		UNCLASSIFIED	264595
604	81675420 (1207, 1208)			264758
605	20436657 (1208, 1210)	Novel Protein sim. GBank gij1175322[spIP44917Y883_HAEIN - HYPOTHETICAL PROTEIN H0883]	UNCLASSIFIED	264603
606	80334582 (1211, 1212)	Novel Protein sim. GBank gij5020284[gibAAD38043.1]AF15136 - (AF151363) Cdc42 GTPase-activating protein [Mus musculus]	UNCLASSIFIED	264764
607	95361506 (1213, 1214)	Novel Protein sim. GBank gij188864 (M74027) - mucin [Homo sapiens]	UNCLASSIFIED	264508, 264908, 85858542, 264682, 264687, 264689, 264534, 18108376, 35698423, 264636, 264555, 264638
608	11810888 (1215, 1216)		UNCLASSIFIED	264682
609	80064775 (1217, 1218)	Novel Protein sim. GBank gij2496701[spIP55552]Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	UNCLASSIFIED	264605
610	79629413 (1219, 1220)			264682
611	87566205 (1221, 1222)			264508, 264905, 264807, 264908, 264909, 264511, 264910, 264756, 264604, 264684, 264766, 264688, 264692, 264628, 264635, 264636, 264637, 264558
612	95287851 (1223, 1224)	Novel Protein sim. GBank gij1877366[emb]CAB07118] - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - nuclease Viral (Superfamily 1) RNA helicase	264600, 264601, 264604, 264769, 264558, 264565
613	7523475 (1225, 1226)			264369
614	79969348 (1227, 1228)	Novel Protein sim. GBank gij5114231[gibAAD40238.1]AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]	UNCLASSIFIED kinase	18108372, 264563
615	38566098 (1228, 1230)	Novel Protein sim. GBank gij1339950[djibAA12741] - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	synthase	264600, 264602, 264629
616	20465331 (1231, 1232)	Novel Protein sim. GBank gij544387[spIP35873]GALE_ERWAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE)/ (UDP- GALACTOSE 4-EPIMERASE)	isomerase	264605
617	91227222 (1233, 1234)	Novel Protein sim. GBank gij2498097[spIQ60769]TNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00641) - Int Zn-finger in Ran binding protein and others.	52845156, 21906765, 35698423, 21906768, 21906769, 22278894, 35698286, 22278996, 265020, 265021, 265007, 265008, 264636, 52844150, 33857023, 264692, 264693, 29331822, 29331824, 55812038, 83373044, 56182181, 60424289, 86714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35696052, 29331828, 27486262, 33657349, 56526486, 265018, 265019, 22279002, 264482, 264448, 29331830, 66712502, 264909

618	20632843 (1235, 1236)	Novel Protein sim. GBank gi 5459388 emb CAB50746.1  - (AL096839) putative aminotransferase [Streptomyces coelicolor]		isomerase	264603	
619	91227224 (1237, 1238)				56994075, 29331826, 33656970, 265008, 33657402, 33109954, 87168559, 264448, 18108374, 83373044	
620	81183143 (1239, 1240)	Novel Protein sim. GBank gi 464335 sp Q05922 DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)		phosphatase	29148498, 284758, 264369, 29148627	
621	80239251 (1241, 1242)	Novel Protein sim. GBank gi 26333557 emb CAB13060  - [Z891.10] yidF [Bacillus subtilis]		UNCLASSIFIED	264556, 284558, 264639	
622	20456427 (1243, 1244)	Novel Protein sim. GBank gi 1857710 gb JA848482  - (U87224) conlactin associated protein [Rattus norvegicus]		UNCLASSIFIED	264605	
623	10131788 (1245, 1246)	Novel Protein sim. GBank gi 1705703 sp P52225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK	Contains protein domain (PF00054) - Laminin G domain	laminin	264906	
624	19534127 (1247, 1248)	Novel Protein sim. GBank gi 1705703 sp P52225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		cytochrome	264596	
625	13084618 (1249, 1250)	Novel Protein sim. GBank gi 2894252 emb CAA17114.1  - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	264688	
626	88062603 (1251, 1252)	Novel Protein sim. GBank gi 416592 sp P32323 AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	29331822, 264905, 264908, 33657023, 33657109, 264558	
627	80255457 (1253, 1254)	Novel Protein sim. GBank gi 3098418 (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 264112, 264593, 265022, 264635	
628	80077096 (1255, 1256)	Novel Protein sim. GBank gi 1711543 sp P50526 SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264600	
629	79851602 (1257, 1258)	Novel Protein sim. GBank gi 1143204 (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	264906, 264907	
630	39565156 (1259, 1260)	Novel Protein sim. GBank gi 3236368 (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	264490	
631	20598718 (1261, 1262)	Novel Protein sim. GBank gi 140687 sp P11666 YGG8_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)			263978	
632	27843890 (1263, 1264)			UNCLASSIFIED	264906, 264600, 264605, 264769, 264689, 264486	
633	80477772 (1265, 1266)			UNCLASSIFIED	264769	
634	17938808 (1267, 1268)			UNCLASSIFIED	265019	
635	79574508 (1269, 1270)			UNCLASSIFIED	264689	
636	79910981 (1271, 1272)			UNCLASSIFIED	264596, 264762, 264693	



637	82455798 (1273, 1274)	Novel Protein sim. GBank gij2326739[emb]CAB10953] - (Z98268) recN [Mycobacterium tuberculosis]		nuclease	264906, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264782, 264786, 264687, 264789, 264689, 35695917, 264693, 264634, 264638, 264639, 264559, 18108385, 264638
638	14897457 (1275, 1276)	Novel Protein sim. GBank gij467862[emb]CAB41074.1] - (AL049645) putative large ATP-binding protein [Streptomyces coelicolor]			
639	80204210 (1277, 1278)	Novel Protein sim. GBank gij458962[dbj]BAA76836.1] - (AB0233209) KIAA0992 protein [Homo sapiens]		struc1	264112, 263874
640	17829578 (1279, 1280)	Novel Protein sim. GBank gij1432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - mapolymerase Skp1 family		265009, 265010
641	78636398 (1281, 1282)			UNCLASSIFIED	264693
642	1988737 (1283, 1284)			UNCLASSIFIED	264555
643	81516220 (1285, 1286)			UNCLASSIFIED	264906, 264908, 264758, 264288, 264632, 264635, 264639, 264564
644	11751367 (1287, 1288)			UNCLASSIFIED	264694
645	95010907 (1289, 1290)			UNCLASSIFIED	264906, 264762, 264693, 264639, 264559
646	80089083 (1291, 1292)			UNCLASSIFIED	264595, 264586
647	80257085 (1293, 1294)			transcriptfactor	264908, 264591
648	80077428 (1295, 1296)	Novel Protein sim. GBank gij4507613[ref]NP_003738.1[ptnks - TANKYRASE	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264600
649	80247447 (1297, 1298)	Novel Protein sim. GBank gij1044963[dbj]169648 - protamine [Monodonta turbinata, gonads, Peptide, 106 aa]		UNCLASSIFIED	263978
650	11798316 (1299, 1300)			UNCLASSIFIED	264686
651	11776932 (1301, 1302)	Novel Protein sim. GBank gij1346918[sp]P12283[PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE LIGASE)]			264602, 264638
652	85516704 (1303, 1304)	Novel Protein sim. GBank gij1722977[sp]Q10638[Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C]		UNCLASSIFIED	264905, 264907, 264909, 263978, 264637
653	82124947 (1305, 1306)			UNCLASSIFIED	22278998, 264510, 264511, 264512, 264593, 21906754, 264603, 264760, 18108376, 264556
654	85010589 (1307, 1308)	Novel Protein sim. GBank gij130327[sp]P26647[PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)]	Contains protein domain (PF01553) - Acyltransferase	UNCLASSIFIED	264906, 264595, 264632
655	79320692 (1309, 1310)			transferase	264592
656	80416739 (1311, 1312)			UNCLASSIFIED	264602, 264605, 264766, 264691
657	20611010 (1313, 1314)			UNCLASSIFIED	264557, 264558

658	87761815 (1315, 1316)	Novel Protein sim. GBank gij5689493[dbj BAA83030.1] - (AB029001) KIAA1078 protein [Homo sapiens]		UNCLASSIFIED	22278986, 60432049, 29331822, 29331824, 29331828, 265007, 265009, 33657402, 33657084, 265017, 264448, 21906765, 21906766, 263957, 20281148, 18108370, 18108374, 264482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gij2137872[pirl 48724 - zinc finger protein PZF - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	22278999, 60432049, 66714117, 29331827, 265007, 264766, 58181562, 18108359, 18108365, 18108370, 18108381
660	81897922 (1319, 1320)	Novel Protein sim. GBank		UNCLASSIFIED	264757
661	80026023 (1321, 1322)	gij134180[sp P15401 SACY_BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTITERMINATOR	Contains protein domain (PF00874) - Transcriptional antiterminator bglG family	UNCLASSIFIED	264510, 265009, 264600, 264602, 264603, 264604, 264605, 32833986, 18108376, 264636, 18108387, 22279000
662	20463731 (1323, 1324)	Novel Protein sim. GBank gij4545229[gb AAD22450.1 AF11618 - (AF116183) SecA homolog [Actinobacillus actinomycetemcomitans]		UNCLASSIFIED	264605
663	20628080 (1325, 1326)	Novel Protein sim. GBank gij5689250[dbj BAA82881.1] - (AB024335) similar to orf5 [Comamonas testosteroni]		dehydrogenase	264769
664	80508512 (1327, 1328)	Novel Protein sim. GBank gij1652848[dbj BAA17766] - (DS0909) DNA photolyase [Synechocystis sp.]		UNCLASSIFIED	264600
665	80079053 (1329, 1330)	Novel Protein sim. GBank gij116841[sp P21640 COBJ_PSEDE - PRECORRIN-3B C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE) (PRECORRIN-3 METHYLASE)		isomerase	264907, 265007
666	79603142 (1331, 1332)	Novel Protein sim. GBank gij3261829[emb CAB10927] - (Z98260) hypothetical protein Rv1230c [Mycobacterium tuberculosis]		glycoprotein	264689, 264602, 264593
667	94631802 (1333, 1334)	Novel Protein sim. GBank gij5688851[dbj BAA82702.1] - (AB017438) Orf5 [Streptomyces coelicolor]		UNCLASSIFIED	264905, 264906, 264908, 264600, 264601, 264603, 264605, 264760, 264689, 264636, 264638, 264639
668	82051891 (1335, 1336)	Novel Protein sim. GBank gij3581853[emb CAA20809] - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	Contains protein domain (PF00453) - Ribosomal protein L20	ribosomal prot	264637
669	12967154 (1337, 1338)	Novel Protein sim. GBank gij2582531 (AF026444) - 2- isopropylmalate synthase [Streptomyces coelicolor]		UNCLASSIFIED	264905, 264906, 264908, 264601, 264762, 264766, 264689, 264638, 18108385, 264486
670	80238549 (1339, 1340)	Novel Protein sim. GBank gij2582531 (AF026444) - 2- isopropylmalate synthase [Streptomyces coelicolor]	Contains protein domain (PF00023) - Ank repeat	synthase	264690, 264692, 264693, 264636, 18108387
671	79601368 (1341, 1342)	Novel Protein sim. GBank gij2114430 (U92703) - Olf-1/EBF-like-3 transcription factor [Mus musculus]		UNCLASSIFIED	264910, 265017
672	79834371 (1343, 1344)	Novel Protein sim. GBank gij4589285[gb AAD26430.1 AF13515 - (AF135154) ferric aicaligin siderophore receptor [Bordetella pertussis]		transcription factor	264759
673	82285788 (1345, 1346)	Novel Protein sim. GBank			
674	79199259 (1347, 1348)	Novel Protein sim. GBank		UNCLASSIFIED	264629

675	87895870 (1349, 1350)	Novel Protein sim. GBank gi 4980755 gb AAD35347.1 AE00170 - (AE001708) D- alanine--D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	264488, 22278999, 68714117, 264508, 284511, 285008, 60433436, 264600, 264601, 264602, 264603, 264604, 264605, 264762, 264887, 264769, 60431602, 18108374, 264638, 264638 265010
676	78896607 (1351, 1352)	Novel Protein sim. GBank gi 1723566 sp Q10479 DF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07			
677	21644312 (1353, 1354)	Novel Protein sim. GBank gi 887208 (U03976) - dynein heavy chain isotype 5C [Tripanestes graillie]		ATPase-associated	264591, 264632
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi 1566274 pr J2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264758, 264682, 264557
679	78868855 (1357, 1358)	Novel Protein sim. GBank gi 3928723 emb CAA22219  - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278996, 264693
680	20726424 (1359, 1360)				
681	84322017 (1361, 1362)	Novel Protein sim. GBank gi 5174493 ref NP_006050.1 pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264600, 264602 264102, 264907, 264908, 265006, 264693, 263972, 83373044, 264566
682	11392476 (1363, 1364)				
683	80083680 (1365, 1366)	Novel Protein sim. GBank gi 4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	UNCLASSIFIED phosphatase	284595 264634
684	20465367 (1367, 1368)	Novel Protein sim. GBank gi 5420387 emb CA846678.1  - (AJ243459) proteophosphoglycan [Leishmania major]			264605
685	80246735 (1369, 1370)				
686	78208808 (1371, 1372)				264809, 263967, 263981
687	80085629 (1373, 1374)				264831
688	78853412 (1375, 1376)	Novel Protein sim. GBank gi 2688962 (AF027768) - Lspa (Serratia marcescens)		peptidase	264693, 264635 264907, 264638
689	88064256 (1377, 1378)	Novel Protein sim. GBank gi 3046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264908, 264907, 265007, 265009, 60433438, 21908754, 264760, 18108358, 21908766, 21908769, 265021, 18108361, 263974, 18108378, 264557, 18108385, 22279002 264510, 264511, 264764, 264769
690	80389750 (1379, 1380)	Novel Protein sim. GBank gi 2498941 sp Q15428 SP62_HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)		UNCLASSIFIED	
691	81854382 (1381, 1382)				264757
692	83608936 (1383, 1384)	Novel Protein sim. GBank gi 5420387 emb CA846678.1  - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	55812038, 55811957, 265018, 55811150, 18108351, 264908, 60431528, 264594
693	78586116 (1385, 1386)	Novel Protein sim. GBank gi 854065 emb CAA56337  - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	264635
694	82455883 (1387, 1388)	Novel Protein sim. GBank gi 267327 sp Q01033 VG48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278996, 264510, 264602, 264603, 264762, 264687, 264769, 264693

695	94147849 (1389, 1390)	Novel Protein sim. GBank gij4468339[embjCAB38059.1] - (AJ010901) MUC4 [Homo sapiens]	Contains protein domain (PF00094) - von Willebrand factor type D domain	UNCLASSIFIED	56182575, 264509, 264905, 264907, 29931830, 264908, 264909, 264511, 265007, 264910, 264758, 264764, 264288, 65274791, 264905, 264595
696	79830882 (1391, 1392)	Novel Protein sim. GBank gij2649950 (AE001058) - glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	
697	11767889 (1393, 1394)	Novel Protein sim. GBank gij1731343[spjQ10694]YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY49.25	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	264682
698	66695862 (1395, 1396)			UNCLASSIFIED	264688, 35695917
699	79582558 (1397, 1398)			UNCLASSIFIED	264682
700	79639098 (1399, 1400)			UNCLASSIFIED	264693
701	80230242 (1401, 1402)	Novel Protein sim. GBank gij1001236[dbjBAA10477] - (DB4003) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	264488, 264510, 264511, 264602, 264605, 264689
702	79814789 (1403, 1404)	Novel Protein sim. GBank gij2498935[spjQ46338]SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT		UNCLASSIFIED	264909
703	20446820 (1405, 1406)	Novel Protein sim. GBank gij3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	oxidase	264804	
704	94312224 (1407, 1408)	Novel Protein sim. GBank gij3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264288, 56181562, 33657109, 264628, 55811576
705	17932141 (1409, 1410)	Novel Protein sim. GBank gij421091[prjS30730] - hypothetical protein o206 - Escherichia coli		UNCLASSIFIED	265006
706	20288062 (1411, 1412)	Novel Protein sim. GBank gij3024872[spjQ35790]Y074_SYNV3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074			264600
707	20638065 (1413, 1414)	Novel Protein sim. GBank gij3420608[gbjAAC31907.1] - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]	transport		264603
708	20708292 (1415, 1416)	Novel Protein sim. GBank gij3649741[embjCAA03985] - (AJ000281) mucin [Homo sapiens]			264601, 264692
709	88001439 (1417, 1418)	Novel Protein sim. GBank gij3080425[embjCAA18744.1] - (AL022604) putative protein [Arabidopsis thaliana]	struct		18108398, 264637, 264908, 264909
710	11356683 (1419, 1420)				264369
711	17931418 (1421, 1422)				265019
712	80258164 (1423, 1424)	Novel Protein sim. GBank gij4758686[refjNP_002323.1]pLRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	Contains protein domain (PF00058) - Low-density lipoprotein receptor repeat class B	apolipoprotein	264591
713	79263126 (1425, 1426)	Novel Protein sim. GBank gij1703266[spjQ11056]AMI2_MYCTU - PUTATIVE AMIDASE CY50.19C		hydrolase	264906, 264907
714	27847651 (1427, 1428)	Novel Protein sim. GBank gij4502351[refjNP_001692.1]pBAAT - bile acid Coenzyme A: amino acid N-acetyltransferase; glycine N-choloyltransferase			264508, 264555

715	78639423 (1428, 1430)	Novel Protein sim. GBank gij1789035 (AE000352) - ori, hypothetical protein [Escherichia coli]		UNCLASSIFIED	264907	
716	78553072 (1431, 1432)				264692	
717	78491842 (1433, 1434)	Novel Protein sim. GBank gij2494074[sp]P55653[GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+)] (SSDH)		dehydrogenase	264636	
718	94318658 (1435, 1436)	Novel Protein sim. GBank gij3873579[emb]CAA94886] - (Z71178) similar to pro-collagen domains: cDNA EST EMBL:D27978 comes from this gene: cDNA EST EMBL:D27977 comes from this gene: cDNA EST EMBL:D34199 comes from this gene: cDNA EST EMBL:D64392 comes from this gene: cDNA EST EMBL... (Z95387) Hypothetical protein Rv2811c [Mycobacterium tuberculosis]	Contains protein domain (PF000093) - von Willebrand factor type C domain	kinase	18108392, 22278984, 22278998, 265008, 265018, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21908769, 18108381, 264691, 264692, 55810764, 264635, 18108381, 18108382, 83373044, 18108388	
719	17679564 (1437, 1438)	Novel Protein sim. GBank gij2104302[emb]CAB08631] - (Z95387) Hypothetical protein Rv2811c [Mycobacterium tuberculosis]		UNCLASSIFIED	265011	
720	79841684 (1439, 1440)				264908	
721	15020180 (1441, 1442)	Novel Protein sim. GBank gij123530[sp]P04929[HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	264629	
722	9862603 (1443, 1444)	Novel Protein sim. GBank gij498253 (U02372) - integrase [Vibrio cholerae]			264910	
723	19755589 (1445, 1446)	Novel Protein sim. GBank gij2253054[emb]CAB10705] - (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	264691	
724	10126494 (1447, 1448)	Novel Protein sim. GBank gij4063015 (AF083061) - protease PrfA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	- protease	264909	
725	78878879 (1449, 1450)			UNCLASSIFIED	264905, 264807	
726	13086282 (1451, 1452)			UNCLASSIFIED	264638	
727	13522872 (1453, 1454)				264634	
728	20288471 (1455, 1456)	Novel Protein sim. GBank gij2633910[emb]CAB13411] - (Z99112) similar to hypothetical proteins [Bacillus subtilis]			264567	
729	11293753 (1457, 1458)			UNCLASSIFIED	264490	
730	18900373 (1459, 1460)	Novel Protein sim. GBank gij2494660[sp]Q45291[GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264584	
731	80058750 (1461, 1462)	Novel Protein sim. GBank gij1146192 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	264605	
732	80258175 (1463, 1464)	Novel Protein sim. GBank gij1168396[sp]P46881AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		struct	264591, 264594, 264595	
733	20446839 (1465, 1466)					
734	20435987 (1467, 1468)	Novel Protein sim. GBank gij3184080[emb]CAA19336] - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264604	
				ubiquitin	264604	

735	11607859 (1469, 1470)	Novel Protein sim. GBank gi1401582 sp P27432 YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELC INTERGENIC REGION			264594
736	10878734 (1471, 1472)	Novel Protein sim. GBank gi1400831 sp P31135 POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264636
737	78945340 (1473, 1474)		Contains protein domain (PF00615) - Regulator of G protein signalling domain	UNCLASSIFIED	265020
738	17895353 (1475, 1476)			oxidase	265008
739	79833670 (1477, 1478)	Novel Protein sim. GBank gi12506867 sp P33225 TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)			264910
740	19881557 (1479, 1480)				264907, 264784, 264634, 264637
741	79827273 (1481, 1482)	Novel Protein sim. GBank gi13261828 emb CAB10925  - [Z98260] mtp [Mycobacterium tuberculosis]	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED	264689, 35696286, 264510, 264908, 18108362
742	82393795 (1483, 1484)	Novel Protein sim. GBank gi13877494 emb CAA88472.1  - (Z46583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family, cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D68340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D6845...		UNCLASSIFIED	29331822, 264910, 264762
743	82300051 (1485, 1486)	Novel Protein sim. GBank gi127420 sp P19888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	UNCLASSIFIED	264488, 264259, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264693, 18108370, 264629, 18108372, 264630, 264631, 264634, 264558, 18108385, 264482, 264564, 264567
744	80230421 (1487, 1488)				18108397, 264511, 264650, 264628, 264638, 264692, 264639, 264766
745	9841963 (1489, 1490)	Novel Protein sim. GBank gi178921 pir S04846 - UDP-N- acetyl-muramoylalanine-D-glutamate-2, 6-diaminopimelate--D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli		glycoprotein	264906
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi13366354 (AF074705) - pyochelin synthetase [Pseudomonas aeruginosa]		synthase	264600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi12887411 dbj BAA24848  - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	oxidase	66714117, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264681, 264288, 264766, 264687, 264766, 264769, 21908768, 35695917, 264691, 264693, 264628, 264634, 264635, 264639, 56182323, 83373044
748	11617923 (1495, 1496)				264690

749	20469119 (1497, 1499)	Novel Protein sim. GBank gi1169727 sp P44948 FPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY- DNA GLYCOSYLASE)		UNCLASSIFIED	264604 264600
750	20286427 (1499, 1500)				
751	21636169 (1501, 1502)	Novel Protein sim. GBank gi15360088 gb AAD42851.1 AF159689 - (AF159689) serine/threonine kinase PKN3 [Myxococcus xanthus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264605, 264559
752	82450366 (1503, 1504)	Novel Protein sim. GBank gi1168662 sp P44426 BIOA_HAEIN - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELAGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	264508, 264907, 264510, 265011, 264782, 264689, 35695855, 264638, 18108387
753	80508718 (1505, 1506)	Novel Protein sim. GBank gi2851530 sp P32399 YHGE_BACSU - HYPOTHETICAL 84.1 KO PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORFB)		UNCLASSIFIED	264908, 264500, 264602, 264604, 264760, 264769, 264634
754	85083741 (1507, 1508)				
755	80185449 (1509, 1510)				
756	94631686 (1511, 1512)	Novel Protein sim. GBank gi13449276 emb CAA20420  - (AL031317) putative dehydrogenase [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264906, 264807, 264808, 264809, 264759, 264602, 264764, 264769, 264828, 264629, 264630, 264632, 264634, 264635, 264637, 264638, 83373044, 18108385
757	78485533 (1513, 1514)				264448, 264690
758	78863176 (1515, 1516)	Novel Protein sim. GBank gi14580331 emb CAB40107.1  - (AJ001206) putative glycogen debranching enzyme [Streptomyces coelicolor]		UNCLASSIFIED	264682, 264685
759	78475667 (1517, 1518)	Novel Protein sim. GBank gi2911858 (AF047659) - No definition line found [Caenorhabditis elegans]		amylase	265007, 18108387, 265007, 18108387
760	87828888 (1519, 1520)	Novel Protein sim. GBank gi13451312 emb CAA20449  - (AL031324) membrane alipase [Schizosaccharomyces pombe]	Contains protein domain (PF00122) - E1-E2 ATPase	UNCLASSIFIED	264684, 264686
761	79877966 (1521, 1522)				29331822, 264908, 52644045, 56182435, 60170831, 21906754, 265017, 265019, 264681, 264687, 264688, 21906788, 21906768, 265020, 265021, 265022, 264635, 22279000
762	80023563 (1523, 1524)	Novel Protein sim. GBank gi13327158 dbj BAA31647  - (AB014572) KIAA0672 protein [Homo sapiens]		UNCLASSIFIED	264768
763	20284813 (1525, 1526)	Novel Protein sim. GBank gi14981268 gb AAD35822.1 AE001744 - (AE001744) lipopolysaccharide core biosynthesis protein KdIB [Thermotoga maritima]		UNCLASSIFIED	264907, 264593, 265020
764	39515024 (1527, 1528)				264600
					264603

765	80025347 (1529, 1530)	Novel Protein sim. GBank gij3845093 (AE001371) - erythrocyte membrane protein PIEMP3 [Plasmodium falciparum]		struct	264905, 264906, 264594, 264686, 33657023
766	82417404 (1531, 1532)			UNCLASSIFIED	264605, 264762, 18108374
767	10296742 (1533, 1534)	Novel Protein sim. GBank gij541121 [pir]S40827 - hypothetical protein o300 - Escherichia coli		UNCLASSIFIED	264907
768	79416080 (1535, 1536)			UNCLASSIFIED	264592, 264595
769	80086554 (1537, 1538)	Novel Protein sim. GBank gij2882501 [emb]CAA06164 - (AJ004832) neuropathy target esterase [Homo sapiens]		esterase	55810764, 264559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gij283437 [pir]S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		UNCLASSIFIED	264905, 264907, 264828, 264908, 265010, 264766, 264628, 264629, 264634, 264638, 264555
771	95329508 (1541, 1542)	Novel Protein sim. GBank gij4769004 [gb]AAD29715.1 [AF140598] ring-box protein 1 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35696286, 264259, 66714117, 264107, 66712502, 56182435, 264112, 55812038, 67168559, 264288, 21906766, 33657023, 65274620, 65274791, 18108381
772	78971362 (1543, 1544)			UNCLASSIFIED	264910
773	78945363 (1545, 1546)			UNCLASSIFIED	265020
774	78856129 (1547, 1548)	Novel Protein sim. GBank gij553132 [emb]CAB51045.1 - (AJ009579) putative alkane 1-monooxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	264909
775	20620141 (1549, 1550)			UNCLASSIFIED	264555
776	78842693 (1551, 1552)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a		265019
777	78960378 (1553, 1554)	Novel Protein sim. GBank gij4505461 [ref]NP_003624.1 [pNRPB - nuclear restricted protein, BTB domain-like (brain)]	Contains protein domain (PF01344) - Keich motif	protease	21906754, 265020, 60170615, 264691
778	20691310 (1555, 1556)			UNCLASSIFIED	264511
779	80054024 (1557, 1558)				264603
780	95288987 (1559, 1560)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	264907, 264600, 264601, 264602, 264603, 264604, 264605, 264486
781	80250049 (1561, 1562)				264905, 264907, 265010, 264600, 264601, 18108362, 18108374, 264558
782	8758529 (1563, 1564)	Novel Protein sim. GBank gij4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	264605
783	16410791 (1565, 1566)				265020
784	80051197 (1567, 1568)			UNCLASSIFIED	264635, 33657023, 29331828, 265017, 264565, 264568
785	56073541 (1568, 1570)	Novel Protein sim. GBank gij3451335 (AC005525) - F22162_1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696052, 264604
786	20438842 (1571, 1572)	Novel Protein sim. GBank gij138748 [sp]P10905 [UGPA, ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA]		transport	264603
787	80258364 (1573, 1574)			UNCLASSIFIED	264593



788	80507844 (1575, 1576)	Novel Protein sim. GBank gij2746079 (AF015310) - BTH1 [Brassica napus]		synthase	264909, 264602, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gij2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium salinarum]		UNCLASSIFIED	265007
790	86284408 (1578, 1580)	Novel Protein sim. GBank gij5706378 [dbj BAA83098.1  - (AB026118) MALT1 [Homo sapiens]	Contains protein domain (PF000047) - glycoprotein Immunoglobulin domain		22276999, 29331824, 264828, 87168559, 265018, 21906765, 21906767, 21906768, 21906769, 265020, 264682, 22279000, 264563
791	84651627 (1581, 1582)	Novel Protein sim. GBank gij5689948 [emb CAB51985.1  - (AL109863) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]			264601, 264605, 264636
792	80056786 (1583, 1584)	Novel Protein sim. GBank gij393194 (L02375) - S-antigen [Plasmodium falciparum]		struct	
793	79638730 (1585, 1586)	Novel Protein sim. GBank gij1345408 [dbj BAA05046  - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - homeobox		265021, 264631, 264635, 264558
794	81839284 (1587, 1588)	Novel Protein sim. GBank gij105884 [pir S24023 - dopamine receptor D4 - human (fragment)]	Homeobox domain	homeobox	264693
795	80074388 (1589, 1590)	Novel Protein sim. GBank gij1877334 [emb CAB07082  - (Z92771) bta [Mycobacterium tuberculosis]		UNCLASSIFIED	264603, 264604, 264910, 264762, 264908, 264639, 264909, 264757
796	86669451 (1591, 1592)			carboxylase	264488, 35696052, 264805, 264807, 265010, 35698423, 264636
797	87771781 (1593, 1594)	Novel Protein sim. GBank gij2905447 [emb CAA71519  - (Y10495) CDV-1R protein [Mus musculus]		struct	80432228, 55811150, 264630, 264637, 264565
798	79865209 (1595, 1596)	Novel Protein sim. GBank gij4467250 [emb CAB37575  - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		transcript factor	22278998, 264093, 264094, 66714117, 21906767, 21906769, 265020, 265022
799	79557816 (1597, 1598)			hydrolase	264687, 264768, 264693
800	79970189 (1599, 1600)				264909, 264910, 264638, 264638
801	80499399 (1601, 1602)	Novel Protein sim. GBank gij2791517 [emb CAA16054  - (AL021246) hypothetical protein RV2477c [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
802	79834598 (1603, 1604)	Novel Protein sim. GBank gij4867211 [gb AAD32237.1  AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]		transport	264508, 264511, 265008, 265009, 264769, 264567, 264486
803	20467520 (1605, 1606)				264905, 264693
804	10174239 (1607, 1608)	Novel Protein sim. GBank gij1176152 [sp P44507 YHAD_HAEIN - HYPOTHETICAL PROTEIN H10091]		struct kinase	264605 264510
805	79599993 (1609, 1610)				
806	80484113 (1611, 1612)	Novel Protein sim. GBank gij2764612 [emb CAA04683  - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	transferase	264508 264769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gij2833311 [sp Q21828 YNF0_CAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]			264764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gij3913092[sp]Q46170[ARCD_CLOPE - ARGININE/ORNITHINE ANTI-PORTER		transport	264909, 264602, 21906764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gij3913016[sp]P74309[ALF1_SYN3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)]	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264906, 264909, 265007, 264910, 264758, 264600, 264602, 264603, 264805, 264687, 264769, 264689, 264636, 264486
810	80192761 (1619, 1620)	Novel Protein sim. GBank gij401472[sp]P30863[YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPULM-LD INTERGENIC REGION	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264369
811	80079280 (1621, 1622)			UNCLASSIFIED	264558
812	10297654 (1623, 1624)			UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gij146168 (J01617) - glutaminyl- tRNA synthetase [Escherichia coli]		synthase	264905, 264602, 264605, 264682, 264687,
815	95419513 (1629, 1630)	Novel Protein sim. GBank gij4589652[dbj]BAA78848.1] - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	264769, 264636
816	19881910 (1631, 1632)				264488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146499, 264905, 264908, 265007, 33657402, 60433358, 60433438, 264758, 265011, 265017, 265018, 265019, 264389, 264288, 264885, 21906765, 21906767, 265020, 265021, 264892, 65274620, 33657109, 264629, 18108376, 264635, 264638, 60170394, 56182323, 264564
817	95293318 (1633, 1634)	Novel Protein sim. GBank gij178114[emb]CAB06254] - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	264600
818	90938180 (1635, 1636)	Novel Protein sim. GBank gij1477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22278999, 60424269, 35696052, 55812038, 21906768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810764, 35696423, 55811576, 264636
819	80254977 (1637, 1638)	Novel Protein sim. GBank gij1001352[dbj]BAA10839] - (D64006) ABC transporter [Synecocystis sp.]		transport	264565
820	80059688 (1639, 1640)	Novel Protein sim. GBank gij586814[sp]P37484[YBYT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION		UNCLASSIFIED	264600, 264602, 264604
821	79762590 (1641, 1642)				
822	80215310 (1643, 1644)			UNCLASSIFIED	264910
823	94992299 (1645, 1646)	Novel Protein sim. GBank gij3878400[emb]CAA95828] - (Z71264) predicted using GeneFinder; Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL-D32742 comes from this gene; cDNA EST EMBL-D33617 comes from this gene; cDNA EST....		UNCLASSIFIED	264510, 264594, 264637
824	80411171 (1647, 1648)	Novel Protein sim. GBank gij1370076[emb]CAA66887] - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain	struct	264509, 264687, 264691

825	20638600 (1649, 1650)	Novel Protein sim. GBank gi 3025132 sp P77391 YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank gi 3242281 emb CAA16669  - (AL021046) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank gi 3417424 emb CAA203112  - (AL031261) putative transport protein			264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank gi 4336692 gb AAD17897  - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52845080, 264508, 264508, 264905, 264509, 264908, 264907, 264908, 264908, 264909, 264512, 264910, 264591, 264758, 264600, 264766, 264768, 21908788, 35695917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264658, 264639, 83373044, 18108385, 264553, 264566, 264486
829	81742215 (1657, 1658)	Novel Protein sim. GBank gi 320539 (AF080002) - UDP-N- acetyluramyl tripeptide synthetase MurC [Helicobacter mobilis]		UNCLASSIFIED	264758, 264634
830	20396091 (1659, 1660)			UNCLASSIFIED	264603
831	87112435 (1661, 1662)			UNCLASSIFIED	56714117, 264910, 264639
832	19536322 (1663, 1664)	Novel Protein sim. GBank gi 1870004 emb CAB08855  - (Z82539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	264908
833	20726654 (1665, 1666)	Novel Protein sim. GBank gi 2500058 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
834	21428762 (1667, 1668)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Kinase Pyruvate kinase		264600, 264602, 264769, 264689, 264636
835	94140482 (1669, 1670)				264768, 263994, 21908767, 264910, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35695052, 22279002, 264508, 264905, 264906, 264446, 263972, 264908, 264909
836	66126552 (1671, 1672)	Novel Protein sim. GBank gi 699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		transport	35695817, 264557
837	79450450 (1673, 1674)			UNCLASSIFIED	264595
838	79184203 (1675, 1676)	Novel Protein sim. GBank gi 728867 sp P40802 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	264687
839	79641125 (1677, 1678)	Novel Protein sim. GBank gi 2496533 sp Q50598 YOD8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264906
840	80059851 (1679, 1680)	Novel Protein sim. GBank gi 4557753 ref NP_000372.1 pMID1 - midline 1 protein finger	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264762, 264556

841	80376318 (1681, 1682)	Novel Protein sim. GBank gij139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN Novel Protein sim. GBank gij2114321[dbj]BAA200371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	Transcription factor	264764
842	80078724 (1683, 1684)	Novel Protein sim. GBank gij2114321[dbj]BAA200371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF003569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 56182323, 264558
843	87002847 (1685, 1686)	Novel Protein sim. GBank gij3882325[dbj]BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	264091, 29331825, 264906, 264768, 264563
844	17941439 (1687, 1688)	Novel Protein sim. GBank gij222472[dbj]BAA20844 - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	Transcription factor	265011
845	18346844 (1689, 1690)			kinase	264829 264907
846	79863441 (1691, 1692)	Novel Protein sim. GBank gij625679[pir]A36929 - virulence regulatory protein VsrB - Pseudomonas solanacearum			264909
847	78695348 (1693, 1694)			UNCLASSIFIED	265020
848	78489365 (1695, 1696)			UNCLASSIFIED	264568
849	79756367 (1697, 1698)			UNCLASSIFIED	264909
850	78817849 (1699, 1700)	Novel Protein sim. GBank gij3183245[sp]P78051[YCJ_K_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase		
851	95320333 (1701, 1702)	Novel Protein sim. GBank gij5454130[ref]NP_006280.1[pTLN] - talin	Contains protein domain (PF01608) - ILWEEQ domain		264488, 52644507, 264489, 18108398, 65274572, 56182575, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 20281171, 264490, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264107, 264905, 264906, 264907, 264908, 52644045, 56182435, 265006, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433356, 33657402, 60433438, 264595, 264758, 264759, 21906754, 33109954, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 264448, 264682, 264764, 264683, 18108354, 264288, 264389, 264685, 264766, 264687, 264768, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 29148629, 55811957, 35695917, 265020, 265021, 265022, 60170815, 52844150, 264691, 264692, 33657023, 264693, 263956, 33657109, 27486261, 27486262, 27486264, 27486265, 35695763, 60431602, 18108370, 20281089, 264629, 18108374, 18108376, 55811576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

853	13032587 (1705, 1706)	Novel Protein sim. GBank gij3402836[emb]CAA76082] - (Y18136) 2-enoate reductase [Moorella thermoacetica]		reductase	264636 264566
854	80052438 (1707, 1708)				
855	79641130 (1709, 1710)			UNCLASSIFIED	264692
856	11594236 (1711, 1712)			UNCLASSIFIED	264591
857	79210185 (1713, 1714)			UNCLASSIFIED	264630, 264634
858	80248910 (1715, 1716)				265008, 265009, 264601, 264602, 264603, 18108351
859	20296634 (1717, 1718)				264559
860	80041749 (1719, 1720)			UNCLASSIFIED	264489
861	65857045 (1721, 1722)			UNCLASSIFIED	33657023, 264630
862	80078467 (1723, 1724)			UNCLASSIFIED	264600
863	80578931 (1725, 1726)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264488, 18108398, 35696286, 264259, 18108351, 264288, 265021
864	94939904 (1727, 1728)			UNCLASSIFIED	264259, 264112, 263974
865	80045310 (1729, 1730)	Novel Protein sim. GBank gij568884[emb]CAB52047.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01479) - S4 domain		264635, 264600, 264636, 264591, 264602, 264693
866	80162031 (1731, 1732)	Novel Protein sim. GBank gij4557878[ref]NP_000341.1[pABCR - ATP binding cassette transporter]	transport		264288, 264557, 264558
867	80062402 (1733, 1734)				
868	10075364 (1735, 1736)			UNCLASSIFIED	264605
869	80062408 (1737, 1738)			UNCLASSIFIED	264909
870	80249651 (1739, 1740)	Novel Protein sim. GBank gij626660[pir]S37755 - Adenylyl-transferase - Escherichia coli	transferase		264605, 264687, 18108374
871	20378285 (1741, 1742)	Novel Protein sim. GBank gij1708180[sp]Q10602]HEMK_MYCTU - HEMK PROTEIN HOMOLOG	UNCLASSIFIED		264601, 264636
872	95197114 (1743, 1744)	Novel Protein sim. GBank gij1545959[emb]CAA67763] - (X99384) paladin [Mus musculus]	UNCLASSIFIED		264603
873	20189728 (1745, 1746)	Novel Protein sim. GBank gij156104 (AE001589) - putative Outer membrane protein [Helicobacter pylori J99]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	UNCLASSIFIED	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 264910, 264591, 60433356, 264596, 52848317, 87168474, 285010, 264602, 264603, 265017, 265018, 264605, 18108351, 264764, 264768, 264768, 52844229, 264768, 21906765, 265021, 264534, 264691, 52645129, 264628, 264629, 35696423, 65274791, 264631, 264632, 264635, 264636, 264556, 264637, 264638, 264639, 60432113, 22278000, 22278002, 264584

874	80077692 (1747, 1748)	Novel Protein sim. GBank gi 134319 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264600
875	86608446 (1749, 1750)	Novel Protein sim. GBank gi 481000 pir J37594 - mucin - human (fragment)			264259, 264448, 264288, 264557, 87168518
876	86465157 (1751, 1752)	Novel Protein sim. GBank gi 3128283 (AF010496) - iron(iii) dicitrate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF000005) - ABC transporter	transport	264907, 2646011, 264602, 264605, 265020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gi 731074 sp P40349 URB1 - USTIMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF003320) - GATA zinc finger	transcript/factor	22278998, 264908, 264369
878	80187289 (1755, 1756)	Novel Protein sim. GBank gi 1351614 sp Q09853 YAED - SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I		ATPase associated	264369, 264555
879	94328962 (1757, 1758)	Novel Protein sim. GBank gi 3875304 emb CAA98434  - (Z74030) predicted using GeneFinder; cDNA EST EMBL:CO7609 comes from this gene; cDNA EST EMBL:CO9023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com...			56182575, 29331824, 264508, 264906, 265018, 18108351, 264448, 264683, 21908768, 21908768, 60170815, 33657023, 65274620, 33657109, 18108374, 35695855, 264563
880	8491135 (1759, 1760)	Novel Protein sim. GBank gi 13120 sp P11214 UR0T - MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF00051) - Kingle domain	cathepsin	264508
881	11290122 (1761, 1762)			UNCLASSIFIED	264508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gi 2632098 emb CAA75667  - (Y15513) Prodos protein [Drosophila melanogaster]		UNCLASSIFIED	264558
883	79582969 (1765, 1766)	Novel Protein sim. GBank gi 1155068 emb CAA64425  - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264688
884	13517921 (1767, 1768)	Novel Protein sim. GBank gi 1155068 emb CAA64425  - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264636
885	80052457 (1769, 1770)	Novel Protein sim. GBank gi 2078027 emb CAB08467  - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 18108362
886	11685136 (1771, 1772)				264690
887	94315307 (1773, 1774)	Novel Protein sim. GBank gi 2655834 emb CAA15904  - (AL021006) sucA [Mycobacterium tuberculosis]		dehydrogenase	35696052, 264506, 264600, 264603, 35695917, 35695855, 264636
888	10083399 (1775, 1776)	Novel Protein sim. GBank gi 5689395 dbj BAAB2981.1  - (AB028952) KIAA1029 protein [Homo sapiens]		UNCLASSIFIED	264908
889	20385917 (1777, 1778)	Novel Protein sim. GBank gi 1881338 dbj BAA19365  - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE. [Bacillus subtilis]			264603
890	19904337 (1779, 1780)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]			264629

891	13516879 (1781, 1782)	Novel Protein sim. GBank gi 4959396 gb AAD34331.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]		UNCLASSIFIED	264636
892	87634157 (1783, 1784)	Novel Protein sim. GBank gi 545526 bbs 143833 - LBP- 1b-transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namatwa cells, Peptide, 541 aa]		transcriptfactor	22278996, 22278999, 29331828, 35696052, 264908, 264909, 265009, 265011, 264602, 265019, 264768, 21906765, 21908768, 21906769, 265020, 265021, 56528488, 264689, 263987
893	79166037 (1785, 1786)	Novel Protein sim. GBank gi 2829888 sp P80808 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIO) LYASE) (CSASE)		synthase	
894	11102240 (1787, 1788)				263978
895	80239868 (1789, 1790)			UNCLASSIFIED	264508, 264600, 264555, 264559
896	79747803 (1781, 1792)				264632
897	94991923 (1793, 1794)		Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	264686, 29331828, 264511
898	87895109 (1795, 1796)				56182575, 60432289, 58182435, 60432228, 55811957, 22279000, 264488
899	11100463 (1797, 1798)				264601
900	80499768 (1799, 1800)	Novel Protein sim. GBank gi 1750127 (U66480) - YncC [Bacillus subtilis]		transport	264769, 264691, 264563
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi 3122879 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - IRNA synthetases class II (A)	synthase	264907, 264602, 264605, 264769, 35695917, 18108378, 264563
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi 335570 emb CAA200011 - (AL031124) 3-isopropylmalate dehydratase large subunit [Streptomyces coelicolor]	Contains protein domain (PF00330) - aconitase family (aconitate hydratase)	isomerase	264909, 265008, 264602, 264604, 264769, 264689, 264693
903	82060208 (1805, 1806)	Novel Protein sim. GBank gi 2960120 emb CAA18018.1 - (AL022121) gbpK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	35696052, 264905, 264510, 264511, 264512, 264805, 264760, 18108351, 264762, 264687, 264768, 264769, 264688, 21908764, 35695917, 27486262, 35695855, 264634, 264636, 264488
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi 728887 sp P40906 ARGI_COCIM - ARGINASE	Contains protein domain (PF00491) - Arginase family	hydrolase	264604
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi 4567200 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264809
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi 3738200 emb CAA21292 - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			264595, 264605
907	87913201 (1813, 1814)				
908	11754482 (1815, 1816)			UNCLASSIFIED	60432289, 264601, 264880
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi 3868940 dbj BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	264638
		Novel Protein sim. GBank gi 4599728 dbj BAA76883.1 - (AB003137) DnaJ homolog protein [Salix gligiana]		UNCLASSIFIED	264602
910	16776205 (1819, 1820)		Contains protein domain (PF00684) - eph DnaJ central domain (4 repeats)		265009

911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P35685 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomalprot	265010, 264604, 60432113
912	20448863 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AAD07921.1  - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26695]		hydrolase	264559
913	20469357 (1825, 1826)				
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 417657 sp Q03604 RIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED - reductase	264604 264636
915	87606703 (1829, 1830)	Novel Protein sim. GBank gi 5689571 db BAA83069.1  - (AB029040) KIAA1117 protein [Homo sapiens]			18108398, 22278996, 66714117, 264908, 264591, 21906768, 265020, 55811578, 264638
916	79444091 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790  - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
917	20195985 (1833, 1834)				
918	81226795 (1835, 1836)	Novel Protein sim. GBank gi 1655699 emb CAA68032  - (Y07752) pterophorin-S [Volvox carter]		UNCLASSIFIED synthase	264605 264259, 29331826, 264908, 265019, 264448, 265020, 264635, 83373044
919	80436785 (1837, 1838)	Novel Protein sim. GBank gi 5689968 emb CAB52005.1  - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265006, 264512, 264600, 264602, 264604, 264768, 18108370, 264563
920	78608095 (1839, 1840)	Novel Protein sim. GBank gi 1168449 sp Q05813 AMP1_STRL1 - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I)		peptidase	264508
921	19858634 (1841, 1842)	Novel Protein sim. GBank gi 3850084 emb CAA21811.1  - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	78982605 (1843, 1844)				265019, 22279002
923	86695830 (1845, 1846)	Novel Protein sim. GBank gi 267079 sp P28514 TB86_ARATH - TUBULIN BETA-6 CHAIN		tubulin	264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
924	21431341 (1847, 1848)				264510
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi 2497689 sp Q0863 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA2) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264603
926	78397657 (1851, 1852)	Novel Protein sim. GBank gi 3882325 db BAA34522.1  - (AB018345) KIAA0802 protein [Homo sapiens]			55811957, 263972, 264639
927	37036201 (1853, 1854)			UNCLASSIFIED	264769



928	80070610 (1855, 1856)	Novel Protein sim. GBank gi 156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]		dehydrogenase	264605
929	20630335 (1857, 1858)				
930	5496348 (1859, 1860)	Novel Protein sim. GBank gi 4115936 gb AA03446.1 - (AF118223) No definition line found [Arabidopsis thaliana]		UNCLASSIFIED	264603
931	10245731 (1861, 1862)	Novel Protein sim. GBank gi 4490809 emb CA838642.1 - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]	Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	284259
932	80420613 (1863, 1864)	Novel Protein sim. GBank gi 5459396 emb CA850754.1 - (AL096839) putative integral membrane transport protein [Streptomyces coelicolor]		transport	264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gi 5689523 dbj BA883045.1 - (AB029016) KIAA1093 protein [Homo sapiens]	Contains protein domain (PF00827) - UBA domain	UNCLASSIFIED	264508, 264905, 264908, 264909, 264600, 264602, 264603, 264605, 264768, 264558, 18108387, 264486
934	80039105 (1867, 1868)	Novel Protein sim. GBank gi 119111 sp P12978 EBN2_EBV - EBNA-2 NUCLEAR PROTEIN			264508, 264688, 264693, 27486261, 18108370, 65274791, 284636, 264559, 22279002
935	80063162 (1869, 1870)				264369, 22279002
936	80026632 (1871, 1872)	Novel Protein sim. GBank gi 845686 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
937	80250273 (1873, 1874)	Novel Protein sim. GBank gi 1360659 pir CGHU1V - collagen alpha 1(V) chain precursor - human		UNCLASSIFIED	22278995, 22278998, 264602, 264687, 32833986, 18108387
938	80026633 (1875, 1876)	Novel Protein sim. GBank gi 2226243 emb CAA74531.1 - (Y14083) hypothetical protein [Bacillus subtilis]		synthase	263978
939	11071694 (1877, 1878)			UNCLASSIFIED	264602
940	94144252 (1878, 1880)	Novel Protein sim. GBank gi 3560166 emb CAA20678 - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264600
941	11398414 (1881, 1882)				264905, 264908, 264907, 264908, 264909, 264511, 264910, 264592, 33657402, 264598, 264758, 264760, 264683, 264766, 264768, 264769, 33657023, 33657109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264565, 18108391
942	19484122 (1883, 1884)				264593
943	80080258 (1885, 1886)	Novel Protein sim. GBank gi 4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	264760
944	80216096 (1887, 1888)	Novel Protein sim. GBank gi 2494764 sp Q50729 GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		synthase	264600, 264687, 264689, 264563
945	80052477 (1889, 1890)	Novel Protein sim. GBank gi 732353 sp P39606 YWCH_BACSU - HYPOTHETICAL 38.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION	Contains protein domain (PF00818) - Ice nucleation protein repeat	UNCLASSIFIED	264511, 264603
946	79248402 (1891, 1892)				264906, 264604, 264605, 265020, 18108387
					285017

947	81802698 (1893, 1894)	Novel Protein sim. GBank gl 2896770 emb CAA17247  - (AL021899) hypothetical protein RV2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18109394, 22278996, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264602, 265018, 264605, 264769, 264689, 264693
948	88165538 (1895, 1896)	Novel Protein sim. GBank gl 2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		fgf	18109398, 56182575, 22278997, 22278999, 60432049, 29331822, 29331826, 264907, 56182435, 55811386, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486265, 263972, 55811576, 264638, 80170394, 264566
949	88081788 (1897, 1898)	Novel Protein sim. GBank gl 4507885 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331825, 21906764, 27486261, 21906766, 52644298, 33657349, 87168518, 56994075, 265020, 265021, 87168559, 52644150, 264637
950	78485872 (1899, 1900)	Novel Protein sim. GBank gl 1079461 pir S43865 - cyclotralin 8, type II - polioo (fragment)	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gl 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	79566854 (1903, 1904)	Novel Protein sim. GBank gl 5305702 gb AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		calhepsin	264910, 264691
953	10196003 (1905, 1906)	Novel Protein sim. GBank gl 2495642 sp Q47142 YFHS, ECOLI - HYPOTHETICAL 41.8 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	264510
954	9883326 (1907, 1908)	Novel Protein sim. GBank gl 2360965 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	264508
955	95313410 (1909, 1910)	Novel Protein sim. GBank gl 5454064 ref NP_006319.1 pSIP1 - SYT interacting protein	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	56994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264762, 264763, 264764, 264766, 264686, 264767, 264687, 264768, 264769, 264689, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108388, 284563, 264564
956	80064224 (1911, 1912)	Novel Protein sim. GBank gl 2052129 emb CAB08155  - (Z94752) rimJ [Mycobacterium tuberculosis]			264605
957	80056206 (1913, 1914)			UNCLASSIFIED	264603, 18108362
958	80036446 (1915, 1916)	Novel Protein sim. GBank gl 1709787 sp Q00451 PRF1_LYCES - 38.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264908, 264910, 264762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gl 2131050 emb CAB09260  - (Z95944) opcA [Mycobacterium tuberculosis]		UNCLASSIFIED	264602, 264692
960	37815406 (1919, 1920)	Novel Protein sim. GBank gl 2129478 pir IS51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11399318 (1923, 1924)				264593

963	80580374 (1925, 1926)				UNCLASSIFIED	264510, 264288, 264555, 264556, 264559, 264486
964	79832019 (1927, 1928)	Novel Protein sim. GBank gij4589622[dbj BAA76833.1] - (AB023206) KIAA0989 protein [Homo sapiens]			UNCLASSIFIED	264112, 264910, 264689
965	91228465 (1929, 1930)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	264488, 265017, 264448, 264634, 264558, 83373044
966	95292815 (1931, 1932)				UNCLASSIFIED	264906, 264592, 264586, 264604, 264788, 21908764, 264892, 264893, 264829, 264638, 264638
967	79255708 (1933, 1934)	Novel Protein sim. GBank gij1731207[sp Q11156 RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase		264780
968	79560268 (1935, 1936)	Novel Protein sim. GBank gij2661836[emb CAA75187] - (Y14964) putative transport protein [Methylophilus methylotrophus]		transport		264693
969	79919470 (1937, 1938)	Novel Protein sim. GBank gij5419879[emb CAB46422.1] - (AL098747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_ma_bind		35698268, 264685, 264686, 35695917, 264892, 18108374, 264635
970	95085947 (1939, 1940)			UNCLASSIFIED		18108392, 18108394, 18108388, 22278995, 22278996, 22278998, 22278999, 29147820, 264828, 265006, 265007, 265008, 265009, 18108348, 33109954, 265010, 265011, 18108351, 264288, 21908767, 21906768, 18108370, 18108374, 18108377, 264630, 264635, 18108380, 83373044, 18108387, 18108388
971	76919770 (1941, 1942)			UNCLASSIFIED		265007, 265020, 22279002
972	20710704 (1943, 1944)					264557
973	20370183 (1945, 1946)	Novel Protein sim. GBank gij1723119[sp P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				264604
974	80057103 (1947, 1948)			UNCLASSIFIED		264555
975	10196018 (1949, 1950)			UNCLASSIFIED		264510
976	80205742 (1951, 1952)	Novel Protein sim. GBank gij3881459[emb CAA92988.1] - (Z68753) predicted using GeneFinder; Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27860 comes from this gene; cDNA EST EMBL:D27879 comes from this gene; cDNA EST EMBL:D84477 comes from this ge...		UNCLASSIFIED		264508, 264806, 264758, 264632, 264639, 284563
977	10355349 (1953, 1954)	Novel Protein sim. GBank gij549456[sp Q5335 XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3		UNCLASSIFIED		264906
978	80025927 (1955, 1956)					
979	80447820 (1957, 1958)	Novel Protein sim. GBank gij3171904[emb CAA75869] - (Y15908) DJA-12C protein [Homo sapiens]		UNCLASSIFIED		264600, 264602, 264603, 264604
980	80025828 (1959, 1960)			UNCLASSIFIED		264767, 264768, 265008, 285007, 264908
981	80098550 (1961, 1962)	Novel Protein sim. GBank gij3509940 (AF017368) - [lacogenital dysplasia protein 2 [Mus musculus]		UNCLASSIFIED		264600, 264602, 264605
				UNCLASSIFIED		264892, 264555, 264556, 264557, 264558

982	80195670 (1983, 1984)	Novel Protein sim. GBank gij2950220[emb]CAA71575] - (Y10545) fused-ccdB [Escherichia coli]		UNCLASSIFIED	264404
983	90985041 (1965, 1966)	Novel Protein sim. GBank gij476389[pir]B43402 - myosin heavy chain-B, neuronal - chicken		struct	65274572, 56182575, 264908, 264908, 265007, 265008, 264758, 265010, 55811150, 33657023, 264634, 264557, 264558
984	20466878 (1967, 1968)			UNCLASSIFIED	264605
985	65461368 (1969, 1970)	Novel Protein sim. GBank gij3451504[emb]CAA07660.1] - (AJ007747) hypothetical protein BbLPS1.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	transferase	56182435, 264600
986	87102868 (1971, 1972)			UNCLASSIFIED	264106, 264110, 265020, 60170615
987	79867231 (1973, 1974)				264909
988	19858661 (1975, 1976)			UNCLASSIFIED	264600
989	88095329 (1977, 1978)			UNCLASSIFIED	264508, 265017, 264534, 264564
990	88057746 (1979, 1980)	Novel Protein sim. GBank gij5725508[g]AAD48080.1]AF06015 - (AF060152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Reprolysin (M128) family zinc metalloprotease	oxidase	264259, 264908, 265009, 264910, 264596, 264369, 264288, 264768, 264628, 264635, 264566
991	10106140 (1981, 1982)			UNCLASSIFIED	264909
992	79845694 (1983, 1984)	Novel Protein sim. GBank gij2105049[emb]CAB08835] - (Z95436) hypothetical protein Rv3845 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylylate and Guanylate cyclase catalytic domain	UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)			reductase	264907
994	11090590 (1987, 1988)	Novel Protein sim. GBank gij3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]			264602
995	94321911 (1989, 1990)	Novel Protein sim. GBank gij5106572[g]AAD39760.1]AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	18108398, 65274572, 22278996, 264490, 60432049, 29331827, 29146498, 264508, 264905, 264907, 264908, 56182435, 265008, 264591, 264592, 60432229, 60431735, 33657402, 264595, 264758, 21906754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21906765, 21906768, 21906769, 55811957, 264692, 264693, 264629, 35696423, 55811576, 35695855, 264636, 264555, 264556, 264558, 83373044, 22278002, 264563
996	91013745 (1991, 1992)	Novel Protein sim. GBank gij2911719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 263978, 55811957, 56526486, 87168518, 264910, 264906, 264565, 264566, 264693, 264768
997	80503347 (1993, 1994)	Novel Protein sim. GBank gij2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35696286, 22278997, 22278999, 264508, 264905, 264908, 265010, 264600, 264602, 264605, 264888, 264769, 265021, 264565, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gij123530[jp]IP04929[HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			264595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi 2506897 sp P46480 YFCA_HAEIN - HYPOTHETICAL PROTEIN H10198		UNCLASSIFIED	264882	
1000	20727844 (1999, 2000)			UNCLASSIFIED	264602	
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gi 2224689 dbj BAA20833  - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	60432049, 264807, 264809, 264511, 264603, 264683, 264684, 264687, 264689, 26148827, 21908769, 264692, 18108385, 22279000 265009, 264369, 265020	
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gi 586121 sp P37709 TRHY_RABIT - TRICHOHYALIN		synthet		
1003	17933491 (2005, 2006)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 8]			265019 264635	
1004	16314987 (2007, 2008)	Novel Protein sim. GBank		UNCLASSIFIED	264508	
1005	79617144 (2009, 2010)	Novel Protein sim. GBank gi 114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	264259 264905	
1006	37815429 (2011, 2012)	Novel Protein sim. GBank gi 4062979 dbj BAA36210.1  - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		synthase	265007, 264602, 264605, 264760, 264636	
1007	78620871 (2013, 2014)	Novel Protein sim. GBank gi 2808807 emb CAA04607.1  - (AJ001206) putative trehalose synthase [Streptomyces coelicolor]		kinase	264102, 264288	
1008	88094444 (2015, 2016)	Novel Protein sim. GBank gi 3639077 AF090113  - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	dehydrogenase	264592	
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gi 3746332 AF016307  - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		UNCLASSIFIED	35696052, 264905, 264764, 264768, 35695917, 264629	
1010	84672537 (2019, 2020)	Novel Protein sim. GBank gi 2342647 gb AAB88591.1  - (U90653) DHC-domain-containing cysteine-rich protein [Homo sapiens]	Contains protein domain (PF00013) - KH domain	phosphorylase	35696052, 264805, 264600, 264601, 264602, 264605, 264762, 264768, 264768, 264689	
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gi 3413411 emb CAA20272  - (AL031231) guanosine pentaphosphate synthetase/ polynucleotide nucleotidyltransferase [Streptomyces coelicolor]		UNCLASSIFIED	264591, 21908768 29331824, 265019, 265020	
1012	85284456 (2023, 2024)					
1013	86095772 (2025, 2026)					
1014	86608828 (2027, 2028)					

1015	95418878 (2029, 2030)	Novel Protein sim. GBank gij4159895 (AF063085) - SELIL [Mus musculus]	Contains protein domain (PF000040) - struct Fibronectin type II domain	22278994, 22278995, 56994075, 22278996, 22278999, 284259, 29331825, 29331828, 264507, 56182435, 264510, 264591, 264593, 60433358, 264594, 55812038, 264758, 21906754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21906765, 21906766, 21906767, 21906768, 55811957, 265022, 33657023, 65274620, 33657182, 32833986, 18108370, 18108377, 55811576, 35696423, 264630, 22279000, 264565
1018	79559694 (2031, 2032)	Novel Protein sim. GBank gij25069694sp41407IACPD, ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)	esterase	264686, 264693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gij5103943jdbjBAA79259.1] - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA (Aeropyrum pernix)	transport	264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gij4493973jembjCAB39032.1] - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w), Hypothetical protein, len: 489 aa [Plasmodium falciparum]	Contains protein domain (PF00496) - transport Bacterial extracellular solute-binding proteins, family 5	22278996, 29148627, 264563
1019	11703607 (2037, 2038)		UNCLASSIFIED	264686
1020	80234432 (2039, 2040)			264508, 264509, 264512, 264600, 264762, 264769, 264689, 18108370, 264636, 264638, 264486
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gij4633807jgbjAAD26859.1]AF12779 - (AF127795) trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]	synthase	264769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gij1781230jembjCAB06277] - (Z83867) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	phosphatase	3369052, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gij3777495 (U92083) - calcium transporting ATPase [Pichia angustia]	Contains protein domain (PF00122) - ATPase, associated E1-E2 ATPase	264593
1024	80057129 (2047, 2048)		UNCLASSIFIED	52646842, 33657402, 33657023, 18108379, 55811576, 264631, 264556, 264557, 264559, 18108388, 264566
1025	78644200 (2049, 2050)	Novel Protein sim. GBank gij3483045jembjCAA20556] - (AL031371) putative transport system permease protein [Streptomyces coelicolor]	transport	264693
1026	80025948 (2051, 2052)	Novel Protein sim. GBank gij1174922jppjQ02322]UVRD_HAEIN - DNA HELICASE II	helicase	264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gij4757728jrlNP_004886.1]pAGTA - angiotensin/vasopressin receptor AII/AVP-like	UNCLASSIFIED	265017

1028	20287928 (2055, 2056)	Novel Protein sim. GBank gij2791409[emb]CAA16003] - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	264600
1029	94665090 (2057, 2058)			UNCLASSIFIED	264595
1030	88095343 (2059, 2060)			UNCLASSIFIED	264907, 264908, 264510, 264512, 265009, 265010, 265011, 264600, 264602, 264603, 264605, 264769, 18108372, 18108374
1031	95289117 (2061, 2062)			UNCLASSIFIED	264805, 264906, 264809, 264585, 264682, 264630, 264634, 264638
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gij4503895[ro]NP_000145.1[pgALK - galactokinase 1		UNCLASSIFIED	264689
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gij2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35896052, 264906, 264510, 18108354, 264687, 264769, 264688, 60431602, 18108385, 264488
1034	79245937 (2067, 2068)	Novel Protein sim. GBank gij405885 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	264806
1035	78958355 (2069, 2070)			UNCLASSIFIED	264892
1036	85804998 (2071, 2072)			UNCLASSIFIED	284903, 66712502, 264908, 264768
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 264809, 60433438, 265019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gij790819 (L39891) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLATLH2 domain		264604, 264634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gij2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	264092, 264093, 264094, 264683, 264689, 263967
1040	80026840 (2078, 2080)	Novel Protein sim. GBank gij2352095 (U97022) - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	isomerase	264595
1041	10156682 (2081, 2082)	Novel Protein sim. GBank gij3256535[dbj]BAA29218.1] - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		kinase	264907
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gij2058299[emb]CAA66953] - (X98309) ARI protein [Drosophila melanogaster]			264605
1043	80057138 (2085, 2086)	Novel Protein sim. GBank gij1870167[emb]CAA70125] - (Y08921) msK [Streptomyces reticuli]	Contains protein domain (PF000005) - ABC transporter	transport	264565, 264567
1044	80025952 (2087, 2088)			UNCLASSIFIED	265006, 264602, 265017
1045	52415482 (2089, 2090)	Novel Protein sim. GBank gij5688890[emb]CAB52053.1] - (AL108732) hypothetical protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	29331825, 264637
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		helicase	264686
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gij4210471[dbj]BAA74535.1] - (AB018033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	264769
1048	79186400 (2095, 2096)	Novel Protein sim. GBank gij3413419[emb]CAA20278] - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N-terminal Domain	UNCLASSIFIED	264687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gij5051636[gb]AAD38326.1[AF07372] - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	264805, 264634
1050	78471521 (2099, 2100)			UNCLASSIFIED	264688

1051	80475471 (2101, 2102)				UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442962 (2103, 2104)	Novel Protein sim. GBank gi 3123275 sp P35136 SERA_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases		dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank gi 5441319 emb CAB46717.1  - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]				264686, 18108374, 29331824, 83373044, 21906754, 52645156, 56182435, 264689, 29331827, 27486261, 35696052, 21908765, 35696423, 21908768, 56182575, 21908769, 55811957, 87168518, 35696286, 22278997, 265020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264906, 52644150, 264909, 264288, 29331822, 52645080, 264786
1054	79580225 (2107, 2108)				UNCLASSIFIED	264686
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gi 5052508 gb AAD38584.1 AF14560 - (AF145609) BCDNA GH02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/DEAH box helicase		helicase	264907, 264602, 264681, 264288, 21908768, 33657108, 55810764, 35695855, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank gi 3021676 gb BAA25358  - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]			mapolymerase	264906
1057	85667216 (2113, 2114)	Novel Protein sim. GBank gi 1226281  (U50308) - No definition line found [Caenorhabditis elegans]			UNCLASSIFIED	264682
1058	80376576 (2115, 2116)					264764
1059	94662754 (2117, 2118)	Novel Protein sim. GBank gi 1170018 sp P46808 GREM_MYCLE - TRANSCRIPTION ELONGATION FACTOR GRE (TRANSCRIPT CLEAVAGE FACTOR GRE)			transcriptfactor	35696052, 35695855, 265009, 264636
1060	79481169 (2119, 2120)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)			glycoprotein	29146499, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gi 90254 pir A28334 - protein- lysine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse			phosphatase	264634
1062	39567937 (2123, 2124)	Novel Protein sim. GBank gi 3334200 sp O49854 GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)			dehydrogenase	264593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank gi 2499966 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)				264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank gi 82654 pir JA0086 - 10K zein precursor - maize				265007, 265008, 18108351, 18108385



1065	80021208 (2128, 2130)	Novel Protein sim. GBank gij2120998[pilj]S70682 - glycosyltransferase homolog - Bordetella pertussis		transferase	264600, 264602, 264689
1066	17896878 (2131, 2132)	Novel Protein sim. GBank gij2506362[sp]P15042[DNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))		synthase	265009
1067	10132178 (2133, 2134)	Novel Protein sim. GBank gij4007669[emb]CAA22355] - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264909 264688, 18108382, 264558, 264600, 264760
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gij4589484[dbj]BAA76770.1] - (AB023143) KIAA0928 protein [Homo sapiens]		UNCLASSIFIED	264604
1069	83002954 (2137, 2138)	Novel Protein sim. GBank gij120304[sp]P15932[FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)]		UNCLASSIFIED	264604, 264760
1070	82101892 (2139, 2140)	Novel Protein sim. GBank gij1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	264602
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gij477532[pilj]A49175 - Motch B protein - mouse (fragment)	Contains protein domain (PF00008) - EGF-like domain	synthase	264687, 264688, 21906784, 35696052, 35695917, 35695855, 264600, 264601, 264602, 265009, 264605, 264508, 264805, 264690, 264906, 264762, 264628, 264768
1072	82356540 (2143, 2144)	Novel Protein sim. GBank gij3893109[emb]CAA76940] - (Y17820) CALO protein [Drosophila melanogaster]		synthase	264909 264908
1073	79814400 (2145, 2146)	Novel Protein sim. GBank gij1176203[sp]P46442[YHCM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)]		UNCLASSIFIED	56994075, 22278998, 264594, 264757, 264596, 265018, 265019, 264681, 264389, 264688, 265020, 18108364, 18108374
1074	80105892 (2147, 2148)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		ATPase-associated	264769
1075	81850293 (2149, 2150)	Novel Protein sim. GBank gij3413828[emb]CAA20296] - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		kinase	264905
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		UNCLASSIFIED	264600
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		UNCLASSIFIED	18108394, 264769, 264634, 264636
1078	20288874 (2155, 2156)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		UNCLASSIFIED	264684
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		UNCLASSIFIED	83373044, 265019, 22278002, 264482, 18108351, 264682, 264908, 264693, 264487, 264758, 264768, 264769, 21806767, 264511, 264910, 264634, 264635, 264905, 264636, 264908, 264637, 264907, 264908, 264764, 264638, 20281099, 264766, 264595
1080	11767188 (2159, 2160)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		UNCLASSIFIED	
1081	94747080 (2161, 2162)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		UNCLASSIFIED	
1082	81490656 (2163, 2164)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		UNCLASSIFIED	

1083	87446717 (2165, 2166)	Novel Protein sim. GBank gii1722945j sp Q10523 Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427.23		UNCLASSIFIED	60424178, 264905, 264906, 264510, 60432229, 264759, 87188474, 264605, 264769, 264689, 18108364, 18108376, 35695855, 264636
1084	37799308 (2167, 2168)	Novel Protein sim. GBank gii18384j sp P32057 WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	264769
1085	86475368 (2169, 2170)	Novel Protein sim. GBank gii1999190 (U90204) - heat shock protein 60 [Tukamurella tyrosinosa]	Contains protein domain (PF00118) - eph		60432229, 264687
1086	79608268 (2171, 2172)	Novel Protein sim. GBank gii172956j sp P46176 RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - ribosomal prot		264486
1087	79603979 (2173, 2174)	Novel Protein sim. GBank gii160198j emb CAA15431 - (AL006583) dJ327.J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00365) - helicase		29331827, 264693
1088	79854963 (2175, 2176)	Novel Protein sim. GBank gii2983155 (AE00693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aerophilus]	UNCLASSIFIED		264905, 264601, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gii14981768j AD36280.1 AE00177 - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00328) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	264488, 264511, 265011, 264682, 264768, 264689, 21908764, 35695917, 265020, 32833986, 18108370, 35695855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gii4007680j emb CAA23366 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12917471 (2181, 2182)	Novel Protein sim. GBank gii2495562j sp P77239 YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264637
1092	80252286 (2183, 2184)	Novel Protein sim. GBank gii2960098j emb CAA17996.1 - (AL022121) ntl [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - nuclease		264566
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gii1001642j dbj BAA10373 - (D64002) dGTP triphosphohydrolase [Synecocystis sp.]	Endonuclease III		264769, 35695917, 35695855, 264600, 264602, 264603, 264605, 18108351
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gii4585587j emb CAB40855.1 - (AL049628) putative adenine glycosylase [Streptomyces coelicolor]	UNCLASSIFIED		264886
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gii15001j sp P19206 BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	nuclease	264906, 265007, 264595, 264600, 264602, 264803, 264604, 264605, 264762, 264768, 264769, 264636, 264558, 18108387, 60432113, 264482, 264486
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gii115001j sp P19206 BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)		synthase	264600, 264602, 264603, 264604, 264605, 35695917, 264692, 264631
1097	78239560 (2193, 2194)			UNCLASSIFIED	265019
1098	79166424 (2195, 2196)	Novel Protein sim. GBank gii114135j sp P08205 JARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		synthase	264687

1089	39523638 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (MIG- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	264603
1100	85736571 (2199, 2200)	Novel Protein sim. GBank gi 3023235 sp O64420 ACOD_MESAU - ACYL-COA DESATURASE (STEARYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)	desaturase		264259, 264636
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	isomerase	264769
1102	79777814 (2203, 2204)			UNCLASSIFIED	264910, 264809
1103	81897259 (2205, 2206)	Novel Protein sim. GBank gi 19065596 (U81788) - kinesin-73 [Drosophila melanogaster]	struct		264757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 2935448 (AF048976) - synaptic ras GTPase-activating protein p135 SyngAP [Rattus norvegicus]	UNCLASSIFIED		29331822, 21908754, 264555, 264556, 264558, 22278002
1105	80255121 (2209, 2210)				264566
1106	79314110 (2211, 2212)			UNCLASSIFIED	264555, 264389
1107	80470019 (2213, 2214)				264908, 264789
1108	80440616 (2215, 2216)	Novel Protein sim. GBank gi 117342 sp P43416 SECY_STRSC - PREPROTEIN TRANSLOCASE SECY SUBUNIT	transport		264807, 264510, 264511, 264600, 264602, 264605, 264768, 264769
1109	80064615 (2217, 2218)	Novel Protein sim. GBank gi 2995310 emb CAA18338  - (AL022268) putative ATP-dependent helicase [Streptomyces coelicolor]	helicase		264602, 264605, 264638
1110	80503554 (2219, 2220)				
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2622039 (AE000868) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			264908, 264593, 265010, 264601, 264603, 264604, 264605, 264682, 264769, 264693, 264638
1112	95010088 (2223, 2224)				18108370, 264557
1113	82456352 (2225, 2226)	Novel Protein sim. GBank gi 3218376 emb CAA18628  - (AL023862) putative oxidoreductase [Streptomyces coelicolor]	UNCLASSIFIED		264908 264600, 264802, 264804, 264805, 264762, 264769, 264585
1114	14988014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 p J154876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse	dehydrogenase		264636
1115	11765583 (2229, 2230)				
1116	79841152 (2231, 2232)		UNCLASSIFIED		264686
					264908

1117	95305465 (2233, 2234)	Novel Protein sim. GBank gii3255965[emb]CA494089] - (Z70200) U5 snRNP-specific 200kD protein [Homo sapiens]	Contains protein domain (PF00270) - helicase DEAD/DEAH box helicase	18108392, 264488, 263994, 264489, 18108398, 56182575, 22278995, 22278996, 35698286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264508, 264905, 264508, 264808, 264907, 264908, 66712502, 264909, 52644045, 56182435, 264510, 264511, 265008, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264596, 264758, 264759, 21906754, 33109954, 33657084, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 264604, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 264448, 264682, 264764, 264683, 264288, 264389, 264684, 264685, 264766, 264767, 264686, 264687, 264768, 264769, 264688, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148784, 35695917, 265020, 265021, 265022, 60170815, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 264691
1118	79563326 (2235, 2236)		UNCLASSIFIED	264907
1119	79642463 (2237, 2238)	Novel Protein sim. GBank gii5420387[emb]CA46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264907
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gii1644450 [U67864] - MEX-3 [Caenorhabditis elegans]	collagen	29331827, 265018, 265019, 264681, 265021, 60170615, 18108387
1121	79471716 (2241, 2242)	Novel Protein sim. GBank gii98800[pir]S17768 - 3-dehydroquinase synthase (EC 4.6.1.3) - Mycobacterium tuberculosis	Contains protein domain (PF00013) - KH domain	264683, 264632, 18108388
1122	79456246 (2243, 2244)		UNCLASSIFIED	264639, 264563
1123	78637119 (2245, 2246)		synthase	264693, 27486265
1124	79811596 (2247, 2248)		UNCLASSIFIED	264909
1125	79757861 (2249, 2250)		UNCLASSIFIED	264910
1126	79756914 (2251, 2252)	Novel Protein sim. GBank gii138154[sp]P03643[VG]GG_BPPIX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)	eph	264905, 264909, 264910
1127	11800930 (2253, 2254)		UNCLASSIFIED	264682
1128	8364885 (2255, 2256)	Novel Protein sim. GBank gii5002704[emb]CA44358.1] - (AJ242630) DNA polymerase I [Methylobacterium sp. DM4]	Contains protein domain (PF00476) - DNA polymerase family A	264511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank gi 56809485 dbj BAA03026.1  - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264768
1130	78420151 (2259, 2260)	Novel Protein sim. GBank gi 4981328 gb AAD35881.1 AE001747 - (AE001747) bioY protein [Thermotoga maritima]		UNCLASSIFIED	264595
1131	80055391 (2261, 2262)	Novel Protein sim. GBank gi 1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	35686288, 22278998, 28331828, 264603, 264805, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank gi 1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	22278998, 264906, 265009, 264600, 264602, 264604, 264805, 264760, 32833988, 18108374
1133	17280437 (2265, 2266)	Novel Protein sim. GBank gi 4982454 gb AAD36931.1 AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	18108374
1134	80235376 (2267, 2268)	Novel Protein sim. GBank gi 4539171 emb CAB39700.1  - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	265018
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gi 4539171 emb CAB39700.1  - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264512, 264534
1136	78842052 (2271, 2272)	Novel Protein sim. GBank gi 4982454 gb AAD36931.1 AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264508, 264600, 264602, 284603, 18108376
1137	90931557 (2273, 2274)	Novel Protein sim. GBank gi 4972746 gb AAD34768.1  - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - collagen TPR Domain	UNCLASSIFIED	22278998, 22278999, 35696052, 264907, 265009, 60433358, 264596, 265010, 264448, 264682, 264767, 264688, 265020, 264692, 55811578, 35695855, 284631, 284632, 22279002
1138	78841163 (2275, 2276)	Novel Protein sim. GBank gi 731607 sp P38739 YHC8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264908
1139	78633561 (2277, 2278)	Novel Protein sim. GBank gi 3650031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264893
1140	39480358 (2279, 2280)	Novel Protein sim. GBank gi 3927800 emb CAA05880  - (AJ003125) procollagen I N-proteinase [Homo sapiens]		UNCLASSIFIED	264593
1141	79638019 (2281, 2282)	Novel Protein sim. GBank gi 3927800 emb CAA05880  - (AJ003125) procollagen I N-proteinase [Homo sapiens]		UNCLASSIFIED	265019, 264693
1142	19635848 (2283, 2284)	Novel Protein sim. GBank gi 3927800 emb CAA05880  - (AJ003125) procollagen I N-proteinase [Homo sapiens]		UNCLASSIFIED	264631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank gi 3927800 emb CAA05880  - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - oxidase	UNCLASSIFIED	56182575, 264808, 264600, 264632, 87168518
1144	80088988 (2287, 2288)	Novel Protein sim. GBank gi 3927800 emb CAA05880  - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Thrombospondin type 1 domain	UNCLASSIFIED	264635, 264636, 264807, 264593, 264908, 264586, 264909
1145	14610262 (2289, 2290)	Novel Protein sim. GBank gi 2499003 sp P76422 THID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)		UNCLASSIFIED	264112
1146	82062092 (2291, 2292)	Novel Protein sim. GBank gi 2896734 emb CAA17213.1  - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]		UNCLASSIFIED	264769, 264689, 35696288, 264760, 264905, 264486, 264559
1147	80071761 (2293, 2294)	Novel Protein sim. GBank gi 2896734 emb CAA17213.1  - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]		UNCLASSIFIED	264557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank gi 2896734 emb CAA17213.1  - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]	kinase	UNCLASSIFIED	264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gi 2896734 emb CAA17213.1  - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]		UNCLASSIFIED	264591

1150	81325074 (2299, 2300)	Novel Protein sim. GBank gij2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]		ATPase_associated	264488, 35696286, 264907, 264908, 264909, 264910, 264593, 264598, 264758, 264784, 264766, 264788, 264893, 264628, 60431850, 264564, 264566, 264567
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gij4324655 [pAAD16978] - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]		polymerase	264595
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gij3874275 [emjCAB07311.1] - (Z92825) predicted using GeneFinder; Similarity to Yeast low affinity glucose transporter HXT4 (PS:32467); cDNA EST EMBL: C12555 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from thi...		glycoprotein	264488, 22278998, 264905, 264629, 264486
1153	80027783 (2305, 2306)	Novel Protein sim. GBank gij4240315 [dbjBAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	264910, 264555, 264557
1154	83002995 (2307, 2308)			UNCLASSIFIED	265008
1155	79411098 (2309, 2310)	Novel Protein sim. GBank gij586655 [spjP37617] [ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZN(II)-TRANSLLOCATING P. TYPE ATPASE)]		UNCLASSIFIED	264690, 264636
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gij418480 [spjP32139] [YIHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264603
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gij2498481 [spjQ50724] [Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C]		UNCLASSIFIED	264906, 264907, 264758, 264768, 264769, 264689, 264638, 264566
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gij4503375 [jefINP_001376.1] [pDPYS - dihydropyrimidinase]		UNCLASSIFIED	264906, 264762, 264687, 264769, 264689, 18108374, 35695855
1159	79186451 (2317, 2318)	Novel Protein sim. GBank gij1136408 [dbjBAA11490] - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]		UNCLASSIFIED	264687
1160	91229893 (2319, 2320)	Novel Protein sim. GBank gij2443342 [dbjBAA22380] - (D88764) alpha 2 type I collagen [Rana catesbeiana]		UNCLASSIFIED	29331822, 29331824, 66714117, 29331826, 60433356, 265018, 265019, 83373044, 18108385, 22279000, 22279002, 264563
1161	7417143 (2321, 2322)	Novel Protein sim. GBank gij4503375 [jefINP_001376.1] [pDPYS - dihydropyrimidinase]		UNCLASSIFIED	264369
1162	79635357 (2323, 2324)	Novel Protein sim. GBank gij4503375 [jefINP_001376.1] [pDPYS - dihydropyrimidinase]		UNCLASSIFIED	264693
1163	79563186 (2325, 2326)	Novel Protein sim. GBank gij4503375 [jefINP_001376.1] [pDPYS - dihydropyrimidinase]		UNCLASSIFIED	29331827, 264906
1164	79650829 (2327, 2328)	Novel Protein sim. GBank gij5052554 [gbjAAD38607.1] [AF145632] - (AF145632) BcDNA: GH06032 [Drosophila melanogaster]		transport	18108398, 29331827, 29331828, 29146488, 29146499, 18108354, 21906768, 29148827, 21908769, 264893, 18108382, 18108385
1165	80491888 (2329, 2330)			UNCLASSIFIED	264602, 264605, 264769, 18108370, 18108374, 264565
1166	88096456 (2331, 2332)	Novel Protein sim. GBank gij4589476 [dbjBAA76766.1] - (AB023139) KIAA0922 protein [Homo sapiens]			264488, 35696286, 22278999, 264259, 66714117, 60432289, 35896032, 264905, 56182435, 265006, 60433438, 264759, 21906754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35696423, 35695855, 264558, 18108385, 60432113

1167	78963862 (2333, 2334)	Novel Protein sim. GBank gij2580433[dbj BAA23138] - (D76414) ppGpp hydrolase [Staphylococcus aureus]		kinase	264488
1168	88094678 (2335, 2336)			UNCLASSIFIED	264259, 29331827, 56182435, 60433438, 265019, 33657023, 35695855, 264586
1169	11805403 (2337, 2338)			UNCLASSIFIED	264681
1170	21832244 (2339, 2340)			UNCLASSIFIED	264602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gij2772814 (AF029249) - procollagen D [Mytilus edulis]		UNCLASSIFIED	264556
1172	78610113 (2343, 2344)	Novel Protein sim. GBank gij4757846[re NP_004317.1 pBCL9 - B-cell CLL/lymphoma 9		UNCLASSIFIED	55810764, 35896052, 264634, 264486
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gij2564053[dbj BAA22946] - (AB007832) Bm trachealless [Bombyx mori]			264508, 264906, 264907, 264909, 264591, 264632, 264638, 264639
1174	20283077 (2347, 2348)	Novel Protein sim. GBank gij2911027[emb CAA17520] - (AL021958) mmsA [Mycobacterium tuberculosis]		dehydrogenase	264600
1175	20711847 (2348, 2350)	Novel Protein sim. GBank gij118333[sp P23234 DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	264601
1176	80252845 (2351, 2352)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00586) - AIR synthase related protein	synthase	264509, 264805, 264593, 264602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gij11879[sp P28643 FABG_CUPLA - 3-OXOACYL-ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264605
1178	84128641 (2355, 2356)	Novel Protein sim. GBank gij5031687[re NP_005594.1 pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated	65274572, 18108398, 22278998, 22278999, 29331828, 264508, 264908, 264828, 33657402, 33109954, 284769, 21806765, 21808766, 21806768, 55811957, 33657023, 264629, 55811578, 35698423, 264636, 264556, 56182323, 60432113, 22279000, 22279002
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gij2960090[emb CAA17888.1] - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264603
1180	11794448 (2359, 2360)	Novel Protein sim. GBank gij2558614[emb CAA04787] - (AJ001493) dehydroquinase dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	264638
1181	17946362 (2361, 2362)			UNCLASSIFIED	265017
1182	81494284 (2363, 2364)	Novel Protein sim. GBank gij5420387[emb CAB46678.1] - (AJ243459) proleophosphoglycan [Leishmania major]			265007, 265009, 264564, 264909, 264693
1183	76574044 (2365, 2366)	Novel Protein sim. GBank gij4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]			264699, 35898423, 264638, 18108385
1184	52559933 (2367, 2368)	Novel Protein sim. GBank gij2129478[pir S51839 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264602
1185	76491185 (2369, 2370)			glycoprotein	263967

1186	20224012 (2371, 2372)			UNCLASSIFIED	264559	
1187	78248834 (2373, 2374)			UNCLASSIFIED	29331825, 285017, 18108351	
1188	79831387 (2375, 2376)	Novel Protein sim. GBank gij2996039 (AF054525) - hypothetical protein [Synecococcus PCC7002]		UNCLASSIFIED	264905, 264906	
1189	79609367 (2377, 2378)				264692	
1190	79830589 (2379, 2380)			UNCLASSIFIED	265018	
1191	80310105 (2381, 2382)			UNCLASSIFIED	264600, 264605, 264764, 35695855, 264638,	
1192	13521641 (2383, 2384)		Contains protein domain (PF01581) - FMRPamide related peptide family		264488	
1193	11103584 (2385, 2386)				264636	
1194	78893947 (2387, 2388)	Novel Protein sim. GBank gij854065jembjCAA583371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	263978	
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gij1790277 (AE000459) - putative oxidoreductase [Escherichia coli]		UNCLASSIFIED	265007, 265008	
1196	13000688 (2391, 2392)			UNCLASSIFIED	264605	
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gij2487360jspIQ50715jIMDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)	Contains protein domain (PF00571) - CBS domain		264689	
1198	95290101 (2395, 2396)				264594	
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gij1709525jspiP54673jP3K1_DICD1 - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)			264603	
1200	9848880 (2399, 2400)				264259, 264757, 33109954, 21906768	
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gij2499877jspiP70845jBLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)		UNCLASSIFIED	264910	
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gij606342 (U18997) - ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]		cathepsin	264766, 264769	
1203	82125373 (2405, 2406)			ribosomalprot	264600, 264558	
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gij2500728jspiQ59912ISECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT		UNCLASSIFIED	264768, 264769, 35695917, 264910, 264760, 264908, 264907, 264629, 264908, 264909,	
1205	80053861 (2409, 2410)				264766	
1206	80241965 (2411, 2412)				264905, 264769, 264636	
1207	79841192 (2413, 2414)			UNCLASSIFIED	264566	
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gij2645560 (AF027954) - Bcl-2 related ovarian killer protein [Rattus norvegicus]	Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family	UNCLASSIFIED	264556, 264557, 264558	
				UNCLASSIFIED	29331824, 264909, 265021, 18108370	
				apoptosis	29331824, 29331825, 29331827, 265007,	
					264764, 264683, 264769, 264688, 264689	



1209	79185742 (2417, 2418)	Novel Protein sim. GBank glij175033[sp]P44398[X]LA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	56426884 (2419, 2420)	Novel Protein sim. GBank glij421095[pir]S30688 - hypothetical protein o246 - Escherichia coli		UNCLASSIFIED - transferase	264907, 264693
1211	94665855 (2421, 2422)	Novel Protein sim. GBank glij3806025[emb]CAB07858] - (293785) predicted using GeneFinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this gene...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		264591, 264592, 264595
1212	78167829 (2423, 2424)	Novel Protein sim. GBank glij226282[pir]1505375A - vir gene [Bordetella pertussis]		kinase	264689, 263967
1213	78659633 (2425, 2426)	Novel Protein sim. GBank glij5726285[gb]AAD48398.1[AF126162] HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	264909
1214	10144306 (2427, 2428)	Novel Protein sim. GBank glij2326739[emb]CAB10953] - (298288) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	264908
1215	80050106 (2429, 2430)	Novel Protein sim. GBank glij417328[sp]P33038[MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYL-PYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOYL-PYRUVYLTRANSFERASE)(EPT)		transferase	265009, 264601, 264602, 264603, 33657109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank glij1805460[dbj]BAA09021] - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		dehydrogenase	264604
1217	85011344 (2433, 2434)	Novel Protein sim. GBank glij2143886[pir]152523 - nucleoporin p82 homolog - rat (fragment)		UNCLASSIFIED	264905, 264907, 264908, 264591, 264766, 264891, 264693, 264629, 264630, 264636, 264564
1218	11093680 (2435, 2436)	Novel Protein sim. GBank glij4240315[dbj]BAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	264601
1219	91216252 (2437, 2438)	Novel Protein sim. GBank glij730805[sp]P39663[SPHR_SYNTP7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR		UNCLASSIFIED	56181686, 28331822, 60432289, 264601, 264692, 264629
1220	81241524 (2439, 2440)	Novel Protein sim. GBank glij1172827[sp]P46546[PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	52644507, 264905, 264909, 265008, 265019, 265020, 52644150, 33657023, 264693, 33657182, 35695763, 264634, 22279000, 22279002, 264482
1221	83045055 (2441, 2442)	Novel Protein sim. GBank glij1172827[sp]P46546[PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)		UNCLASSIFIED	264766, 265020, 264908
1222	20711865 (2443, 2444)	Novel Protein sim. GBank glij1172827[sp]P46546[PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)		phosphatase	264601
1223	11815647 (2445, 2446)	Novel Protein sim. GBank glij1172827[sp]P46546[PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)		kinase	264593
1224	80432645 (2447, 2448)	Novel Protein sim. GBank glij1172827[sp]P46546[PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	264593, 264600, 264601, 264603, 264605, 264766, 18108376, 264635, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gij12105050[emb]CAB08836] - (Z95436) hypothetical protein RV3644c [Mycobacterium tuberculosis]			264768
1226	80237518 (2451, 2452)	Novel Protein sim. GBank gij12105050[emb]CAB08836] - (Z95436) hypothetical protein RV3644c [Mycobacterium tuberculosis]		polymerase	264905, 264512, 264689
1227	78422138 (2453, 2454)	Novel Protein sim. GBank gij1708768[sp]P98133[FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)]		UNCLASSIFIED	264808, 264637, 264639
1228	79208027 (2455, 2456)	Novel Protein sim. GBank gij165330[db]BAA1881] - (D90917) acriflavine resistance protein [Synchocystis sp.]	Contains protein domain (PF00873) - AcrB/AcrD/AcrF family		264605, 264634
1229	84329135 (2457, 2458)	Novel Protein sim. GBank gij116230[sp]P28598[CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60)] (GROEL PROTEIN)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	UNCLASSIFIED	87168474, 265011, 87168559, 264681, 264689, 264693, 65274620, 18108374, 264909, 264605, 18108388
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]		UNCLASSIFIED	264908, 264909
1231	79843141 (2461, 2462)	Novel Protein sim. GBank gij118298[sp]P20730[CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]		UNCLASSIFIED	265017, 264564
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]		UNCLASSIFIED	265008, 265010, 18108381
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]		UNCLASSIFIED	264634, 264762
1234	79242158 (2467, 2468)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]	Contains protein domain (PF00125) - Core histone H2A/H2B/H3/H4	UNCLASSIFIED	265018, 55811150, 264565, 264757
1235	79914423 (2469, 2470)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]		UNCLASSIFIED	264758, 264601, 264766, 264687, 18108372, 264555, 264559
1236	81927147 (2471, 2472)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]		UNCLASSIFIED	
1237	83371762 (2473, 2474)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]		UNCLASSIFIED	
1238	87411577 (2475, 2476)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 26331822, 29331824, 35696052, 264508, 264906, 52644045, 52646317, 264288, 264769, 264693, 264632, 264634, 264558, 87168518, 264563
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]	protein-coupled receptor LGR4 [Rattus norvegicus]	oncogene	264509, 264511, 264759, 264760, 264764, 264557
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]			264769
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264601, 264604, 264638
1242	78775890 (2483, 2484)	Novel Protein sim. GBank gij1729671[sp]P40280[H2A_MAIZE - HISTONE H2A]			264906, 264907, 264908, 264634

1243	79778458 (2485, 2486)	Novel Protein sim. GBank gi 3355671 emb CAA19971  - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 264909
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gi 2970846 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gi 4586338 dbj BAA76357.1  - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gi 3531849 emb CAA20805  - (AL031541) putative phenylalanine-RNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264836, 264557, 264564
1247	80064831 (2493, 2494)	Novel Protein sim. GBank gi 2821884 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank gi 1352403 sp P09467 F16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264258, 28331826, 264106, 264508, 264907, 264828, 265009, 60433356, 264757, 264758, 21808754, 285010, 265011, 285018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gi 2791407 emb CAA16001  - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]		transport	264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2499, 2500)	Novel Protein sim. GBank gi 112785 sp P05100 3MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE 1 (3-METHYLADENINE-DNA GLYCOSYLASE 1, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	79850448 (2501, 2502)				264909
1252	79458087 (2503, 2504)				264683, 263978
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gi 5670176 gb AAD46616.1 AF16131 - (AF161317) NRAMP manganese transport protein MntA [Salmonella typhimurium]		UNCLASSIFIED	glycoprotein
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gi 103160 pir J22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21906787, 55811957, 264892, 264556, 264639
1255	79169728 (2509, 2510)				264638
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gi 2985353 emb CAA04608.1  - (AJ001206) pepZ [Streptomyces coelicolor]		UNCLASSIFIED	60432289, 264800, 264605, 264764, 264687, 264769, 264689, 27486265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gi 3193306 (AF089300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)				
1259	80166012 (2517, 2518)				264602, 263978
1260	80084608 (2519, 2520)				264906, 264448, 264908
					264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gij5689511[dbj BAA83039.1] - (AB029010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - cadherin	29331824, 264906, 264809, 264768, 264769, 264689, 264693, 264639, 18108384, 264563
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gij95100[pir S21334 - hypothetical protein 4 - Agrobacterium tumefaciens]	UNCLASSIFIED	264634
1263	20710997 (2525, 2526)	Novel Protein sim. GBank gij3550958 (AF004840) - CDO [Rattus norvegicus]	struct	264602
1264	80083386 (2527, 2528)	Novel Protein sim. GBank gij1085002[pir S55056 - Mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans]	UNCLASSIFIED	264634
1265	80253578 (2529, 2530)	Novel Protein sim. GBank gij1085002[pir S55056 - Mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans]	UNCLASSIFIED	264563
1266	79914604 (2531, 2532)	Novel Protein sim. GBank gij1085002[pir S55056 - Mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans]	UNCLASSIFIED	264768, 264836, 264838, 264567
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gij1085002[pir S55056 - Mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans]	transport	264259, 21908754, 264369
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gij4886445[emb CAB43370.1] - (AL050269) hypothetical protein [Homo sapiens]	UNCLASSIFIED	18108388, 22278995, 56994075, 60424269, 29331827, 264109, 264512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87168559, 264600, 265018, 265019, 264369, 264688, 21908767, 265020, 52644150, 264691, 33657023, 33657348, 18108374, 264556, 18108385, 60432113, 22279002, 264488
1269	79821946 (2537, 2538)	Novel Protein sim. GBank gij3334791[emb CAA19939] - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]	UNCLASSIFIED	264508, 264905, 264906, 264687, 264693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gij2851634[sp Q50591 Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01]	dehydrogenase	265010, 264601
1271	76840498 (2541, 2542)	Novel Protein sim. GBank gij1655665[emb CAB03731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]	ATPase associated	35696052, 264908
1272	79462878 (2543, 2544)	Novel Protein sim. GBank gij1655665[emb CAB03731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]	UNCLASSIFIED	264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gij1655665[emb CAB03731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]	UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)	Novel Protein sim. GBank gij1123726[sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.9)]	UNCLASSIFIED	264905, 264908, 264909, 264769
1275	20730763 (2549, 2550)	Novel Protein sim. GBank gij1123726[sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.9)]	eph	264602
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gij2129478[pir S51939 - chitinase [EC 3.2.1.14] precursor - beet]	UNCLASSIFIED	264369
1277	20438195 (2553, 2554)	Novel Protein sim. GBank gij1175473[sp P44555 YAAJ_HAEIN - HYPOTHETICAL PROTEIN H10183]	UNCLASSIFIED	264556
1278	11088365 (2555, 2556)	Novel Protein sim. GBank gij1175473[sp P44555 YAAJ_HAEIN - HYPOTHETICAL PROTEIN H10183]	UNCLASSIFIED	264603
1279	21638756 (2557, 2558)	Novel Protein sim. GBank gij1929513 (U64318) - ATP synthase subunit beta [Mycobacterium thermorescens]	synthase	264605
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gij4938504[emb CAB43862.1] - (AL078465) putative protein [Arabidopsis thaliana]	struct	263976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gji1136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	29331825, 29331828, 264766, 83373044
1282	87537885 (2563, 2564)	Novel Protein sim. GBank gij3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gij3281721 (emb)(CAB07057) - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20636325 (2567, 2568)	Novel Protein sim. GBank gij3929022 (AF057696) - LspB [Haemophilus ducreyi]			264604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gij417154 (sp)P33126 (HS82_ORYSA - HEAT SHOCK PROTEIN 82)	Contains protein domain (PF00183) - eph		264766, 264688, 263967
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gij2078004 (emb)(CAB08451) - (Z95207) gorA [Mycobacterium tuberculosis]	reductase		264605, 264639
1287	80417530 (2573, 2574)			UNCLASSIFIED	265011, 264602, 264766, 264687, 264769, 264688, 18108370, 264638, 18108385, 264563
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gij5353510 (gb)AAD42161.1 (AF08891) - (AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - collagen C1q domain		35686052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 33657402, 264595, 264758, 265011, 265019, 264760, 18108351, 264681, 264784, 264288, 264685, 264766, 264687, 264768, 264789, 265020, 265021, 264534, 264692, 18108370, 264628, 18108374, 35688423, 264555, 264556, 264557, 264558, 18108385, 264564, 264566, 264567, 264486, 18108391
1289	11813647 (2577, 2578)	Novel Protein sim. GBank gij116995 (sp)P46023 (GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR)	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	UNCLASSIFIED	264637
1290	19526027 (2578, 2580)	Novel Protein sim. GBank gij2072674 (emb)(CAB08305) - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	Im7	264563
1291	80470266 (2581, 2582)	Novel Protein sim. GBank gij1835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Helicases conserved C-terminal domain	helicase	265007, 265008, 264769
1292	84723316 (2583, 2584)	Novel Protein sim. GBank gij2129173 (pirl)F64453 - oxalacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript factor	264082, 264259, 29331822, 29331824, 264508, 264908, 264909, 264512, 265008, 265009, 264591, 265018, 264369, 264288, 264686, 264768, 264693, 18108374, 264632, 56182323, 264639, 83373044, 22278002, 264482, 264563
1293	80067538 (2585, 2586)	Novel Protein sim. GBank gij2129173 (pirl)F64453 - oxalacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		UNCLASSIFIED	265008, 55812038, 264369, 264556
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gij5441778 (emb)(CAB46803.1) - (AL096811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]	biolindap		264602, 264605, 264760, 18108351, 264688, 33657023, 264559
1295	11666651 (2589, 2590)		dehydrogenase		264689

1296	11687904 (2591, 2592)	Novel Protein sim. GBank			UNCLASSIFIED	264591, 264639
1297	79839300 (2593, 2594)	gl14982191[gb]AAD36686.1(AE00180 - (AE001805) DNA-directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01357) - 5'-3' exonuclease		polymerase	264693
1298	94239506 (2595, 2596)	Novel Protein sim. GBank gl1943770 (U97191) - F53F10.1 gene product [Caenorhabditis elegans]		struct		18108348, 265017
1299	80255378 (2597, 2598)	Novel Protein sim. GBank gl13445181 (AC005498) - R31665_2 [Homo sapiens]				264488, 264906, 264908, 22278002, 264566
1300	80084867 (2599, 2600)	Novel Protein sim. GBank gl14062973[gb]BAA36204.1 - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]	Contains protein domain (PF01352) - KRAB box	transcriptfactor		264605
1301	17939614 (2601, 2602)			UNCLASSIFIED		264906
1302	95416198 (2603, 2604)					85658542, 265020
1303	9684121 (2605, 2606)					264908
1304	79377196 (2607, 2608)			UNCLASSIFIED		264508
1305	19905999 (2609, 2610)					264566
1308	13069230 (2611, 2612)	Novel Protein sim. GBank gl13242273[emb]CAB070171 - (Z92669) hypothetical protein Rv0236c [Mycobacterium tuberculosis]		UNCLASSIFIED		264636
1307	82201029 (2613, 2614)	Novel Protein sim. GBank gl1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120	reductase		264907, 264592, 264764
1308	21426814 (2615, 2616)	Novel Protein sim. GBank gl1958191[pir]S16298 - ferric enterobactin transport protein fepC - Escherichia coli		transport		264555
1309	79263011 (2617, 2618)	Novel Protein sim. GBank gl15458220[emb]CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED		264906, 18108354
1310	20466319 (2619, 2620)					264605
1311	87613142 (2621, 2622)					35696288, 29331827, 264908, 265008, 264764, 264766, 264688, 21908787, 21908769, 35695917, 264691, 264693
1312	88061720 (2623, 2624)	Novel Protein sim. GBank gl14455118[gb]AAD21084 - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00066) - Zinc finger, C2H2 type	dna_rna_bind		22278995, 22278998, 22278998, 264805, 264908, 265011, 265017, 285019, 264887, 21906768, 265020, 265021, 33657023, 22279002, 264584
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gl14929733[gb]AAD34127.1(AE151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - Ribosomal protein S16	ribosomalprot		22278996, 22278999, 264259, 20281099, 29146498, 264508, 264908, 66712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21908767, 29148627, 21906768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22278000, 264563, 18108390
1314	56928053 (2627, 2628)					264693
1315	84357192 (2629, 2630)	Novel Protein sim. GBank gl12589223 (AF026565) - ring finger protein [Mus musculus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept		264691

1316	95361609 (2631, 2632)	Novel Protein sim. GBank glij5689407[dbj BAA82987.1] - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181886, 20281171, 28331822, 29331824, 60424269, 29331825, 35896052, 5284045, 264591, 60432229, 265018, 265019, 55811150, 56181562, 21906765, 21906767, 21906768, 35895917, 60170815, 33657023, 65274620, 33857109, 35895763, 35895855, 18108387, 87168518, 60432113, 22278002, 264584
1317	88055187 (2633, 2634)	Novel Protein sim. GBank glij4836757[gb AAD30541.1]AF13491 - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264093, 264806, 264908, 284369, 284884
1318	95322893 (2635, 2636)	Novel Protein sim. GBank glij4680204[gb AAD27567.1]AF114171 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108382, 56182323, 18108385, 22279000
1319	84238546 (2637, 2638)				264808, 264909, 265008, 265008, 264592, 265019, 264766, 56181562, 18108368, 284628, 264829, 18108377, 284636
1320	86603587 (2639, 2640)	Novel Protein sim. GBank glij4240183[dbj BAA74870.1] - (AB020854) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35896288, 55812038, 265018, 21906768, 265020, 263978, 22278002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank glij4886505[emb CAB43377.1] - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00851) - BTB/POZ domain	transcriptfactor	60432049, 29331828, 264907, 284808, 264909, 264910, 55812038, 264601, 264762, 264764, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank glij5262591[emb CAB45736.1] - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331828, 264908, 265020, 33657023, 264693, 264404
1323	84845931 (2645, 2646)	Novel Protein sim. GBank glij5459516[dbj BAA82407.1] - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56894075, 264259, 29331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21908766, 21908787, 35895917, 265020, 264693, 65274781, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank glij5031717[ref NP_005704.1]pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278996, 22278998, 29331828, 264905, 264607, 29331830, 264808, 264510, 265008, 264595, 264759, 21908754, 285018, 264288, 264768, 264769, 21906768, 265022, 18108376, 264631, 264632, 264634, 264636, 264638, 264593, 264564, 264565, 264566
1325	94847471 (2649, 2650)	Novel Protein sim. GBank glij3284501 (U64857) - similar to the DPTUKunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35898288, 264805, 264806, 264907, 264908, 264909, 264910, 264593, 33857402, 264758, 85658542, 264760, 264768, 264769, 264691, 35898423
1326	87316288 (2651, 2652)	Novel Protein sim. GBank glij1397275 (U61947) - C08G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635

1327	95322897 (2653, 2654)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 264091, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264805, 56182435, 264112, 265008, 285009, 21906754, 285010, 285011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21906767, 21906769, 29148629, 265020, 284690, 264691, 264692, 264693, 263967, 33857109, 33657182, 27486262, 33657349, 18108370, 18108374, 55810764, 35695855, 264634, 58182323, 83373044, 87188518, 60432113, 22279000, 22279002, 264563, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	264488, 22278997, 29331828, 264595, 18108351, 264766, 22279002, 264482, 264567
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gi 4678224 gb AAD26969.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gi 437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264555, 264558, 56526488
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi 4589586 dbj BAA76815.1  - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 50170831, 264448, 264686, 21906765, 55811957, 265020, 33657023, 33657109, 263973, 55811576, 35696423, 35695855, 56182323
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gi 5459516 dbj BAA82407.1  - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52644045, 58182435, 284510, 21906754, 87168559, 265018, 265019, 264448, 264288, 264389, 264688, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	88098476 (2665, 2666)	Novel Protein sim. GBank gi 5689527 dbj BAA83047.1  - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433356, 60433438, 55812038, 265010, 284639, 56526488
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi 2662536 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]		phosphatase	264905
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gi 4240285 dbj BAA74921.1  - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21906754, 87168559, 265017, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 33657109, 27486264, 18108374, 264558, 264638, 264557, 60170394, 264559, 18108385, 264563



1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi 465445 sp P33485 VNUA_PRVKA - PROBABLE NUCLEAR ANTIGEN			UNCLASSIFIED	264509, 264905, 264512, 264764, 264693, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi 568947 dbj BAA83019.1  - (AB028990) KIAA1067 protein [Homo sapiens]			UNCLASSIFIED	56182575, 56994075, 22278989, 22278989, 264092, 264259, 60432289, 29331826, 264906, 264908, 264909, 264112, 265008, 265009, 60433356, 55812038, 33657084, 265011, 265017, 265018, 265019, 264682, 264448, 264683, 264369, 264688, 264689, 21906766, 21906769, 265020, 264691, 27486281, 20281069, 18108379, 55811576, 35695855, 56182323, 60432113, 22279002, 264587
1338	80366114 (2675, 2676)				UNCLASSIFIED	29331822, 265010, 264268, 264689, 18108370, 35695855
1339	80248231 (2677, 2678)	Novel Protein sim. GBank gi 1176422 (U43194) - rhophilin [Mus musculus]			UNCLASSIFIED	35696052, 264909, 264688, 264556, 264558
1340	89316311 (2678, 2680)					264905, 264907, 87168559, 264764
1341	86107485 (2681, 2682)					264681, 264685, 264686, 264692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi 5019564 emb CAB44507.1  - (AL035542) dJ994E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Contains protein domain (PF00001) - tm7 7 transmembrane receptor (rhodopsin family)			264629
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi 4557543 ref NP_001384.1 pECM2 - extracellular matrix protein 2	Contains protein domain (PF00560) - struct Leucine Rich Repeat			264910, 264686, 264534
1344	20562559 (2687, 2688)					263978
1345	91225546 (2689, 2690)	Novel Protein sim. GBank gi 2144101 p p 55210 - litteroxylate carrier - rat (fragment)		glycoprotein		264909, 60170394
1346	80255717 (2691, 2692)	Novel Protein sim. GBank gi 3881052 emb CAA19523  - (AL023843) predicted using GeneFinder, similar to serine/threonine kinase: cDNA EST yk246a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk246a12.5 comes...	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain			22278989, 264907, 264681, 264685, 264689, 265020, 264693, 22279000, 22279002, 264568
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi 4504379 ref NP_003858.1 pHG38 - orphan G protein- coupled receptor HG38	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat	glycoprotein		264908, 264908, 264909, 265008, 264910, 265011, 265017, 264764, 264768, 264767, 264769, 264831, 264634, 264638, 264567, 264486
1348	97352335 (2695, 2696)	Novel Protein sim. GBank gi 3399720 dbj BAA32100  - (AB010999) peptidylarginine deiminase type IV [Rattus norvegicus]		UNCLASSIFIED		264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22279002, 264486

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gii2144101 pir  55210 - l(ricarboxylate carrier - rat (fragment))		UNCLASSIFIED	52646842, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265008, 264512, 264910, 60170831, 264591, 60433438, 264757, 21906754, 265017, 265018, 264605, 264760, 264762, 264288, 264766, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265020, 264534, 264691, 264692, 33657023, 264693, 33657348, 18108374, 18108376, 35696423, 60170394, 22279000, 22279002, 264563, 264564
1350	87093136 (2699, 2700)			UNCLASSIFIED	52646842, 264259, 29331825, 264908, 264511, 264604, 264288, 21906769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22279002, 264486
1351	87381327 (2701, 2702)	Novel Protein sim. GBank gii4887239 gb AAD32246.1  - (AF064584) BAW protein [Fugu rubripes]		UNCLASSIFIED	264906, 264907, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gii2144101 pir  55210 - l(ricarboxylate carrier - rat (fragment))		UNCLASSIFIED	35696286, 60424269, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264596, 55811386, 265011, 264605, 55811150, 264762, 264784, 264766, 52644229, 56181562, 35695917, 265022, 33657023, 264693, 35695783, 60431528, 264629, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264583, 264564, 264566
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gii4889108 gb AAD27763.1 AF07703 - (AF077030) hypothesized 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 264908, 265008, 33657402, 21906754, 265011, 37188559, 264684, 264369, 264769, 264689, 21906765, 21906768, 52644150, 33657023, 264692, 264693, 18108374, 83373044, 87168518, 22279000
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gii1469199 dbj BAA09487  - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278997, 264259, 66714117, 264511, 21906754, 265010, 264769, 264689, 21906765, 21906768, 21906769, 264532, 27486262, 264629, 264638, 264556, 264638, 264639, 264482, 264484

1356	85313981 (2711, 2712)	Novel Protein sim. GBank gij113865 (U40342) - ninein [Mus musculus]		struct	18108397, 22278995, 22278996, 22278998, 264094, 28331828, 264905, 265006, 265007, 265008, 265010, 265017, 265018, 265019, 264764, 18108354, 264689, 21806785, 265022, 18108364, 35898423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gij897693jemb CAA90330  - (Z50028) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		264259, 29331822, 29331825, 264510, 87186559, 265018, 264448, 264288, 21806785, 21806786, 21806788, 265021, 264693, 18108376
1358	38719453 (2715, 2716)	Novel Protein sim. GBank gij556219 (L36831) - transcription regulator [Mus musculus]			264757
1359	87771643 (2717, 2718)			UNCLASSIFIED	264907, 264909, 264510, 264511, 264512, 18108351, 264764, 264534, 33657023, 18108374, 264634, 264635, 264638, 264639, 18108385, 264488, 264587
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gij2598282jemb CAA75612  - (Y15417) acetate-CoA ligase [Coprinus cinereus]		synthase	60432289, 264605
1361	87583527 (2721, 2722)	Novel Protein sim. GBank gij5689443jdbj BAA83005.1  - (AB028976) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00338) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	35896286, 22278997, 22278999, 264258, 29331828, 264508, 264509, 264905, 264907, 264908, 265007, 265009, 33109854, 21806754, 87188474, 265011, 264761, 264683, 264288, 264766, 264789, 264689, 21806788, 265020, 265021, 33657023, 55811576, 35898423, 264634, 60432113, 22279002, 264482, 264488
1362	85287961 (2723, 2724)	Novel Protein sim. GBank gij5689411jdbj BAA82989.1  - (AB028960) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	eph	56182575, 56181686, 60432049, 264259, 29331822, 56182181, 29331827, 35898052, 28331828, 264905, 264906, 264908, 264595, 55812038, 85858542, 55811150, 264681, 264288, 264389, 56181582, 60431528, 55810764, 35898423, 60431850, 264558, 264488, 28331826, 264907, 264687, 264689, 264693
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gij1130484 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	
1364	88178468 (2727, 2728)				60432289, 60433356, 60433438, 87188559, 264603, 18108351, 21806786, 35898423, 60432113
1365	83003108 (2729, 2730)	Novel Protein sim. GBank gij4589582jdbj BAA76803.1  - (AB023176) KIAA0959 protein [Homo sapiens]		oncogene	264766
1366	87003282 (2731, 2732)	Novel Protein sim. GBank gij1084944jpirj J54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	265007

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gjl4884088[emb]CAB43240.1 - (AL050018) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - UNCLASSIFIED SAND domain	264488, 52846842, 52846385, 22278995, 56994075, 35896286, 22278996, 22278998, 22278999, 284259, 29331824, 66714117, 29331825, 60432289, 35696052, 264905, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265009, 60170831, 33657402, 55812038, 21906754, 265011, 87188559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264369, 264888, 264767, 264688, 21906765, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264534, 60170815, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264635, 264555, 264637, 264556, 52844332, 60170394, 264558, 18108381, 18108385, 56526486, 22279000, 264583, 264587
1368	94320078 (2735, 2736)	Novel Protein sim. GBank gjl464561[sp]P35289[RB15_RAT RAS-RELATED PROTEIN RAB-15]	Contains protein domain (PF00071) - Ras family oncogene	264259, 29331822, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87168559, 264600, 264601, 264760, 264764, 264765, 264768, 52644229, 264689, 35695917, 265020, 265021, 264631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264566, 264488, 264587, 21906764, 21906768, 264555, 264638, 264559, 264567
1369	86634033 (2737, 2738)	Novel Protein sim. GBank gjl2062702 (U90550) - butyrophilin [Homo sapiens]	UNCLASSIFIED	265008, 60432229, 60433356, 33657084, 21906764, 21906768, 264555, 264638, 264559, 264567
1370	95316910 (2739, 2740)	Novel Protein sim. GBank gjl5031823[ref]NP_005823.1[pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2]	potassium_channel	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264766, 264768, 21906767, 35695917, 18108362, 35696423, 264632, 264635, 264636, 264555, 264638, 264558, 264639, 18108385, 65274727, 264404, 264563, 264568, 264488
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gjl5032203[ref]NP_005714.1[pTSPA - tetraspan 5]	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins glycoprotein	22278996, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695855, 264558, 22279002, 264583

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gll840708[dbj BAA09334] - (D50685) trans-sialidase [Trypanosoma cruzi]		collagen	263978
1373	80499421 (2745, 2746)			UNCLASSIFIED	264769, 21906765, 21906767, 22278989, 264691, 264910, 55812038, 265010, 264681, 264684
1374	95087036 (2747, 2748)	Novel Protein sim. GBank gll111876[pir JC1241 - beta-interferon-induced protein - rat]		interferon	264907, 264510, 265007, 264512, 265008, 60432229, 264689, 65274781, 264555, 264558, 264557, 83373044, 80432113
1375	84236842 (2749, 2750)	Novel Protein sim. GBank gll5649176[gb AA03500.2] - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52844507, 52845158, 52846842, 52846365, 56182575, 56181686, 22278988, 56994075, 35996286, 22278987, 22278988, 22278989, 264259, 29331822, 52845080, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33658970, 264905, 264509, 264908, 264907, 264907, 264908, 29331830, 264908, 265006, 264511, 265007, 265008, 265009, 33657402, 60433356, 52646317, 33109954, 33657084, 52844286, 87188474, 87168559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264784, 264288, 264389, 264788, 52844229, 21906765, 21906766, 21906767, 21906768, 21908789, 55811957, 35695917, 265020, 265021, 52844150, 33657023, 264693, 65274620, 52845129, 33657109, 27486261, 33657349, 27486265, 35695783, 18108376, 55810764, 35698423, 35695855, 264830, 264631, 264634, 264636, 264555, 264638, 18108385, 87168518, 80432113, 22278000, 22279002, 264563, 264564, 264566, 264567
1376	87398050 (2751, 2752)	Novel Protein sim. GBank gll138350[sp P28888 VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED	264768, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35696052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264809, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 58528486, 265010, 265011, 264600, 264563, 264762, 264564, 264565, 264764, 264486, 264768
1377	88984242 (2753, 2754)	Novel Protein sim. GBank gll1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - ATPase associated E1-E2 ATPase	ATPase_associated	29331824, 264591, 265019, 264686, 264768, 55811957, 264693, 22278002

1378	87595071 (2755, 2756)	Novel Protein sim. GBank gij4107015[dbj BAA36293] - (AB001772) PEM-5 [Ciona savignyi]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264369, 264288, 29148627, 55811957, 264691, 18108366, 33657109, 18108368, 264635, 263991, 18108385
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gij3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627962 (2759, 2760)	Novel Protein sim. GBank gij4837737[gb AAD30682.1] - (AF096834) germ cell specific Y-box binding protein [Homo sapiens]	nud_recpt		264510, 264512, 265008, 264288, 264564
1381	88179656 (2761, 2762)	Novel Protein sim. GBank gij4731580[gb AAD28508.1 AF12538 - (AF125384) L82A [Drosophila melanogaster]	UNCLASSIFIED		87168559, 265017, 264628, 22279002
1382	94847576 (2763, 2764)		UNCLASSIFIED	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433356, 85658542, 265017, 265018, 264885, 264768, 21906766, 35695917, 33657023, 27486261, 27486262, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)		UNCLASSIFIED		18108396, 264692
1384	86915895 (2767, 2768)		UNCLASSIFIED		264488, 264508, 264509, 264905, 264906, 264908, 264909, 264511, 264512, 264910, 264760, 18108351, 264768, 264769, 35695855, 264630, 264638, 264555, 264638, 264483, 264564, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gij2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]	UNCLASSIFIED		35696052, 5581386, 264888, 21906765, 265020, 33657023, 18108385
1386	91013048 (2771, 2772)	Novel Protein sim. GBank gij2384910 (AF022982) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]	Inf		60432289, 29331828, 264906, 264907, 56182435, 265011, 264881, 60170615, 33657023, 83373044, 264566
1387	87797958 (2773, 2774)	Novel Protein sim. GBank gij4160304[emb CAA10600] - (AJ132192) HSI binding protein 3 [Mus musculus]	UNCLASSIFIED		264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gij4895164[gb AAD32753.1 AC007231] putative disease resistance protein [Arabidopsis thaliana]	glycoprotein		65274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264692, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22279000

1388	91256016 (2777, 2778)	Novel Protein sim. GBank gij5689387jdbj BAA82977.1  - (AB028948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29146499, 264906, 66712502, 55812038, 265017, 265018, 265019, 18108351, 264369, 21908765, 21908766, 21908767, 21908768, 265020, 265021, 264692, 33657023, 33657349, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 83373044, 22279000, 264583, 284584, 52645156, 52646365, 264259, 52645080, 29331825, 29331826, 264906, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181582, 52644229, 21908765, 21908769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486261, 27486284, 65274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1389	94111916 (2778, 2780)	Novel Protein sim. GBank gij3702285 (AC005763) - R33083_1 [Homo sapiens]	peptidase		29331826, 29331828, 29331830, 264448, 264288, 33657023, 18108385, 264555, 264556, 83373044
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gij1346910 sp P28650 PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP-ASPARTATE LIGASE) [Mus musculus]	Contains protein domain (PF00709) - Adenylosuccinate synthetase		52646842, 65274572, 22278994, 22278995, 35698286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656870, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21908764, 21908767, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486282, 27486285, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264568, 18108391, 264763, 264631
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gij726286 (U22394) - mSin3A [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	
1393	80408472 (2785, 2786)			UNCLASSIFIED	264629
1394	15028819 (2787, 2788)			UNCLASSIFIED	265009, 18108381
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gij2274845 dbj BAA21534  - (D88481) N-WASP [Rattus rattus]		UNCLASSIFIED	

1396	95363253 (2791, 2782)	Novel Protein sim. GBank gij2135904 pir  54810 - pH-EIF1 - human			22278997, 22278999, 264259, 29331825, 60432289, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433356, 265010, 264602, 265017, 265018, 265019, 18108354, 52644229, 18108358, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 18108368, 18108374, 56182323, 18108385, 264563, 264567, 35696286, 264907, 66712502, 264510, 35695917, 264892, 264693, 35696423
1397	87631317 (2793, 2794)		UNCLASSIFIED		
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gij5420389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]			264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 87168474, 265018, 265019, 264682, 264768, 21906767, 265020, 33657023, 27486261, 55811576, 264632, 264639, 83373044, 87168518, 22279002
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gij2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F.5.2 IN CHROMOSOME III	UNCLASSIFIED		264768, 18108370, 264555, 264557
1400	95419064 (2799, 2800)	Novel Protein sim. GBank gij283920 pir  S27839 - tensin - chicken	Contains protein domain (PF00017) - VHS domain Src homology domain 2		56182575, 22278994, 22278997, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264288, 264685, 264687, 56181562, 264769, 21906768, 21906767, 55811957, 264691, 264692, 264628, 264629, 55811578, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226378 (2801, 2802)	Novel Protein sim. GBank gij3256185 emb CAA15485  - (AL008635) dJ510H16.1 [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00790) - VHS domain	55274572, 60432289, 264909, 264758, 264768, 21906769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gij1515427 (U57523) - nel homolog [Homo sapiens]	tgf	Contains protein domain (PF00008) - EGF-like domain	264905, 264907, 264908, 264909, 264112, 264693, 33657109, 264634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gij5262615 emb CAB45747.1  - (AL080156) hypothetical protein [Homo sapiens]			55274572, 66712502, 265017, 264448, 264288, 21906765, 21906769, 264693, 55811576, 65274791, 60432113
1404	90935393 (2807, 2808)		UNCLASSIFIED		55274572, 22278998, 29331822, 29331828, 66712502, 265008, 60433438, 265017, 264693, 18108385



1405	95095068 (2809, 2810)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]			264488, 56994075, 35698286, 29331822, 28331824, 29331826, 29331828, 35698052, 264508, 264908, 264907, 264908, 264510, 264511, 264910, 33857402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33857023, 33857109, 264628, 264634, 83373044, 22279002, 284563, 284482, 264486, 264567, 264907, 264605
1406	87612369 (2811, 2812)	Novel Protein sim. GBank gi 624076 gb AAC86425.1  - (U42580) contains Pro-rich P <sub>x</sub> motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramoecium bursaria Chlorella virus 1]	collagen		
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gi 2827886 (AF015037) - endooligopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35698286, 22278999, 264094, 264259, 68714117, 29331826, 29331827, 29331828, 29146488, 284107, 264908, 265006, 265008, 264910, 60433438, 285011, 285017, 18108351, 264448, 264288, 264688, 21908765, 21908769, 264692, 33857109, 18108370, 264828, 263972, 18108374, 35698423, 55811576, 264631, 284557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gi 2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - oncogene EGF-like domain		264488, 264489, 35698286, 264109, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264885, 264766, 264687, 264689, 21908767, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 58182323, 264639, 264563, 264564, 264565, 264566, 264567, 264693
1409	66844385 (2817, 2818)	Novel Protein sim. GBank gi 2662165 dbj BAA23714  - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gi 2483780 sp Q60994 ACR3 MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)	Contains protein domain (PF00356) - complement C1q domain		29331826, 264112, 264512, 265008, 265010, 264601, 264686, 264788, 21908767, 263974, 264631, 264566

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gij312155 sp P91343 YM3M, CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	22278995, 22278997, 22278999, 29331822, 60432289, 29331828, 264907, 265017, 265019, 264682, 21906767, 21906768, 21906769, 265020, 264690, 264691, 33657023, 33657109, 27486284, 264628, 263972, 264634, 264558, 18108385 264757
1412	84390919 (2823, 2824)			UNCLASSIFIED	
1413	95416559 (2825, 2826)	Novel Protein sim. GBank gij387812 emb CAA94370  - (Z70310) predicted using Genefinder. Similarly to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:TD1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	homeobox	56994075, 29331822, 35696052, 29331828, 29331830, 264909, 52844045, 264510, 52844296, 85658542, 87168474, 265017, 265018, 264681, 264687, 21906768, 35695917, 265020, 52644150, 264692, 263987, 27486284, 35695763, 264639, 18108387, 264566
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gij3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264682, 264683, 265022, 264636
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gij1871187 (U90439) - unknown protein (Arabidopsis thaliana)			52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 66712502, 29331830, 52644045, 264113, 264511, 33657402, 264757, 21908754, 55811386, 265017, 265018, 265019, 264781, 264683, 264369, 264288, 264686, 264689, 21906768, 21906767, 29148627, 21906769, 55811957, 265020, 265021, 264690, 33657023, 65274620, 52645129, 27486262, 27486284, 60431528, 264629, 35695855, 56182323, 264559, 60432113, 264404, 22278002, 264482

1416	94325977 (2831, 2832)	Novel Protein sim. GBank gij5106557jgb/AAAD39749.1IAF12305 - (AF123052) MLL septin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - struct Cell division protein	18108392, 18108394, 18108397, 18108398, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29146498, 264905, 264907, 264908, 264828, 264809, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87188474, 265010, 265011, 87168559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264682, 264683, 264766, 52644229, 264688, 264689, 21906765, 21906766, 21906767, 29146627, 21906768, 55811957, 29146629, 285020, 52644150, 18108361, 33657023, 18108362, 18108368, 264628, 18108370, 264628, 18108374, 18108376, 55811576, 65274791, 264634, 264636, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000 264107, 264448
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gij4958935jdbjBAA78095.1I - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]	ATPase-associated	
1418	87594276 (2835, 2836)		UNCLASSIFIED	264259, 264908, 265010, 52644229, 21906764, 21906768, 264690, 264639, 18108388
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gij2072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]	struct	264259, 60432289, 265006, 87168474, 264289
1420	87298628 (2839, 2840)	Novel Protein sim. GBank gij517442jreilNP_008023.1pCPNE - copine VI (neuronal) (Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D87355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...	ATPase-associated	29331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gij3876090jembjCAA93459.1I - (Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D87355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...	kinase	18108358, 18108398, 18108397, 21906766, 18108398, 21906767, 56162575, 21906768, 21906769, 56181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 29331822, 56162181, 29331824, 66714117, 29331825, 33657109, 29331826, 27488281, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 66712502, 283972, 55811576, 35696423, 35695855, 264512, 265007, 60431850, 60432229, 60431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906754, 55811388, 87168518, 87168558, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264488, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gjl450939[le]NP_000928.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)			56994075, 35698288, 87168559, 55811957, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)				264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gjl437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00820) - RhoGAP domain	UNCLASSIFIED	29331822, 29331825, 29331827, 29146498, 264905, 264906, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264766, 264887, 21906765, 21906766, 21906767, 21906768, 29148627, 55811957, 29148629, 265021, 264691, 264692, 56526486, 22279002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gjl100798[pil]S14959 - proline- rich protein - wheat		UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gjl2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P23386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 60424178, 35698286, 22278897, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21806754, 265018, 264288, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gjl5916074[gb]AAD45616.1 AF06194 - (AF061943) prolate- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 56994075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 265008, 265009, 264683, 264288, 18108354, 21906765, 21906768, 29148629, 33657023, 18108374, 35695855, 83373044, 22279002, 264564
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gjl138350[sp]P28968[VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		glycoprotein	56181686, 264259, 264907, 265007, 265009, 264595, 265010, 264688, 65274620, 264629, 65274791, 22279002, 264566
1429	87888689 (2857, 2858)			UNCLASSIFIED	264112, 264585, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gjl1181619[dbj]BAA11555] - (D82384) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 264593, 265018, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gjl5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gjl414787 (L18966) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148629, 263969
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gjl2460316 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	264882, 264691

1435	84708213 (2869, 2870)	Novel Protein sim. GBank gi 3870850 dbj BAA34789.1  - (AB015330) HRIHF2007 [Homo sapiens]			transcript factor	22278997, 22278998, 22278999, 60432048, 264259, 29331822, 29331824, 66714117, 29331826, 33656970, 264508, 264905, 66712502, 29331830, 284909, 265007, 265008, 264910, 265009, 60433356, 60433438, 264596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906787, 21906768, 21906769, 265020, 265021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108376, 55811578, 264636, 60170394, 56182323, 284559, 83373044, 87168518, 60432113, 22278000, 22278002, 264563, 264482, 264585, 263978, 264557, 264559
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gi 3183977 emb CAA39515  - (X56044) protein H19C [Mus musculus]			UNCLASSIFIED	
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22, CAEL - HYPOTHETICAL 32.0 KD PROTEIN C08F5.2 IN CHROMOSOME III			UNCLASSIFIED	
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gi 1805906 (AD000092) - hypothetical human serine-threonine protein kinase R31240.1 [Homo sapiens]		Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	kinase	264488, 264508, 264906, 264909, 264757, 264600, 264601, 264605, 264768, 264769, 264690, 33696423, 284558, 264563, 264566
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gi 3876299 emb CAA94892  - (Z71180) similar to BPTIKUNITZ inhibitor domain; cDNA EST EMBL:D88293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis...]		Contains protein domain (PF00450) - Serine carboxypeptidase	calhepsin	22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 284259, 60432048, 29331822, 29331824, 60432269, 29331826, 29331827, 29331828, 35696052, 33656970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265006, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811388, 265011, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 18108355, 264767, 21906766, 21906768, 21906769, 265020, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264638, 56182323, 83373044, 18108387, 87168518, 60432113, 22278000, 264486
1440	87423643 (2879, 2880)	Novel Protein sim. GBank gi 2662165 dbj BAA23714  - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			UNCLASSIFIED	264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

1441	85317662 (2881, 2882)	Novel Protein sim. GBank gij493956[emb]CAB11123.2] - (Z98551) predicted using hexExon: MAL3P6.28 (PFC0845c). Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe), C.elegans protein ZK287.5 (TR....	Contains protein domain (PF00646) - helicase F-box domain.	18108382, 264488, 263394, 264488, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 66714117, 29331826, 29331827, 29331828, 35696052, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264582, 264593, 33657402, 60433438, 264595, 264758, 21906754, 85658542, 87188474, 265010, 87168559, 264600, 264602, 265017, 264604, 265018, 264605, 264608, 264764, 264683, 264288, 264766, 264768, 264769, 52644228, 264689, 21908765, 21908766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 52844150, 264691, 264692, 33657023, 65274620, 33657109, 35695763, 264628, 18108370, 264628, 18108374, 55811576, 35696423, 65274781, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 56182323, 264558, 60170394, 264639, 264559, 83373044, 18108385, 18108388, 56526488, 22279000, 22279002, 264563, 264483, 264564, 264566, 264567, 264488
1442	83367491 (2883, 2884)	Novel Protein sim. GBank gij5103027[dbj]BAA78765.1] - (AB023419) mSox7 [Mus musculus]	transcript factor	264806, 265007, 264693, 264558
1443	87109935 (2885, 2886)	Novel Protein sim. GBank gij4887229[gb]AAD32244.1[AF150755] microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - spectrin repeat	52845080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gij3874447[emb]CAB02772] - (Z81039) predicted using GeneFinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...	UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 29331828, 264288, 35695917, 33657023, 264635, 60170394
1445	94990470 (2889, 2890)	Novel Protein sim. GBank gij2959886[emb]CAA11022] - (AJ222868) L-peritaxin [Mus musculus]	UNCLASSIFIED	264369
1446	85079268 (2891, 2892)	Novel Protein sim. GBank gij5081610[gb]AAD39464.1[AF135440] huntington yeast partner C [Mus musculus]		264369
1447	86945392 (2893, 2894)	Novel Protein sim. GBank gij5081610[gb]AAD39464.1[AF135440] huntington yeast partner C [Mus musculus]	Contains protein domain (PF01846) - FF domain	18108398, 35696286, 22278997, 66714117, 29331828, 265009, 264758, 265018, 264288, 21906766, 21906767, 264692, 264634, 264566
1448	94990477 (2895, 2896)	Novel Protein sim. GBank gij3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain	29331827, 264509, 264909, 265008, 264595, 18108357, 18108385, 264566, 264486

1449	87860858 (2897, 2898)				UNCLASSIFIED	66714117, 264906, 264908, 264591, 264601, 264764, 264632
1450	87456696 (2899, 2900)	Novel Protein sim. GBank gij1707074 (U80450) - MO1E11.2 [Caenorhabditis elegans]			UNCLASSIFIED	35696286, 35696052, 265008, 265009, 60170831, 33109954, 264883, 264889, 35696423, 35695855, 56526486
1451	87787970 (2901, 2902)	Novel Protein sim. GBank gij14160304[emb]CAA10600] - (AJ132182) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	29331826, 264683, 264693, 263978, 264630
1452	85692898 (2903, 2904)	Novel Protein sim. GBank gij2832906[dbj]BAA24608.1] - (D89340) dipeptidyl peptidase III [Rattus norvegicus]			peptidase	264681, 33657023, 264629
1453	86130434 (2905, 2906)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]			kinase	264510, 264768
1454	11204696 (2907, 2908)					264556
1455	87797896 (2909, 2910)				UNCLASSIFIED	29331822, 66714117, 29331825, 264805, 29331830, 265008, 265008, 265009, 265011, 265019, 18108351, 21908768, 33657109, 18108376, 264632, 56182323, 87188518
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gij729230[sp]P41004[CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3]			transport	22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 264107, 265017, 21906765, 21906766, 21906767, 21906769, 29148829, 18108370, 22278000
1457	80076900 (2913, 2914)	Novel Protein sim. GBank gij729230[sp]P41004[CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3]			UNCLASSIFIED	264107, 264566
1458	87800460 (2915, 2916)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 264102, 264107, 264110, 265009, 60432229, 265019, 265020, 263972, 263976, 264635, 22278002, 264566
1459	85360920 (2917, 2918)	Novel Protein sim. GBank gij5524667[gb]AAD44333.1[AF159356] Munc13-4 protein [Rattus norvegicus]	Contains protein domain (PF00168) - C2 domain		kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264786, 265021, 264692, 33657023, 33657109, 35695855, 264566
1460	95354602 (2919, 2920)				UNCLASSIFIED	29331822, 264591, 55811957, 264691, 264693, 65274620
1461	84741513 (2921, 2922)	Novel Protein sim. GBank gij1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate		gaba	22278997, 29331822, 35686052, 265009, 264758, 265017, 265018, 265019, 264780, 264369, 264687, 21906765, 21906768, 265022, 33657109, 27480261, 264555, 83373044
1462	87320218 (2923, 2924)				UNCLASSIFIED	264555, 264556
1463	88090605 (2925, 2926)	Novel Protein sim. GBank gij170466[emb]CAA66912] - (X98259) M-phase phosphoprotein 8 [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR)romalin Organization Modifier domain		struct	60432048, 264259, 29146499, 264906, 264907, 264512, 265017, 264763, 264768, 18108370, 18108374, 264636, 18108385, 18108398

1464	87620482 (2927, 2928)	Novel Protein sim. GBank gll3874447[emb CAB02772] - (Z81039) predicted using GeneFinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264569, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331825, 35696052, 20281100, 264905, 29331830, 264909, 265007, 33657402, 21906754, 265017, 265018, 264882, 264884, 264369, 264288, 264766, 21906765, 21906766, 21906767, 21906769, 35695917, 264691, 33657023, 264692, 35696423, 35695855, 264630, 264631, 264639, 264565
1465	87425192 (2928, 2930)	Novel Protein sim. GBank gll4589598[db BAA76821.1] - (AB023194) KIAA0977 protein [Homo sapiens]		glucanase	264488, 22278994, 56994075, 60432049, 264259, 56182181, 60432289, 29331827, 52844045, 264511, 265007, 265008, 264596, 55812038, 55811386, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 265021, 33657023, 33657182, 55811576, 264557, 18108382, 60432113
1466	87606227 (2931, 2932)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264512, 265017, 264689, 264558
1467	87614328 (2933, 2934)	Novel Protein sim. GBank gll4507241[ref NP_003137.1 pSSRP - structure specific recognition protein 1		struct	264683, 264636
1468	95342862 (2935, 2936)	Novel Protein sim. GBank gll4507241[ref NP_003137.1 pSSRP - structure specific recognition protein 1			22278998, 264758, 265018, 265019, 21906769, 265020, 33657109, 22279002
1469	79236174 (2937, 2938)	Novel Protein sim. GBank gll1906596 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 285009, 265010, 265011, 18108354, 18108365, 18108368, 18108374, 18108381, 18108382, 18108384, 18108388
1470	94990482 (2939, 2940)	Novel Protein sim. GBank gll5649170[gb AA043131.2 AF159092] syld709613 protein [Homo sapiens]		UNCLASSIFIED	18108394, 18108398, 56182575, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432229, 60433356, 264595, 80433438, 284758, 33109954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264369, 18108357, 264769, 18108358, 21906767, 21906769, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87168518, 60432113, 264404, 22279002, 264482, 264567, 264487
1471	87826842 (2941, 2942)	Novel Protein sim. GBank gll38761746[emb CAB01750] - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL: T01651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331822, 29331824, 29331825, 264828, 264803, 264689, 264693, 18108374, 55811576



1472	87756816 (2843, 2944)	Novel Protein sim. GBank gi 4680707 gb AAD27743.1 AF132988) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	264905, 18108351, 21906765, 264486
1473	87791609 (2845, 2946)	Novel Protein sim. GBank gi 3688780 (AF042180) - testis- specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - MHC Nucleosome assembly protein (NAP)		18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 66714117, 29331825, 29331826, 35696052, 264906, 264907, 56182435, 265007, 264758, 265018, 265019, 264760, 264764, 264288, 264685, 264686, 264768, 21908789, 55811957, 265021, 264691, 264693, 264629, 55811576, 264634, 264638, 56182323, 22279002, 264566, 264486
1474	85800389 (2847, 2948)	Novel Protein sim. GBank gi 2494890 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - struct WD domain, G-beta repeat		264488, 35695917, 35696286, 264692, 33657023, 264693, 33657109, 35696052, 264508, 264905, 264906, 264907, 264629, 264908, 264909, 35696423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264639, 264758, 60432113, 264604, 264605, 264565, 264566, 264764, 264488, 264685, 264768, 264681, 264682, 264288, 264566
1475	86871935 (2849, 2950)		Contains protein domain (PF00041) - Fibronectin type III domain	UNCLASSIFIED	
1476	87548855 (2951, 2952)	Novel Protein sim. GBank gi 4757752 ref NP_004684.1 pANGP - angiopoietin 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein	60424179, 56181686, 29331824, 60424269, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33657402, 264595, 264596, 55812038, 265011, 264601, 264762, 18108351, 264288, 264369, 264685, 264766, 264689, 55811857, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35696423, 264634, 264635, 264636, 60431850, 264555, 264638, 264557, 264639, 18108382, 18108388, 60432113, 22279002
1477	87774279 (2953, 2954)	Novel Protein sim. GBank gi 2498308 sp Q60870 DP1_MOUSE - POLYPOSI LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)		UNCLASSIFIED	264259, 264107, 264905, 265008, 265010, 265011, 264682, 264288, 265020, 265021, 263974
1478	11754412 (2855, 2856)				264686

1479	91640140 (2957, 2958)	Novel Protein sim. GBank gij5499741[gb]/AAD43978.1[AF15296] chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 66714117, 264906, 264907, 56182435, 265006, 60170831, 33657402, 264758, 33109954, 21906754, 265017, 265018, 264448, 264288, 264767, 264687, 52644229, 21906764, 264689, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 18108370, 60431528, 263976, 55811576, 264556, 264557, 60170394, 87168518, 264404, 22278000, 22279002, 264563, 264482
1480	94312412 (2959, 2960)	Novel Protein sim. GBank gij3550456[emb]/CAA06329.1[ (AJ005073)] Alix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35696286, 56994075, 22278998, 22278997, 22278998, 22278999, 264091, 264259, 35696052, 29146499, 264103, 264105, 264108, 264907, 52644045, 264112, 265007, 265008, 265009, 60433356, 60433438, 264598, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170815, 52644150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2861, 2862)	Novel Protein sim. GBank gij4836807[gb]/AAD30566.1[AF14679] PFT27 [Mus musculus]		MHC	265006, 265007, 265010, 18108374
1482	85320442 (2963, 2964)	Novel Protein sim. GBank gij4585372[gb]/AAD25403.1[AF12292] Wnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264908, 264910, 264758
1483	94115503 (2965, 2966)	Novel Protein sim. GBank gij535428 (U13736) - calmodulin- like protein [Plum salivum]	Contains protein domain (PF00036) - EF hand	struct	264259, 29331822, 52645080, 29331825, 29331826, 33656970, 29331830, 265007, 55812038, 33109954, 265017, 264288, 21906768, 21906769, 264636, 18108380, 87168518, 22279000
1484	94131544 (2967, 2968)	Novel Protein sim. GBank gij1911774[bbn]180090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 264259, 264107, 264909, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906766, 29148627, 33657023, 27486262, 18108374, 35696423, 83373044, 60432113
1485	80194441 (2869, 2970)	Novel Protein sim. GBank gij5360129[gb]/AAD42883.1[AF15511] NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264369, 265020, 18108374

1486	94125066 (2871, 2972)	Novel Protein sim. GBank gi 4589510 dbj BAA76780.1  - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	56182575, 22278999, 264908, 264907, 21908754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264568, 21908754, 264486
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gi 5019275 emb CAB44431.1  - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase [form XL-III] [Bos taurus]		synthase	
1488	87732028 (2975, 2976)	Novel Protein sim. GBank gi 5712131 gb AAD47379.1 AF120499 - (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	IgI	264686, 264768, 264688, 264692, 264693, 264509, 264908, 264907, 18108370, 264908, 264628, 264908, 264510, 265008, 264512, 265007, 265008, 265008, 264555, 264556, 264557, 264558, 264782, 264564, 264882
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gi 2497303 sp Q62786 FPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	21908767, 22278999, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35896423, 35895855, 265007, 265008, 265009, 83373044, 21908754, 56528486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87380127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21908767, 21908768, 55811957, 60170615, 33657109, 35895855, 264635, 60170394, 56528486, 22279002, 264583
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gi 295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gi 1656005 (U71205) - rti [Mus musculus]	Contains protein domain (PF00071) - Ras family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2885, 2886)	Novel Protein sim. GBank gij5689515[dbj BAA83041.1] - (AB029012) KIAA1089 protein [Homo sapiens]		UNCLASSIFIED	264488, 52846365, 65274572, 56182575, 22278994, 35896286, 56994075, 22278999, 60432049, 29331824, 29331828, 35696032, 264508, 264905, 264908, 52844045, 264909, 56182435, 265008, 265008, 265010, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264682, 264685, 264686, 52844229, 21906765, 21906766, 21906768, 21906769, 265020, 265021, 60170815, 52844150, 33657023, 18108364, 18108365, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 264629, 18108374, 52844332, 56182323, 87168518, 22279002, 264564, 264566, 264567
1494	87605265 (2887, 2888)	Novel Protein sim. GBank gij728832[sp P39189]ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF01352) - KRAB box	kinase	264907, 265009, 264769, 18108370, 55811576, 264639, 264565, 264488
1495	87605267 (2889, 2890)	Novel Protein sim. GBank gij4589588[dbj BAA76816.1] - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	22278997, 264259, 264906, 264907, 265008, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264566, 264486, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	35696286, 264906, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gij3874925[emb CAA92591] - (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:TO1018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene;...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264910, 264758, 265011, 264784, 264288, 264690, 264634, 264635, 56526486
1498	80834938 (2995, 2996)	Novel Protein sim. GBank gij728836[sp P39193]ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		oncogene	264488, 65274572, 29331822, 265017, 265018, 21906765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	86451589 (2997, 2998)	Novel Protein sim. GBank gij2570168 (U54556) - microfilament sheath protein SHP3 [Ulomomolus sigmodontis]		glucoamylase	263978, 264568
1500	80499386 (2998, 3000)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycopetide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	22278999, 264769, 18108379
1501	85795297 (3001, 3002)			UNCLASSIFIED	264559
1502	80205141 (3003, 3004)				264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264556, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gij3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989) [Homo sapiens]	Contains protein domain (PF00535) - Glycosyl transferases	transferase	29331822, 265007, 264369

1504	79540051 (3007, 3008)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264693	29331826, 35696052, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 55812038, 264758, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264566
1505	86102872 (3008, 3010)	Novel Protein sim. GBank gll4753775[emb]CAB41970.1] - (AJ132545) protein kinase [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		29331826, 35696052, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 55812038, 264758, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264566
1506	94143219 (3011, 3012)	Novel Protein sim. GBank gll1304201[db]BAA06170] - (D29766) alternatively spliced product [Rattus norvegicus]	Contains protein domain (PF00018) - SH3 domain	glycoprotein		65274572, 56182575, 56994075, 22278997, 22278998, 22278999, 264091, 264082, 60432049, 264259, 52645080, 29331822, 29331827, 264108, 29331830, 264908, 58182435, 264110, 264511, 264512, 55812038, 21906754, 87168559, 264600, 265017, 265018, 264681, 18108354, 284369, 264687, 264689, 21908765, 29148827, 21908768, 21908769, 29148829, 52844150, 33657023, 18108376, 65274791, 56182323, 264558, 264559, 18108385, 87168518, 60432113, 22279000, 264565, 264639
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gll5689513[db]BAA83040.1] - (AB029011) KIAA1088 protein [Homo sapiens]		helicase		
1508	11618758 (3015, 3016)	Novel Protein sim. GBank				
1509	87318451 (3017, 3018)	Novel Protein sim. GBank gll5031975[re]NP_005875.1[pPAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		264259, 29331822, 29331824, 29331828, 264591, 33109954, 264563
1510	95362843 (3019, 3020)	Novel Protein sim. GBank gll113161[sp]P28614[ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN]		UNCLASSIFIED		264259, 29331822, 265007, 18108374, 264556
1511	88318073 (3021, 3022)	Novel Protein sim. GBank gll728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]		UNCLASSIFIED		264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1512	95345390 (3023, 3024)	Novel Protein sim. GBank gll4559353[gb]AAD23014.1[AC006585] putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family			52845156, 18108396, 56994075, 60432289, 265006, 60433356, 60433438, 21906754, 87168474, 87168559, 265018, 264782, 264783, 264687, 21906765, 21906769, 27486262, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1513	87436228 (3025, 3026)	Novel Protein sim. GBank gll1330394 [U58761] - C01F1.6 gene product [Caenorhabditis elegans]				35696052, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 264766, 264689, 264892, 264829, 264636

1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi 4559353 gb AAD23014.1 AC006585 putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 65274572, 22278994, 35696288, 56994075, 264259, 52645080, 29331822, 29331825, 35896052, 29331830, 52644045, 58182435, 265006, 60433358, 60433438, 55812038, 21906754, 52646317, 52644296, 87168474, 87168559, 264448, 52644229, 21906765, 21906768, 21906767, 21906768, 35895917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486282, 27486284, 27486265, 35695763, 18108376, 35696423, 35695855, 52644332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163536 (3028, 3030)	Novel Protein sim. GBank gi 3879501 emb CAA87795  - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin		
1516	88073539 (3031, 3032)	Novel Protein sim. GBank gi 498015 (L27479) - X123 [Homo sapiens]	UNCLASSIFIED		265008, 56182323, 22279002
1517	87783325 (3033, 3034)	Novel Protein sim. GBank gi 3415134 (AF082024) - Phyb1 [Pimpinella brachycarpa]			264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi 728838 sp P39195 ALU8_HUMAN - IIII ALU SUBFAMILY SX WARNING ENTRY IIII	im7		68714117, 264508, 264509, 264905, 264510, 264910, 264591, 264595, 264288, 264766, 264769, 18108374, 264636, 264638, 264486 264589, 264489, 60432049, 265009, 33657402, 264596, 21906754, 265019, 264369, 21906765, 21908788, 21906769, 264691, 65274620, 33657182, 27486281, 18108374, 264557, 264639, 87168518, 22279002
1519	94328689 (3037, 3038)	Novel Protein sim. GBank gi 5262681 emb CAB45771.1  - (AL080188) hypothetical protein [Homo sapiens]			
1520	87592855 (3038, 3040)	Novel Protein sim. GBank gi 2662161 dbj BAA23712  - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED		18108392, 60432049, 264259, 29331824, 265007, 60433356, 265010, 21906768, 264636
1521	86970696 (3041, 3042)	Novel Protein sim. GBank gi 5052351 gb AAD38516.1 AF13542 - (AF135421) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - synthase Nucleotidyl transferase		18108394, 264259, 66714117, 265011, 264603, 265019, 18108384, 35896423, 264557, 264558, 18108388
1522	78980687 (3043, 3044)	Novel Protein sim. GBank gi 3776567 (AC005388) - Strong similarity to F21B7.33 gi 2809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]	UNCLASSIFIED		29331824, 265018, 265020, 265021 65274572, 21906768, 264693
1523	91005151 (3045, 3046)		UNCLASSIFIED		
1524	80203723 (3047, 3048)		UNCLASSIFIED		284112, 21906754, 263974
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gi 4759040 ref NP_004283.1 pRIN1 - ras inhibitor	UNCLASSIFIED		264693, 264687, 264689, 264690, 264692, 264693

1526	85105344 (3051, 3052)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)				35698286, 56182181, 60431735, 264595, 55812038, 264605, 264683, 21908765, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gi 2782496 (AF041107) - ulip 2 [Rattus norvegicus]				56182575, 264259, 60432049, 29331822, 60432289, 264908, 66712502, 60433438, 87168558, 265017, 264288, 21908766, 21908769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)				UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21908765, 21908766, 21908767, 21908768, 21908769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank gi 4086663 gb A020053  - (AF131826) Unknown [Homo sapiens]			UNCLASSIFIED	264488, 263894, 56182575, 22278995, 35698286, 22278997, 264259, 29331822, 60432289, 29331827, 35698052, 264509, 264908, 264907, 264908, 264909, 52844045, 56182435, 264511, 265009, 264910, 60433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264369, 264288, 264768, 18108357, 264768, 52844228, 21908765, 21908766, 21908767, 21908768, 265021, 265022, 52644150, 33657109, 264629, 35698585, 60432113, 22278002, 264583, 264584, 264488, 264587
1530	85012765 (3059, 3060)	Novel Protein sim. GBank gi 2828710 (AF043642) - matrin cyclophilin [Rattus norvegicus]				264488, 264489, 35698286, 29331825, 35698052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264486
1531	95418351 (3061, 3062)	Novel Protein sim. GBank gi 1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - Kinase PDZ domain (Also known as DHR or GLGF).			56182575, 35698286, 264097, 264259, 29331822, 29331825, 29331826, 29331827, 35698052, 264509, 56182435, 264510, 264511, 265007, 60433358, 55811386, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33637023, 35695763, 55810764, 35698423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264566

1532	85718224 (3063, 3064)	Novel Protein sim. GBank gll3874716[emb]CAA91265] - (Z66494) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D87438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...			UNCLASSIFIED	264689
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gll1490324[emb]CAB01543] - (Z78141) unknown [Mus musculus]	strud			29331824, 29146499, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263967, 20281149, 18108374, 263981, 264566
1534	95343841 (3067, 3068)	Novel Protein sim. GBank gll81286[pir]S22697 - extensin - Volvox carteri (fragment)			UNCLASSIFIED	264905, 264907, 264766, 264637
1535	90936732 (3069, 3070)					65274572, 22278997, 264259, 60432049, 29331822, 60432289, 29331827, 29146499, 265006, 265008, 60170831, 60433438, 33109954, 87168559, 265018, 18108357, 21906768, 29146629, 265021, 265022, 18108377, 58182323, 60432113, 22279000, 22279002
1536	87602858 (3071, 3072)	Novel Protein sim. GBank gll106024[pir]B32891 - finger protein 2, placental - human	transcript/factor	Contains protein domain (PF00096) - Zinc finger, C2H2 type		264686, 18108357, 18108394, 21906767, 21906768, 29146629, 35696286, 265020, 265021, 52644150, 264693, 66714117, 29331825, 29331826, 264508, 264905, 20281149, 264909, 18108374, 35696423, 35895855, 265009, 264634, 264636, 264638, 18108385, 56526468, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766
1537	95345556 (3073, 3074)	Novel Protein sim. GBank gll3876332[emb]CAB02096] - (Z79754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426112.5 comes from this gene; cDNA EST yk34210.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...				65274572, 56182575, 60432049, 264259, 29331826, 265006, 265007, 60433356, 60433438, 264601, 18108351, 264448, 264369, 264288, 33657023, 65274620, 33657109, 60432113
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gll403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds.], gene product [Gallus gallus]	kinase	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388



1539	95337628 (3077, 3078)	Novel Protein sim. GBank gij3218411[emb CAA19575.1] - (AL023859) SPBC19C7.07c, putative RNA splicing endonuclease gamma subunit, len:284aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAF008W, RNA splicing endonuclease gamma subunit, (275aa), fasta scores, opt:269, E(0.6e-2....		nuclease	22278994, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 60424269, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656870, 58182435, 265009, 33657402, 60433356, 60433438, 55812038, 21906754, 87168559, 285017, 285018, 265019, 18108351, 284288, 52644228, 18108359, 21906764, 21906767, 21908768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27486281, 18108370, 18108376, 35898423, 55811576, 65274781, 264558, 58182323, 60170394, 83373044, 87168518, 60432113, 22278000, 22279002, 264566
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gij5052634[gbl AAD38647.1 AF14567 - (AF145672) BcDNA, GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gij5052349[gbl AAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 284259, 29331822, 35696052, 284508, 284509, 264905, 264907, 264908, 284511, 284512, 284910, 284592, 284781, 284782, 284448, 264764, 284288, 264687, 21806769, 55811957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 284628, 18108374, 264632, 264634, 264635, 284639, 18108385, 264563, 264564, 264565, 264566, 264486
1542	80937549 (3083, 3084)	Novel Protein sim. GBank gij5305702[gbl AAD41778.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 285008, 285009, 265011, 264682, 18108354, 18108355, 52844150, 18108358, 264636, 18108381, 18108382
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gij728832[sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		nuclease	264108, 33108954, 285019, 264683, 35695917, 264690, 264692, 33657109
1544	8757295 (3087, 3088)	Novel Protein sim. GBank gij3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nuc_ recpt	35696286, 56994075, 22278999, 35696052, 60433356, 60433438, 265011, 264683, 33657109, 35696423, 264631, 87168518, 22278000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gij1086591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP:P22082) in a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 284693, 55811576
1546	79476589 (3091, 3092)			UNCLASSIFIED	264905, 264686
1547	86969584 (3093, 3094)	Novel Protein sim. GBank gij2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	264259, 29331822, 66714117, 265007, 55811386, 285010, 284600, 265017, 285018, 264288, 264768, 265020, 285022, 55811576, 18108380, 264563

1548	84233065 (3095, 3096)	Novel Protein sim. GBank gl 3043692 dbj BAA25510  - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank gl 5689519 dbj BAA83043.1  - (AB029014) KIAA1091 protein [Homo sapiens]		eph	60424179, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35686052, 264905, 264906, 264908, 264909, 265006, 264511, 265008, 60431735, 60433356, 21908754, 55811386, 87168558, 265017, 265018, 265019, 55811150, 264682, 264288, 264369, 56181562, 264769, 21908765, 21908768, 21906769, 55811957, 265020, 264691, 33657109, 60431528, 35696423, 35695855, 56526486, 60432113, 22279002, 264563, 264568
1550	95201907 (3099, 3100)	Novel Protein sim. GBank gl 544483 sp P35350 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	65274572, 60432289, 265008, 264910, 265011, 265017, 265019, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank gl 4758566 ref NP_004798.1 pHS6S - heparan-sulfate 6-sulfotransferase		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264906, 264907, 264909, 285007, 264512, 264910, 21908754, 265018, 265019, 264681, 264764, 264766, 264688, 264769, 21908769, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	264259, 29331828, 66712502, 284764, 264288, 264686, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gl 4589570 dbj BAA76807.1  - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	- dehydrogenase	56182575, 35696286, 29146499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233069 (3107, 3108)	Novel Protein sim. GBank gl 3043692 dbj BAA25510  - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	- transferase	35696286, 22278997, 264259, 29331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265018, 264681, 264369, 264688, 264767, 264768, 21908765, 21906769, 35695917, 264693, 18108370, 80431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gi 2257495 d BAA21392  - (AB004534) p 015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331826, 35696052, 264508, 264905, 284906, 284907, 284908, 52644045, 264909, 264910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265018, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35698423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526486
1556	91228268 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35696052, 264630, 35698423, 265018, 264632, 264682, 29331822, 265020, 265011, 60432288, 264509, 284908, 284907, 284908, 264909, 264910, 284758, 55811386, 264761, 264762, 264766, 264769, 264690, 263978, 264634, 264635, 264639, 264564, 264486
1557	87640609 (3113, 3114)	Novel Protein sim. GBank gi 3329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; zf-C3HC4.hmm, score: 34.08); most similar to drosophila goliath protein (SW: Q06003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278994, 22278996, 22278997, 22278998, 22278999, 60432046, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 264448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811576, 83373044, 87168518, 22278000, 22279002
1558	94840376 (3115, 3116)	Novel Protein sim. GBank gi 5360105 gb AAD42871.1 AF155105 - (AF155105) putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			264259, 29331822, 60432289, 35696052, 264107, 264110, 21906754, 33109854, 87168559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1559	88224865 (3117, 3118)	Novel Protein sim. GBank gi 112908 sp P02750 AZGL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264908, 264603, 264638
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gi 3880146 emb CAA92704  - (Z68319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from this gene		UNCLASSIFIED	
1581	86609159 (3121, 3122)			UNCLASSIFIED	264510, 264594
1582	83359682 (3123, 3124)			UNCLASSIFIED	263967
1583	85506694 (3125, 3126)			UNCLASSIFIED	264910, 264764, 264766
1584	87766371 (3127, 3128)	Novel Protein sim. GBank gi 1168287 sp P45953 ACDV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD)	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED	18108394, 35696286, 264259, 29331822, 60432289, 35696052, 29331828, 264508, 66712502, 264908, 56182435, 265007, 264910, 80170831, 21906754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 21906765, 21906768, 265021, 60170615, 264692, 35698423, 35695855, 264557, 56182323, 60432113, 22278002, 264482

1565	87783381 (3129, 3130)	Novel Protein sim. GBank gii128726[sp]P05307[PDI_BOVIN - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)]		isomerase	264488, 264689, 18108398, 55811957, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264638, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264596, 265011, 264603, 22279002, 18108351, 264762, 264565, 264567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gii1388044[emb]CAA20329] - (AL031268) VM106R.1 [Caenorhabditis elegans]		Inf	22278996, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 66712502, 264908, 265008, 18108351, 52644229, 21906765, 21906767, 21906768, 21906769, 33657109, 264555, 264639, 264482
1567	84999006 (3133, 3134)	Novel Protein sim. GBank gii4929699[gb]AAD34110.1[AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		UNCLASSIFIED	56182575, 21906769, 264692
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gii4827063[ref]NP_005072.1[pZNF1 - zinc finger protein 142 (clone pHZ-49)]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	- transcript factor	29331827, 29331830, 264511, 265009, 264758, 21908767, 21908768, 264691, 264693, 22279000, 22279002
1569	90936668 (3137, 3138)	Novel Protein sim. GBank gii5689451[db]BAA83009.1] - (AB028980) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265019, 264764, 21906765, 21906769, 55811957, 60170615, 52644150, 264692, 33657023, 33657109, 18108377, 264563, 264567
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gii1256430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gii4507731[ref]NP_001061.1[pTUBG - tubulin, gamma polypeptide]	Contains protein domain (PF000091) - TubulinFtsZ family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21906765, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384
1572	81201664 (3143, 3144)			UNCLASSIFIED	35696052, 264905, 264906, 264908, 264910, 264758, 264766, 35695917, 264637
1573	80207066 (3145, 3146)			UNCLASSIFIED	263972

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gi 4758334 ref NP_004256.1 pFADS - delta-6 fatty acid desaturase		Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	cytochrome	18108394, 264887, 18108397, 18108398, 22278996, 22278997, 22278999, 264259, 29331825, 29331827, 29146498, 29146499, 264107, 264907, 264909, 52644045, 264511, 265008, 264910, 265009, 264591, 21908754, 265011, 265019, 18108351, 264682, 264763, 264764, 18108354, 264389, 264288, 264885, 264766, 264686, 264768, 264688, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 264690, 264691, 264693, 20281069, 18108370, 18108374, 18108378, 35695855, 264634, 18108384, 18108385, 22279002, 264563, 264568
1575	95340019 (3149, 3150)	Novel Protein sim. GBank gi 3881810 emb CAA94856  - (Z70783) similar to EF-hand calcium binding protein; cDNA EST EMBL: C08700 comes from this gene [Caenorhabditis elegans]		Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 264909, 265008, 265008, 265009, 265010, 87168559, 55911150, 264448, 18108354, 264389, 264288, 18108357, 55811957, 265020, 265021, 60170815, 264691, 33657023, 33657109, 60431528, 65274791, 35695855, 18108385, 60432113, 22278002, 264482
1576	95314019 (3151, 3152)	Novel Protein sim. GBank gi 2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]			UNCLASSIFIED	184568, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 285008, 264910, 21908754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264638, 83373044, 264488
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gi 2489130 sp P70315 WASP_MOUSE - WISKOTT- ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)			UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)					264259, 29331826, 265017, 264689, 264693, 60432113
1578	88085141 (3157, 3158)	Novel Protein sim. GBank gi 2978255 db BAA25190  - (AB007407) myeloid zinc finger protein-2 [Mus musculus]		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35696288, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gi 4324682 gb AAD16986  - (AF108674) late gestation lung protein 1 [Rattus norvegicus]		Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278999, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gi 2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]				22278995, 29331822, 29331824, 29331826, 56182435, 264585, 55812038, 87168559, 265017, 264288, 21908764, 55811957, 35695917, 264692, 55811576, 264637, 56182323, 264559, 83373044, 60432113

1582	95358052 (3163, 3164)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (A1243459) proteophosphoglycan [Leishmania major]		phosphatase	264259, 604322289, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264639, 56526486, 22279000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gij5578958[emb]CAB51351.1] - (AL050306) dJ47587.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	60170831, 33657402, 264682, 21906766, 35895855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gij5531815[gib]AAD44482.1] - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	60424179, 52646842, 65274572, 56182575, 22278995, 35696286, 22278998, 22278998, 22278999, 264259, 29331822, 56182181, 60424268, 60432268, 29331827, 29331828, 35696052, 29146498, 68712502, 29331830, 52644045, 56182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810784, 55811576, 35696423, 65274791, 35695855, 56182323, 83373044, 18108387, 87168518, 60432113, 22279002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gij4240132[dbj]BAA74846.1] - (AB020630) KIAA0823 protein [Homo sapiens].	Contains protein domain (PF00023) - Ank repeat	phosphatase	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 265006, 265007, 265008, 60433356, 33109854, 87168474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108364, 18108370, 264629, 263972, 18108383, 18108388, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gij3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			265017, 265018, 264689, 33657023, 263978, 264636, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gij3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264907, 264908, 264511, 264910, 264591, 264594, 264629, 264631, 264563, 264483, 264567
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gij1077573[pir]S52680 - probable ribosomal protein L34, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265006, 264758, 21906754, 264761, 264762, 21906765, 21906769, 60170615, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gij2137756[pir]I46746 - semaphorin C - mouse (fragment)		UNCLASSIFIED	55274572, 264490, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264596, 265011, 264688, 21906766, 21906768, 55811957, 27486265, 264639, 18108385, 56526486, 60432113

1590	85318825 (3179, 3180)			UNCLASSIFIED	284489, 22278986, 264259, 29331824, 29331825, 29331826, 29331827, 285006, 60433356, 21906754, 265017, 265018, 265019, 264448, 264785, 264288, 52644229, 21906765, 21906767, 21906768, 21906769, 285021, 264692, 27486285, 35695783, 56528486, 60432113, 22279000, 22279002, 284584
1591	56877160 (3181, 3182)				
1592	87862533 (3183, 3184)	Novel Protein sim. GBank gi 4557749 ref NP_000237.1 pMHC2 - MHC class II transactivator		MHC	264259, 284905, 29331830, 264595, 265017, 264448, 264288, 264690, 264629, 87188518
1593	94991661 (3185, 3186)			UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35696423, 22279000, 264565, 264567
1594	67773752 (3187, 3188)	Novel Protein sim. GBank gi 3877072 emb CAA07060  - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	264488, 29331827, 284905, 264906, 264907, 264908, 264909, 264910, 284592, 264593, 264757, 264602, 284604, 264760, 264881, 264288, 264766, 284768, 29148629, 35695917, 264692, 264628, 264629, 264630, 264632, 264634, 264635, 264636, 264639, 264563, 264564, 264566
1595	78918425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - telraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	UNCLASSIFIED	29331826, 284908, 55811957
1596	79933928 (3191, 3192)			UNCLASSIFIED	28146498, 264758, 263867
1597	86971857 (3193, 3194)	Novel Protein sim. GBank gi 5257114 gb AAD41244.1 AF094480 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450	cyto450	264092, 29331824, 284508, 264682, 264369, 264686, 264630, 264563
1598	87862839 (3195, 3196)				264259, 264634
1599	87849829 (3197, 3198)	Novel Protein sim. GBank gi 4506797 ref NP_000324.1 pSCA7 - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	52645080, 29331824, 29331828, 264511, 265009, 265011, 264605, 264448, 264784, 265020, 264692, 264693, 18108370, 264635, 18108385
1600	80056002 (3199, 3200)				28331826, 264603, 264691, 284563
1601	15023246 (3201, 3202)			UNCLASSIFIED	284635
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF12853 - (AF12853) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain	struct	29146499, 264112, 264762, 18108351, 29146627, 263974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283920 pir I527939 - tensin - chicken		collagen	264490, 29331824, 264807, 264909, 264511, 265008, 264592, 265010, 265011, 264782, 264784, 264369, 264288, 264687, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108385
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4786831 gb AAD29633.1 AF11682 - (AF116827) unknown [Homo sapiens]	ATPase-associated		263977

1605	91221129 (3209, 3210)				struct	264905, 264509, 264908, 264907, 264908, 264909, 264604, 264766, 264768, 264892, 264693, 33657109, 264629, 35695855, 264635, 264638, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gij4505313[ref]NP_003794.1[pm]YOM - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	struct		22278996, 22278998, 264259, 33657402, 265017, 18108351, 264448, 21906767, 21906769, 52644150, 264691, 87168518, 264689
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gij5174473[ref]NP_005888.1[pm]PI - Intracisternal A particle-promoted polypeptide		transcriptfactor		
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gij2224629[db][BAA20802] - (AB002342) KIA0344 [Homo sapiens]		UNCLASSIFIED		264094, 264906, 264907, 264908, 264910, 264591, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	94311572 (3217, 3218)	Novel Protein sim. GBank gij4684073[emb][CAB43213.1] - (AL049934) hypothetical protein [Homo sapiens]				52844507, 52645156, 52646365, 52646842, 56182575, 22278994, 56994075, 35698286, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 28331828, 35696052, 33656970, 284508, 264509, 264907, 52844045, 56182435, 264510, 264511, 264512, 33657402, 21906754, 52646317, 33109954, 52644286, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264769, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 52645129, 27486261, 27486262, 35695763, 264628, 18108370, 18108376, 35696423, 264638, 52644332, 18108387, 87168518, 22278000, 264563, 264488
1610	85468200 (3219, 3220)	Novel Protein sim. GBank gij283920[pm][S27939 - lensin - chicken]		UNCLASSIFIED		264593, 264757, 55812038, 265018, 265020, 264691, 264692, 264693, 264631, 264634, 264635, 264555, 22279000, 264564
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gij107284[pm][A35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)]	(Contains protein domain (PF00008) - peroxidase EGF-like domain			35696286, 21906765, 264691, 35696423
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gij3874846[emb][CAA94337] - (Z70307) Similarly to B subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL:C09951 comes from this gene; cDNA EST EMBL:C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED		264488, 264509, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED		264759



1614	91228634 (3227, 3228)	Novel Protein sim. GBank gi 4680673 gb AAD27726.1 AF13295 - (AF132951) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 264908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 264683, 264288, 264768, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 56182323, 83373044, 264566 22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22278002
1615	86121909 (3228, 3230)	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1  - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22278002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi 3878260 emb CAB01696  - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07649 comes from this gene; cDNA EST EMBL:C09081 comes from this gene; cDNA EST yk39912.3 comes from this gene; cDNA ...	UNCLASSIFIED	UNCLASSIFIED	264488, 52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52645080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 35695970, 264905, 264909, 264584, 52646317, 21906754, 35657084, 52644298, 87168474, 87168558, 265017, 265018, 265019, 264681, 264448, 264684, 52644229, 21906764, 264689, 21906765, 21906766, 21906769, 35695917, 265020, 265021, 52644150, 33857023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657348, 27486265, 35695763, 18108376, 35696423, 35695855, 264557, 52644332, 264558, 18108385, 87168518
1617	38090742 (3233, 3234)	Novel Protein sim. GBank gi 466053 sp P34879 YO41_CAEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264766, 264768, 264689, 264693, 18108374, 264635, 264636, 264638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi 4240231 dbj BAA74894.1  - (AB020678) KIAA0871 protein [Homo sapiens]		siRNA	35696286, 22278999, 264092, 29331824, 29331825, 35696052, 33657084, 21906765, 27486284
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gi 5031763 ref NP_005515.1 pHRY - hairy (Drosophila) - homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcription factor	52646842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 56182435, 265007, 265008, 264910, 60170831, 60432229, 60433356, 80433438, 265019, 264448, 264288, 264686, 21908768, 265021, 60170615, 33657023, 65274620, 33657109, 18108374, 18108376, 35696423, 35695855, 56182323, 56526486
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi 1351047 sp P45843 SCRT_DROME - SCARLET PROTEIN		UNCLASSIFIED	264684

1821	87076708 (3241, 3242)				UNCLASSIFIED	264910
1822	94741739 (3243, 3244)	Novel Protein sim. GBank gi 3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain		UNCLASSIFIED	18108392, 65274572, 18108398, 22278996, 22278997, 22278999, 29148498, 29148499, 264905, 264908, 264909, 264828, 52644045, 264592, 60433356, 21906754, 264602, 265017, 264369, 21906768, 55811957, 265021, 60170615, 264635, 264557, 60170394, 83373044, 18108385, 22279000, 22279002, 264566
1823	87779106 (3245, 3246)	Novel Protein sim. GBank gi 731086 sp P40389 UV22_SCHPO - UV-INDUCED PROTEIN UV122	ribosomal prot			18108398, 264259, 264909, 56182435, 87168474, 264448, 21906768, 35695917, 264691, 87168518, 264563
1824	87338178 (3247, 3248)	Novel Protein sim. GBank gi 387566 emb CAB05478  - (Z83104) cDNA EST EMBL: T00015 comes from this gene; cDNA EST EMBL: D33665 comes from this gene; cDNA EST EMBL: D38540 comes from this gene; cDNA EST yk240f8.3 comes from this gene; cDNA ES... comes from this gene; cDNA ES...			UNCLASSIFIED	66714117, 29331825, 264909, 265008, 264758
1825	95354748 (3249, 3250)	Novel Protein sim. GBank gi 4589622 dbj BAA76833.1  - (AB023206) KIAA0989 protein [Homo sapiens]	kinase			264489, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 264108, 264508, 33657084, 265017, 265018, 18108351, 264683, 284369, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 264691, 65274620, 18108368, 263972, 18108376, 35696423, 264631, 264634, 22279000, 22279002
1826	94734369 (3251, 3252)	Novel Protein sim. GBank gi 5679070 gb AAD46844.1 AF160904 - (AF160904) BcDNA.HL05936 [Drosophila melanogaster]				52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265009, 60432229, 60433356, 60433438, 21906754, 52646317, 52644296, 265011, 87168559, 5264604, 265018, 264448, 264369, 264288, 264768, 52644229, 264689, 21906765, 21906768, 35695917, 265021, 265022, 52644150, 33657023, 65274620, 27486261, 27486262, 27486265, 35695763, 263972, 52644332, 60170394, 87168518, 80432113, 264567
1827	83368773 (3253, 3254)				UNCLASSIFIED	264288
1828	85708459 (3255, 3256)	Novel Protein sim. GBank gi 3668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]	eph			264288, 264686, 264767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gij4240175jdbj BAA74866.1  - (AB020650) KIAA0843 protein [Homo sapiens]		struct	284555
1630	87778027 (3259, 3260)			UNCLASSIFIED	28331822, 29331827, 265010, 284693, 284634, 22278002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gij1915892 emb CAA69995  - (Y08740) lom-1A protein [Gallus gallus]		UNCLASSIFIED	55811857, 264258, 33657023, 264693, 29331822, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 264910, 264634, 284636, 284637, 56182323, 284559, 284759, 18108385, 264583, 264764, 264768
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gij2556501 dbj BAA22896  - (D83850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264768, 264691, 264692, 29148499, 284509, 284905, 264907, 264511, 284512, 264482, 264681, 264763, 264682, 264683, 264488, 284259, 284807, 264908, 264909, 264628, 264629, 264631
1633	87773683 (3265, 3266)				265007, 284637, 22278002
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gij4887228 gb AAD32244.1 AF150755 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	
1635	84232600 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35696052, 52644045, 264511, 265008, 265009, 265010, 265011, 265018, 265019, 284448, 284369, 21908765, 21908768, 265021, 264690, 264482
1636	80413227 (3271, 3272)	Novel Protein sim. GBank gij455751 ref NP_001339.1 pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	UNCLASSIFIED - kinase	22278995, 264594, 284783, 265020, 264558
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gij3420051 (AC004680) - unknown protein [Arabidopsis thaliana]			21906765, 21908787, 22278998, 35696288, 22278999, 284258, 264692, 284693, 29331824, 33657109, 264508, 264906, 18108370, 264629, 265007, 33657402, 21908754, 264602, 284604, 264784, 264683, 264566, 264288
1638	87101854 (3275, 3276)				284488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696052, 264908, 56182435, 264112, 265008, 265009, 264757, 284758, 55811386, 264603, 284760, 18108351, 264764, 264288, 264766, 284768, 21908767, 55811857, 264691, 33657023, 65274620, 18108370, 55810784, 55811576, 284558, 284639, 83373044, 18108385, 87168518
1639	84322184 (3277, 3278)	Novel Protein sim. GBank gij5420389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	

1640	94143185 (3279, 3280)	Novel Protein sim. GBank gjl2842469 emb CAA16847.1  - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56894075, 35696286, 60432049, 60432289, 29331827, 35698052, 52644045, 56182435, 264510, 265006, 265007, 285008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21906765, 21906766, 21906788, 35695917, 265021, 60170615, 52644150, 33657023, 33657109, 33657349, 18108374, 35696423, 65274791, 35695855, 264632, 264555, 56182323, 22279000
1641	87625160 (3281, 3282)			UNCLASSIFIED	29146499, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264558, 264559, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gjl1575333 (U60416) - myr 8 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - DIL domain	struct	22278999, 29147820, 29331826, 29331828, 33656970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87188518, 22279002, 264564
1643	94131766 (3285, 3286)				29331825, 29331827, 29331828, 21908754, 265019, 264288, 264893, 33657349, 18108370, 18108376, 264555, 83373044, 22279002, 264482
1644	88095125 (3287, 3288)			UNCLASSIFIED	264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1645	95013858 (3289, 3290)			UNCLASSIFIED	264685, 264693
1646	95362891 (3291, 3292)	Novel Protein sim. GBank gjl1076802 pir S49915 - extensin like protein - maize		UNCLASSIFIED	22278994, 56994075, 35696286, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87188559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486261, 27486265, 33657349, 60432113, 264563, 264564
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gjl5002573 emb CAB44336.1  - (Y17466) alpha-N-acetylgalactosamine alpha-2,6-galactyltransferase [Fugu rubripes]		UNCLASSIFIED	29331822, 264906, 264908, 264369, 21908768, 60170615, 264639, 22279000
1648	87642098 (3295, 3296)		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385

1648	95347628 (3297, 3298)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696288, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52644045, 264809, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55612038, 21906754, 285011, 284601, 284602, 265017, 265018, 265019, 284682, 284448, 264764, 284683, 264288, 284768, 264685, 264687, 284768, 264688, 264769, 52644229, 264689, 21906765, 21908766, 21906767, 21906768, 55811957, 35695917, 265021, 265022, 52644150, 284692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108376, 35696423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 284080, 264404, 60432113, 22279000, 22279002, 264482, 264585, 264586, 264487, 265011, 264602, 21906767, 18108374, 18108377, 18108385
1650	87418539 (3299, 3300)	Novel Protein sim. GBank gi 3647335 emb CAA21059  - (AL031644) possible zinc-finger protein (Schizosaccharomyces pombe)			
1651	91639773 (3301, 3302)	Novel Protein sim. GBank gi 484278 emb CAB43247.1  - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108387, 35696288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21908754, 265010, 265011, 265017, 265019, 284448, 18108354, 264288, 264688, 21906765, 21906766, 21906768, 21906769, 265022, 264692, 264693, 264629, 35695855, 264558, 264637, 264557, 264559, 83373044, 56526486, 22279000, 22279002, 264584
1652	86598622 (3303, 3304)	Novel Protein sim. GBank gi 1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00169) - PH domain	struct	22278997, 29146498, 56182435, 21908754, 264369, 21906785, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002
1653	94255983 (3305, 3306)	Novel Protein sim. GBank gi 3776054 emb CAA06273  - (AJ004999) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	18108398, 22278995, 22278998, 284259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433436, 21906754, 265017, 285019, 264448, 264683, 264288, 265021, 265022, 264692, 18108384, 65274781, 18108384, 60432113, 264567, 33657109, 264565
1654	78756471 (3307, 3308)			UNCLASSIFIED	

1655	86689346 (3308, 3310)	Novel Protein sim. GBank gij3355717[emb CAA73496] - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52644507, 35696286, 22278998, 22278999, 29331824, 29331825, 29331828, 33656970, 264908, 52644045, 264511, 264910, 52646317, 264288, 52644229, 33657023, 33657109, 52644332, 264557, 56182323, 56526486, 60432113
1656	79662297 (3311, 3312)	Novel Protein sim. GBank gij1890141[dbj BAA18947] - (D83206) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gij4557645[jref NP_001524.1]pHNR - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	dna_mn_bind	29331827, 265009, 21906766, 21906767, 265020, 265022, 33657109, 264638, 56526486, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gij3877072[emb CAA87060] - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal prokaryotic L21 protein	UNCLASSIFIED	52646365, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146488, 264905, 264908, 52644045, 265006, 60433356, 264757, 60433438, 21906754, 265011, 18108351, 264448, 264369, 264288, 264766, 264768, 21906765, 21906767, 21906768, 21906769, 29148629, 265021, 265022, 18108362, 263969, 263971, 18108374, 35696423, 18108383, 22279000, 264482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gij539218[pir S38038] - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52646317, 21906766, 21906767, 21906768, 87168518, 22278996, 265020, 22278999, 87168559, 264603, 265017, 264631, 265018, 265019, 22279002, 284482, 264635, 264565
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gij2497012[sp Q10010]YSV4_CAEEL - HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	264488, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265009, 264910, 264592, 264596, 265010, 264600, 264602, 265017, 265018, 264605, 264760, 264764, 264288, 264766, 264688, 264768, 264769, 264689, 21906766, 35695917, 264690, 33657023, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264563, 264483, 264564, 264565, 264566, 264486, 264567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gij4759100[ref]NP_004759.1pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278998, 264259, 29331824, 29331826, 29331827, 29331828, 264509, 86712502, 29331830, 264908, 52644045, 265007, 264512, 60433356, 60433438, 55812038, 21906754, 265019, 264448, 264768, 264768, 264768, 21906768, 21906769, 265020, 33657023, 33657109, 65274791, 87168518, 264482, 264563, 264564, 264565, 264567
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gij1730502[sp]P52875[PF27_MOUSE - TRANSMEMBRANE PROTEIN PFT27			18108392, 29331822, 29331828, 20281100, 264106, 265008, 265007, 265008, 18108348, 21906766, 18108365, 18108366, 18108374, 83373044, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gij4884136[emb]CAB43275.1 - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - kinase WW domain		52645158, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331828, 29331827, 29331828, 33656870, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33109954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264768, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 264691, 33657023, 264693, 263967, 33657109, 264630, 52644332, 83373044, 67168518, 60432113, 22279000
1664	94234078 (3327, 3328)	Novel Protein sim. GBank gij3043692[dbj]BAA23510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263894, 35696286, 29331824, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265008, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264800, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264768, 264687, 264768, 264769, 21906764, 21906765, 21906767, 35695917, 265021, 264534, 60170815, 264690, 264691, 264692, 33657109, 33657182, 264628, 18108370, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264566, 264486

1665	91226552 (3329, 3330)	Novel Protein sim. GBank gij1083506 pir S50065 - sialoadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	immunoglob	264488, 29331826, 29331828, 264509, 264906, 264907, 264909, 264510, 264511, 264910, 264592, 264593, 264595, 264758, 264596, 264600, 264760, 264762, 264764, 264766, 264768, 264629, 264630, 264634, 264636, 83373044, 264564, 264566, 264567, 264486
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gij3913431 sp O42643 DDX8_SCHPO - PUTATIVE PRE- MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	helicase	56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29146498, 265009, 33109954, 87168559, 265019, 264288, 264688, 21908767, 21908769, 264691, 33657182, 18108370, 18108374, 18108385, 22279002
1667	91226555 (3333, 3334)	Novel Protein sim. GBank gij5689535 dbj BAA83051.1  - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transport	264259, 29331822, 29331826, 264905, 264906, 264908, 264510, 265009, 264595, 264758, 265011, 87168559, 265017, 265018, 265019, 264448, 264768, 264686, 21906765, 21906767, 21906769, 285020, 285021, 60170615, 264690, 264692, 264693, 18108368, 18108370, 263972, 55810764, 284555, 83373044, 60432113, 22279000, 22279002
1668	68095135 (3335, 3336)	Novel Protein sim. GBank gij2076894 gbj AAB53983.1  - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE- bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	66714117, 264508, 264509, 264906, 264907, 264908, 264511, 264910, 264764, 264687, 264689, 33657109, 35696423, 35695855, 264632
1669	91227848 (3337, 3338)	Novel Protein sim. GBank gij3875371 embj CAA85414.1  - (Z36948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor UZAF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes fr...		UNCLASSIFIED	29331825, 33108954, 264369, 264767, 264689, 33657109, 83373044
1670	87628009 (3339, 3340)			UNCLASSIFIED	264259, 29331824, 29331827, 60433438, 265022, 264636
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gij462451 sp P34244 KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 22278997, 29331825, 264909, 21906754, 265017, 265018, 265019, 264682, 264683, 264768, 264688, 21906768, 21906767, 21906769, 264691, 264555, 264556, 22279000, 264566
1672	88291834 (3343, 3344)	Novel Protein sim. GBank gij1814270 (U74586) - double- stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	264906, 264909, 264632, 18108381



1673	88095137 (3345, 3346)	Novel Protein sim. GBank gij2076894 gbjAAB33983.1  - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE_bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - kinase domain (C1 domain)	264488, 264569, 18108394, 56994075, 22278998, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264810, 60170831, 264592, 264594, 264595, 264758, 264801, 264760, 264762, 264683, 264784, 264288, 264768, 264686, 264768, 264687, 264769, 264689, 264690, 33657023, 264692, 264693, 33657109, 264628, 264629, 18108374, 35698423, 35695855, 264631, 264632, 264634, 264635, 264637, 264558, 264638, 264639, 264563, 264482, 264564, 264565, 264566, 264567, 264488
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gij5262467 emb CAB45693.1  - (AL080082) hypothetical protein [Homo sapiens]	kinase	29331822, 29331824, 264906, 52644045, 60433358, 87188559, 264448, 264288, 264686, 264691
1675	87608466 (3349, 3350)	Novel Protein sim. GBank gij3128366 (AF010496) - 50S ribosomal protein i9 [Rhodobacter capsulatus]	UNCLASSIFIED	56181688, 35696286, 22278997, 22278998, 264259, 29331824, 29331827, 35698052, 68712502, 264764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35698423, 35695855, 264637, 264639, 18108385, 264594
1676	85358086 (3351, 3352)	Novel Protein sim. GBank gij4164065 gbjAA003327  - (AF111091) latrophilin 3 splice variant bbar [Bos taurus]	UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21906765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gij3327046 dbj BAA31591  - (AB014516) KIAA0616 protein [Homo sapiens]	UNCLASSIFIED	264908
1678	86868829 (3355, 3356)	Novel Protein sim. GBank gij550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	UNCLASSIFIED	29331824, 264102
1679	81214106 (3357, 3358)	Novel Protein sim. GBank gij550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35696286, 29331824, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 264683, 18108354, 18108356, 18108359, 21906765, 29148627, 29148629, 264690, 18108361, 18108362, 18108364, 18108365, 18108368, 264628, 18108378, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gij2394478 (AF024500) - No definition line found [Caenorhabditis elegans]	transport	65274572, 22278994, 22278999, 66714117, 29331827, 56182435, 21906754, 265018, 264288, 21906769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gij5689537 dbj BAA83032.1  - (AB028023) KIAA1100 protein [Homo sapiens]	UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811957, 264690, 33857023, 35696423, 83373044, 264563
1682	86042710 (3363, 3364)		UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3365, 3366)	Novel Protein sim. GBank gij5031717[et]NP_005704.1pGPPB - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263994, 35696286, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264758, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264369, 264766, 264768, 35695917, 264692, 33657109, 35696423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80063409 (3367, 3368)			UNCLASSIFIED	264563, 264566
1685	94323182 (3369, 3370)	Novel Protein sim. GBank gij1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Guanylate kinase		60424179, 52646842, 22278994, 35696286, 22278998, 264259, 52645080, 29331824, 29331826, 265007, 33657084, 265018, 264681, 264448, 264683, 264369, 264689, 21908765, 21908767, 21908768, 21908769, 265021, 264692, 65274620, 33657109, 27488262, 264635, 52644332, 56182323, 22279000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gij2244707[dbj]BAA21115.1[- (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	55182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264565, 264486, 264587
1687	94718400 (3373, 3374)	Novel Protein sim. GBank gij4680679[gbj]AAD27729.1[AF13295] - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264906, 264907, 264908, 264510, 265006, 265007, 264910, 264556, 18108381, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1688	94325048 (3377, 3378)	Novel Protein sim. GBank gij4240193[dbj]BAA74875.1[- (AB020659) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264569, 35696286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274791, 83373044, 264089
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gij3800736 (AF031572) - seven-pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - cadherin		264369, 21908766, 264692, 264639, 87168518
1691	86095223 (3381, 3382)	Novel Protein sim. GBank gij273208 (AF039713) - No definition line found [Caenorhabditis elegans]	Cadherin domain		264768, 33657109, 29331827, 29148629, 264510, 264106, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264907, 264908, 33657023, 264567, 264766, 263974
1692	86106709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gij121271[sp]P02207[GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	29331826, 264508, 264905, 264907, 264595, 265010, 265011, 21908768, 33657023, 264629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gi 5453932 ref NP_008225.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01183) - RNA polymerases L / 13 to 16 kDa subunit	mapolymerase	35696286, 22278998, 22278998, 22278998, 264259, 29331822, 29331825, 29331826, 29331828, 35696052, 29148499, 284905, 284908, 52844045, 264511, 265006, 285007, 265009, 264592, 60433358, 21906754, 265010, 265011, 18108351, 294763, 264682, 264448, 264683, 264288, 264768, 264689, 21906768, 60170615, 264691, 284692, 264693, 18108370, 18108374, 263978, 35698423, 35698555, 264558, 18108381, 18108385, 87188518, 264482, 264486 284634
1695	94719325 (3389, 3390)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gi 4220517 emb CAA22890  - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264259, 285010, 18108351, 264764, 21906766, 18108370
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gi 505662 (U10362) - GP36b glycoprotein [Homo sapiens]		glycoprotein	284682
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi 5052031 gb AAD38411.1 AF15573 - (AF155739) axotrophin [Mus musculus]			56994075, 22278998, 22278998, 264509, 38557402, 284758, 87188474, 87188559, 265017, 265018, 264448, 264687, 29148627, 21908768, 29148629, 265020, 265022, 33657023, 264558, 87188518, 22278902
1699	87424783 (3397, 3398)	Novel Protein sim. GBank gi 543344 pir S41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35696286, 264635
1700	87859161 (3399, 3400)			nuc_rept	29331824, 52844045, 285008, 265009, 263968, 263971
1701	86570488 (3401, 3402)			UNCLASSIFIED	284082, 284110, 263977
1702	87785092 (3403, 3404)	Novel Protein sim. GBank gi 3877439 emb CAA96652  - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		MHC	22278995, 22278997, 264092, 28146498, 29148489, 264107, 264508, 264907, 264110, 264112, 265009, 60170831, 21908754, 265011, 265017, 264782, 18108351, 284288, 21908765, 35695917, 265021, 60170815, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263978, 35695855, 264555, 263981, 60170394, 18108385, 56528486, 87188518, 60432113 284909, 265017, 264628, 264629, 264638
1703	79588651 (3405, 3406)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	
1704	86622978 (3407, 3408)	Novel Protein sim. GBank gi 1263289 (U47856) - fibronin-4 [Araneus diadematus]		UNCLASSIFIED	264369
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gi 4519621 dbj BAA75670.1  - (AB017814) OASIS protein [Mus musculus]			264569, 35696286, 264907, 265010, 284687, 264768, 264682, 264693, 264636, 264568
1706	87790967 (3411, 3412)	Novel Protein sim. GBank gi 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			22278996, 22278998, 264259, 264509, 265018, 264764, 264685, 264686, 21906768, 21908768, 265022, 264691, 264558, 22279000

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gij4321664[gb AAD15797] - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108396, 22278997, 264259, 29147620, 29331826, 29148498, 284905, 284906, 285008, 264593, 264595, 264758, 264596, 265018, 264760, 18108351, 264764, 264766, 264889, 264693, 18108370, 35696423, 55811576, 264558, 87168518, 60432113, 264587
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gij5174591[ref NP_005947.1 pMTHF - 5,10-methylene-tetrahydrofolate dehydrogenase, 5,10-methylene-tetrahydrofolate cyclohydrolase, 10-formyl-tetrahydrofolate synthetase	Contains protein domain (PF01268) - Formate-tetrahydrofolate ligase	synthase	56182575, 22278996, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 265009, 60170831, 33657402, 33109954, 87168559, 265019, 18108351, 284448, 21906765, 21906767, 21906768, 28148627, 29148629, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264583
1709	80222583 (3417, 3418)			UNCLASSIFIED	264107, 55811857, 263974, 263976, 263977, 263981
1710	20754572 (3419, 3420)			UNCLASSIFIED	264556
1711	81013729 (3421, 3422)	Novel Protein sim. GBank gij5031735[ref NP_005760.1 pHEC- - N-acetylglucosamine 6-O-sulfotransferase		sulfotransferase	55274572, 29331824, 29331826, 264768, 60431528, 35696423, 60432113, 264563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gij5454168[ref NP_008453.1 pXAP4 - HBV associated factor	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	kinase	56994075, 264093, 264259, 29331822, 264099, 29331824, 29331827, 264107, 264110, 264511, 264592, 265011, 265018, 264683, 264686, 264688, 265020, 33657023, 263987, 33657109, 283974, 35696423, 35695855, 264630, 264636, 264558, 264566
1713	94143453 (3425, 3426)	Novel Protein sim. GBank gij160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00843) - B-box zinc finger.	UNCLASSIFIED	22278995, 264508, 264758, 18108351, 18108370, 263974, 18108374, 284634, 56182323, 83373044, 60432113
1714	87420048 (3427, 3428)				22278997, 264757, 21906765, 265020, 265021, 264692, 56526486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gij5689537[dbj BAA83052.1  - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	284509, 284905, 284906, 284907, 264908, 264909, 264910, 264591, 265011, 264766, 264768, 264769, 264691, 264692, 264632, 264634, 264635, 284636, 284637, 264558, 264839, 264584
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gij4589468[dbj BAA76761.1  - (AB012808) mBOCT [Mus musculus]		transport	56182575, 29331824, 60432289, 264109, 264909, 265007, 264600, 265019, 264686, 265020, 264693, 55811576, 264558, 60432113, 22279002

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gij2765411[emb CAA74749]- (Y14391) GTP-binding protein [Homo sapiens]	UNCLASSIFIED	264569, 264259, 29331825, 29331826, 29331828, 35696052, 284508, 284905, 284907, 284908, 284909, 264512, 265009, 264910, 264592, 264595, 264758, 264759, 285017, 284681, 284764, 284766, 284686, 18108357, 35695917, 264690, 284692, 284693, 284628, 284629, 35695423, 284630, 284631, 284635, 284636, 18108380, 284638, 284639, 18108388, 18108391
1718	87032828 (3435, 3436)	Novel Protein sim. GBank gij2833262[sp Q14999]Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)	UNCLASSIFIED	285011, 284681, 284682, 284684, 284688, 284689, 21906765, 285021, 284691, 33657023, 284693, 18108370, 35695855, 284632, 284634, 284636, 18108388, 22279002
1719	94315259 (3437, 3438)	Novel Protein sim. GBank gij4505197[ref NP_003473.1]pMILL2 - myeloid/lymphoid or mixed-lineage leukemia 2	UNCLASSIFIED	18108396, 65274572, 35696286, 22278997, 60432049, 56182181, 66714117, 60432289, 29331828, 35696052, 29331828, 284906, 29331830, 56182435, 264592, 60431735, 60433438, 55812038, 284759, 265010, 264600, 284601, 285017, 284448, 284764, 284288, 284769, 21906766, 21906769, 55811957, 265020, 265021, 52844150, 33657023, 33657109, 33657182, 27486262, 33657349, 35695763, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 284631, 56182323, 284559, 284584, 284486, 56182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 284508, 284905, 284906, 284907, 284908, 284909, 284511, 264810, 264758, 21906754, 265011, 284601, 284760, 284762, 284288, 264766, 284686, 18108357, 284689, 21906765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274781, 264630, 20281071, 284634, 284635, 284636, 284637, 284556, 284638, 284639, 56182323, 87168518
1720	94853063 (3439, 3440)	Novel Protein sim. GBank gij2129478[pir S51939]- chitinase (EC 3.2.1.14), precursor - beet	UNCLASSIFIED	22278994, 22278999, 29331822, 285006, 265007, 265008, 55812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21906765, 21906766, 21906768, 21906769, 265020, 33657109, 18108370, 18108374, 284556, 60170394, 83373044, 18108385, 284486
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gij4886461[emb CAB43381.1]- (AL050280) hypothetical protein [Homo sapiens]	UNCLASSIFIED	55994075, 29331824, 29331828, 285009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gij5689375[idb BAA82966.1]- (AB030644) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - kinase Tudor domain	

1723	95358181 (3445, 3446)	Novel Protein sim. GBank gi 426962 gb AAD20633  - (AF128082) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264769, 21906767, 21906768, 56182575, 55811957, 22278997, 22278998, 265020, 264259, 264692, 33857023, 29331822, 29331824, 29331825, 60432289, 33857182, 33856970, 33857349, 29146499, 284508, 264907, 18108370, 264629, 264908, 264909, 18108374, 55811578, 284510, 265008, 264511, 265007, 284910, 264632, 264591, 80432229, 264592, 60433356, 264594, 60433438, 264595, 83373044, 55812038, 33109954, 33857084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264566, 264764, 264288, 264567, 264486, 264369, 264766
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gi 2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	264905, 18108359, 264693, 264628, 264631, 264636, 264555, 264558, 264558, 264559
1725	85655181 (3449, 3450)	Novel Protein sim. GBank gi 3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Anky repeat	homeobox	35696286, 264259, 29331822, 35696052, 284508, 264509, 264905, 264908, 264907, 264908, 264909, 284910, 265009, 264591, 264601, 264760, 18108351, 264681, 264764, 264288, 264766, 264768, 21906769, 35695917, 264628, 35696423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264566
1726	85754255 (3451, 3452)	Novel Protein sim. GBank		UNCLASSIFIED	29146498, 264683, 264689
1727	85280362 (3453, 3454)	gi 4689348 gb AAD27861.1 AF13256 - (AF132562) BcDNA LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264905, 265011, 264689, 21908768

1728	95349515 (3455, 3456)	Novel Protein sim. GBank gij4406549[gbj AAD20027] - (AF131738) Unknown [Homo sapiens]		UNCLASSIFIED	60424178, 18108397, 56182575, 22278995, 56994075, 35698286, 22278997, 22278998, 22278999, 264094, 60432049, 264259, 28331822, 28331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35698052, 264905, 264906, 264907, 28331830, 66712502, 264908, 56182435, 264511, 285008, 285009, 60432229, 60433356, 33857402, 60433438, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 55811150, 264681, 264448, 264682, 264763, 264683, 264288, 264684, 264369, 264685, 264766, 264687, 264769, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 285022, 264535, 264981, 264692, 33657023, 284693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810764, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 58526486, 87188518, 60432113, 22279000, 22279002, 264584, 264586
1729	91227948 (3457, 3458)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	284906, 284907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	85483474 (3459, 3460)			UNCLASSIFIED	28331822, 28331825, 29331828, 264907, 264908, 264909, 265011, 264764, 264629
1731	88266068 (3461, 3462)	Novel Protein sim. GBank gij631600[pri IS47094 - hypothetical protein - rabbit]		UNCLASSIFIED	52648842, 284907, 264809, 56182435, 55811388, 87168559, 285018, 285019, 284760, 52644228, 55811576
1732	91218878 (3463, 3464)	Novel Protein sim. GBank gij4240231[dbj BAA74894.1] - (AB020678) KIAA0871 protein [Homo sapiens]		struct	56182575, 28331822, 28331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21906768, 21906769, 35695917, 265020, 265021, 264638, 56182323
1733	87611718 (3465, 3466)	Novel Protein sim. GBank gij1575756 (U70674) - m-Numb [Mus musculus]	Contains protein domain (PF00640) - Phosphotyrosine interaction domain (PTB/PTD)	- synthase	284907, 264910, 33657402, 265010, 264681, 264683, 264684, 264686, 264769, 264691, 264692, 264693, 264628, 264638, 264558
1734	87795261 (3467, 3468)				264693

1735	88318638 (3469, 3470)	Novel Protein sim. GBank gij4836807 gb AAD30566.1 AF14679 - (AF14679) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016	264488, 18108394, 18108398, 22278998, 60432049, 264259, 29331822, 264908, 265008, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 284682, 18108354, 264769, 264689, 21906765, 21906768, 21906769, 29148628, 29148784, 265021, 265022, 52644150, 18108384, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390
1736	95362884 (3471, 3472)	Novel Protein sim. GBank gij4885647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED	264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433358, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gij2143607 pir S68695 - B/K protein - rat	Contains protein domain (PF00168) - C2 domain	29331822, 29331830, 264591, 265011, 285018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gij2225941 emb CAA69714  - (Y08460) Mdes protein [Mus musculus]	UNCLASSIFIED	264908, 264909, 265008, 264910, 264566
1739	87328576 (3477, 3478)		UNCLASSIFIED	35696052, 264603, 264557
1740	83592939 (3479, 3480)	Novel Protein sim. GBank gij4809 emb CAA44309  - (X62452) YCR601 [Saccharomyces cerevisiae]	traffic	264604, 21906764, 18108364, 264629, 35695855, 264636
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gij4883898 gb AAD31695.1 AF13042 - (AF13042) serine protease-like protein [Homo sapiens]	UNCLASSIFIED	60432289, 29331827, 264509, 265009, 60432229, 264759, 265017, 264767, 264688, 264689, 21906769, 265020, 33657109
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gij4505193 ref NP_003667.1 pMLD1 - membrane fatty acid (lipid) desaturase	UNCLASSIFIED	264908, 264910, 264758, 265011, 264631, 264638, 264566
1743	86966475 (3485, 3486)		UNCLASSIFIED	265017, 265020, 264692
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gij728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	UNCLASSIFIED	22278998, 264508, 264907
1745	20290075 (3489, 3490)		UNCLASSIFIED	264558
1746	84326110 (3491, 3492)	Novel Protein sim. GBank gij7311756 sp P38873 YHY6_YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-IK11 INTERGENIC REGION	UNCLASSIFIED	65274791, 264639, 264559
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gij1658503 (U75467) - Alu [Drosophila melanogaster]	transcription factor	52846842, 29331824, 28331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264369, 264769, 264689, 35695917, 60170815, 264691, 33657023, 65274791, 35695855, 60170394, 22279000, 264482



1748	88003580 (3485, 3486)	Novel Protein sim. GBank gij4504511[ref]NP_001530.1[phsJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	eph	264489, 56182575, 28331824, 56182435, 264112, 265007, 265019, 264764, 21906768, 265020, 264691, 55811576, 264635, 264555, 264558, 264557, 264559 264106
1749	83363091 (3487, 3488)	Novel Protein sim. GBank gij5650780[gjAAD45948.1[AF15196 - (AF151968) RGS protein, RGS-17 (Gallus gallus]	Contains protein domain (PF00615) - Regulator of G protein signalling domain	oncogene	
1750	94321664 (3499, 3500)	Novel Protein sim. GBank gij4996894[gjAAC28444.2] - (AF065164) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]			
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gij2760161[dbjBAA24184] - (AB010054) outer arm dynein light chain 2 [Anthodaris crassipalpa]	Contains protein domain (PF00560) - Leucine Rich Repeat	ATPase_associated	33657402, 264288, 52844150, 263974, 83373044
1752	86456530 (3503, 3504)	Novel Protein sim. GBank gij3915482[spjP74346]YG29, SYN3 - HYPOTHETICAL 38.0 KD PROTEIN SLR1629	Contains protein domain (PF00849) - RNA pseudouridylylase synthase	deaminase	264510, 264583, 264682, 21906765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gij2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acyltransferase	phosphatase	56994075, 22278996, 264908, 60170831, 264682, 264764, 264369, 264288, 264685, 264687, 21906766, 264692, 264693, 65274620, 65274791, 35895855, 264637, 264584
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gij731421[spjP39981]VEH4 YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION		transport	264488, 35696286, 264509, 264806, 264807, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264604, 264762, 264763, 264685, 264768, 264691, 264628, 35696423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264584, 264585, 264586, 264587, 264686
1755	78470282 (3509, 3510)	Novel Protein sim. GBank gij1176422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	
1756	82862614 (3511, 3512)	Novel Protein sim. GBank gij4432860[gjAAD20708] - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]			52646842, 22278994, 22278995, 56994075, 22278996, 22278997, 264259, 29331822, 60432289, 29331827, 33858970, 265008, 265009, 60432229, 60433358, 60433438, 33109854, 21906754, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 87168518, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gij5441615[emb]CAB46856.1] - (AJ386557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_rna_bind	22278997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264583, 265019, 264768, 21906768, 65274620, 18108385, 60432113, 264586, 264487

1758	87812971 (3515, 3516)	Novel Protein sim. GBank gij38810401emb CAA164031 - (AL021497) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265006, 265007, 265009, 264591, 33657402, 33109954, 87189474, 264800, 265017, 265018, 21906769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 264632, 52644332, 22278002, 264563
1759	36984372 (3517, 3518)		UNCLASSIFIED	264759
1760	87329716 (3519, 3520)	Novel Protein sim. GBank gij5262748 emb CAB45688.11 - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]	UNCLASSIFIED	56182575, 60432049, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264910, 60432229, 264592, 264595, 55812038, 264758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811957, 35695817, 264690, 264692, 264628, 264629, 55811576, 35696423, 264632, 264634, 264636, 264557, 264639, 60432113, 264585, 264486
1761	87409586 (3521, 3522)	Novel Protein sim. GBank gij127749 sp P10569 MYSC_ACACA - MYOSIN IC HEAVY CHAIN	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gij3169158 (AC004770) - BC269730_2 [Homo sapiens]	desaturase	22278999, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21906765, 21906766, 21906767, 21906768, 265021, 264690, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gij4808026 gb AAD30062.11 - (AF132856) suppressor of G2 allele of skp1 homolog [Homo sapiens]		56181686, 29331825, 35696052, 264905, 264906, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35696423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gij1360669 pir ICGHU1V - collagen alpha 1(V) chain precursor - human	collagen	22278998, 264259, 35696052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264288, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22279002
1765	81230091 (3529, 3530)	Novel Protein sim. GBank gij486806 pir IS35503 - finger protein neutralized - fruit fly (Drosophila melanogaster)	UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264910, 265009, 21906754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264766, 18108358, 21906768, 21906767, 29148627, 29148629, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)	glycoprotein	52645156, 87188559, 60170615, 33657023, 264693, 33657109, 27486261, 264555, 83373044
1767	87755998 (3533, 3534)	Novel Protein sim. GBank gi 4176443 emb CAA18263.1  - (AL022238) dJ1042K10.4 [novel protein] [Homo sapiens]	UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)		UNCLASSIFIED	29331824, 29331825, 264591, 56182323
1769	87388988 (3537, 3538)		UNCLASSIFIED	264563
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi 115204 sp P00736 CTR_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin	284488, 264768, 264769, 58182575, 55811957, 264690, 264691, 35686052, 264905, 264509, 264906, 264907, 264628, 264808, 264909, 264910, 264834, 264635, 264636, 264558, 264757, 264758, 55812038, 65274444, 264760, 264563, 264762, 264784, 264684, 264768
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 391418 sp P5658 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KO SUBUNIT (O-GLCNAc TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain	264758, 264600, 264369, 55811957, 265020, 83373044, 22278000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb AAD34351.1 AF12136 - (AF121360) DNZDHC/NEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHC zinc finger domain	22278998, 28331828, 33109954, 265018, 265019, 264764, 21906765, 265020, 265021, 264559
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	65274572, 56182575, 22278998, 35686286, 22278999, 264259, 29331824, 60424269, 29331825, 60432289, 35686052, 264106, 284509, 264906, 264907, 29331830, 264908, 52644045, 264511, 265008, 265007, 265008, 60170831, 60433438, 264758, 55811386, 87188559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52644150, 264691, 33657023, 264692, 264693, 60431528, 35686423, 35685855, 264636, 58182323, 18108387, 58526486, 22279000, 22278002, 264563, 264564, 264565, 264566, 264567
1774	94232673 (3547, 3548)	Novel Protein sim. GBank gi 2495689 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	UNCLASSIFIED	65274572, 56182575, 35686052, 55812038, 33109954, 21906754, 265017, 21906767, 21906768, 21906769, 265020, 264691, 264636, 56182323, 22278002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gij1469199[dbj BAA09487] - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278997, 29331822, 29331828, 60432289, 29331828, 35696052, 29331830, 66712502, 264828, 56182435, 264511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21906754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 264448, 264288, 264689, 21906765, 21906768, 21906767, 21906768, 265020, 265021, 265022, 264691, 33657023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811578, 35695855, 264832, 264634, 264638, 264639, 56182323, 83373044, 56528486, 87168518, 60432113, 22279000, 22279002, 264482, 264486, 264910
1776	94133756 (3551, 3552)	Novel Protein sim. GBank gij4589676[dbj BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gij3219939[sp P87115 YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1		nucl_rept	56994075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21906765, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811578, 35695855, 22279000, 22278002, 264564
1778	94851624 (3555, 3556)	Novel Protein sim. GBank gij3875648[emb CAA91454.1] - (Z66561) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...		UNCLASSIFIED	29331826, 29331827, 35696052, 264512, 285007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906768, 21906767, 21906768, 21906769, 285020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gij4589676[dbj BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29148627, 35696286, 29147620, 265008, 265007, 265008, 18108385, 65274727, 264482, 264359, 264768
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56528486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264908, 264639
1782	88094807 (3563, 3564)	Novel Protein sim. GBank gij729225[sp P4123 CTXN_RAT - CORTEXIN			264259, 29331822, 264508, 264905, 264906, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264288, 264768, 264769, 264635, 264638, 264637, 264639, 264563
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gij2257543[dbj BAA21436] - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]		interferon	264768

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gi 1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PH domain	35686286, 264259, 35688052, 264508, 264905, 264906, 264907, 68712502, 264908, 264909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 264601, 264602, 264604, 264605, 18108351, 264782, 264763, 264764, 264389, 264768, 264687, 264768, 264688, 21905768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35696423, 264631, 264632, 264635, 264637, 264638, 264639, 18108385, 22278000, 22279002, 264565, 264566, 264488
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gi 4589552[db][BAA76798.1] - (AB023171) KIAA0954 protein [Homo sapiens]	UNCLASSIFIED	65274572, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 264805, 264906, 264908, 66712502, 56182435, 264511, 265007, 60433356, 55811150, 264683, 264369, 264687, 52644229, 21908767, 52644150, 33657023, 65274620, 33657182, 65274781, 35695855, 264555, 65274727, 22279002
1786	85206465 (3571, 3572)	Novel Protein sim. GBank gi 117788[sp]P26770[CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)]	UNCLASSIFIED	264908, 35696423, 264636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gi 3877175[emb][CAA90338.1] - (Z50028) cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL.D68896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264905, 264908, 264909, 264585, 264764, 264766, 264692, 60431528, 264629, 264638, 264564, 264566
1788	91226778 (3575, 3576)	Novel Protein sim. GBank gi 2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	264488, 83373044
1789	86094528 (3577, 3578)		UNCLASSIFIED	264488, 29331828, 264909, 18108351, 264288, 265021, 264555, 264638
1790	82489734 (3579, 3580)			35696052, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 264758, 265011, 265019, 264764, 264766, 264769, 264628, 264635

1781	95197259 (3581, 3582)	Novel Protein sim. GBank gij2114321[dbj BAA200371 - (DB8733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	284488, 284686, 284687, 284768, 18108394, 284759, 18108397, 284259, 284691, 284692, 33657023, 284693, 284509, 284905, 284906, 284628, 284907, 284629, 284908, 284909, 284510, 285006, 284511, 285008, 284630, 285009, 284631, 284910, 284632, 284634, 284635, 284555, 284636, 284592, 284637, 284593, 284638, 18108381, 284639, 284758, 285010, 285011, 284602, 22279000, 284604, 284760, 284564, 284681, 284782, 284565, 284763, 284683, 284566, 284764, 284288, 284684, 284567, 18108354, 18108391, 284685, 284766
1782	87782690 (3583, 3584)	Novel Protein sim. GBank gij4337106[gb AAD18082] - (AF129756) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 284259, 284508, 265007, 33657402, 87188559, 284369, 33657023, 35695855, 20281071, 264559, 18108387, 87168518
1783	95337877 (3585, 3586)	Novel Protein sim. GBank gij5579331[gb AAD45504.1 AF145732] endoplasmic reticulum alpha-mannosidase 1 [Homo sapiens]	Contains protein domain (PF01532) - Glycosyl hydrolase family 47	ATPase-associated	65274572, 22278995, 22278996, 22278997, 22278999, 284093, 264259, 29331824, 66714117, 60432289, 29331827, 29331828, 284103, 284105, 29331830, 265007, 264910, 265009, 60170831, 60433356, 21906754, 265010, 265017, 265018, 264681, 284682, 284288, 52644228, 21906765, 21906768, 21908767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 52844150, 33657023, 33657109, 18108370, 18108374, 65274791, 20281071, 60432113, 22279000, 264482, 264564
1784	87759806 (3587, 3588)	Novel Protein sim. GBank gij4914604[emb CAB43677.1] - (AL050389) hypothetical protein [Homo sapiens]	Contains protein domain (PF01798) - Putative snRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278999, 264259, 29331822, 29331824, 29331825, 29146498, 29146499, 264508, 264905, 52644045, 264112, 265006, 265008, 264910, 60433356, 264757, 55812038, 87168474, 265011, 265017, 18108351, 264763, 264448, 264683, 284369, 21906765, 21906766, 21906767, 21906769, 29148784, 35695917, 60170615, 33657023, 284629, 18108374, 18108376, 35696423, 35695855, 284558, 284557, 284638, 284558, 18108385, 264564
1795	79747856 (3589, 3590)			UNCLASSIFIED	264632, 284635, 284636, 284595, 284596, 284907, 284566, 284909
1796	86599466 (3591, 3592)	Novel Protein sim. GBank gij585084[sp Q07803 EFGM_1 AT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)]		glycoprotein	264488, 284907, 284909, 284594, 264595, 264768, 284687, 21906765, 21906767, 264628, 284630, 264559

1797	91223219 (3593, 3594)	Novel Protein sim. GBank gl 1842111 (U87586) - decoy (Arabidopsis thaliana)		ribosomalprot	22278998, 22278997, 22278998, 22278999, 29331822, 264910, 60170831, 21908754, 52644229, 21908768, 21908789, 35695917, 265022, 52644150, 264681, 33657023, 263987, 33657109, 22279000
1798	91221276 (3595, 3596)	Novel Protein sim. GBank gl 2832506(db) BAA24508.1 -(D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 284757, 80433438, 21908754, 33657084, 87168559, 265017, 18108351, 264682, 284448, 264288, 21908765, 21908768, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22279000, 264486
1799	86321713 (3597, 3598)	Novel Protein sim. GBank gl 5689541 db BAA83054.1 -(AB029025) KIAA1102 protein [Homo sapiens]		eph	264908, 21908754, 21908767, 21908769, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080118 (3599, 3600)	Novel Protein sim. GBank gl 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	284691, 284558, 284566
1801	95060723 (3601, 3602)	Novel Protein sim. GBank gl 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			52644045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gl 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35686286, 66714117, 284508, 284509, 56182435, 284512, 18108351, 284688, 55811957, 264692, 55811576, 35695855, 284486
1803	95060725 (3605, 3606)	Novel Protein sim. GBank gl 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264769, 264689, 21908769, 35696286, 35695917, 264259, 264691, 264692, 264693, 20281099, 18108364, 35696052, 264508, 284509, 284905, 284908, 18108370, 284628, 264907, 66712502, 264908, 284909, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 285008, 265007, 264512, 265008, 264910, 284631, 284632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 284596, 18108385, 18108387, 265011, 284760, 284583, 18108351, 284762, 264564, 264448, 264565, 264763, 264683, 264764, 264566, 264288, 264486, 264567, 284765, 284766

1804	87770203 (3607, 3608)	Novel Protein sim. GBank gij3879914[emb]CAA98538.1] - (Z74043) predicted using Genefinder: cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk34314.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21906754, 264766, 21906765, 21906768, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3608, 3610)	Novel Protein sim. GBank gij5453844[ref]NP_008461.1pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644229, 35696423, 264636, 60432113
1806	94133762 (3611, 3612)	Novel Protein sim. GBank gij4589876[dbj]BAA78857.1] - (AB023230) KIAA1013 protein [Homo sapiens]	struc1		264094, 264105, 264908, 35698423, 265008, 265007, 265008, 264555, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gij4884079[emb]CAB43235.1] - (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264488, 35696286, 66714117, 35696052, 66712502, 264592, 60433438, 52644296, 265010, 264683, 264369, 264689, 55811957, 35695917, 33657109, 35695783, 55810764, 18108379, 35696423, 35695855, 56182323, 264563, 264564, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gij1916927 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264686, 28148629, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88066316 (3618, 3620)	Novel Protein sim. GBank gij1352944[sp]P47179YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264488, 35696052, 264905, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264686, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264567
1811	88066272 (3621, 3622)	Novel Protein sim. GBank gij2134984[pir]j37275 - death-associated protein kinase (EC 2.7.1.-) - human	Contains protein domain (PF00023) - kinase Ank repeat		264488, 264259, 264508, 264509, 264905, 264906, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264766, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	78245772 (3623, 3624)				29331822, 29331824, 265018, 18108351, 21906769



1813	88090972 (3625, 3626)	Novel Protein sim. GBank gi 5051636 gb AAD38326.1 AF07372 - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucosylase	56182575, 264259, 29331824, 66714117, 29331828, 35698052, 264509, 264805, 264806, 264907, 264908, 66712502, 264909, 265007, 264910, 264591, 264593, 55612038, 265011, 265018, 264760, 264682, 264764, 264683, 264369, 264768, 264768, 264769, 21908768, 21908768, 264691, 264693, 18108374, 35695855, 264634, 264635, 264637, 264639, 264559, 22278000, 22278002, 264566
1814	88178047 (3627, 3628)	Novel Protein sim. GBank gi 3643608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 35698286, 22278988, 264082, 264084, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29331827, 29331828, 264105, 264107, 52644045, 56182435, 265009, 60432229, 60433356, 87168474, 87168559, 264369, 264288, 21908765, 35695917, 265021, 265022, 33657023, 33657109, 18108374, 35696423, 264638, 35692848, 264482
1815	85296473 (3629, 3630)	Novel Protein sim. GBank gi 117788 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)		siuct	22278989, 264508, 264509, 264907, 264808, 264910, 265011, 264760, 264766, 264634, 264636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi 1176823 sp P41846 Y096_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 264509, 264907, 264908, 264909, 265009, 264591, 265011, 265017, 264687, 264689, 265022, 264691, 18108362, 18108368, 18108370, 18108374, 18108379, 264839, 264557, 264584, 264587
1817	88095268 (3633, 3634)	Novel Protein sim. GBank gi 3766377 emb CAA21429  - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - histone WD domain, G-beta repeat		264488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644229, 21906765, 21908767, 21908768, 52644150, 33657023, 33657109, 27488262, 18108370, 18108374, 60170394, 56182323, 22279002
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gi 3879121 emb CAA94370  - (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	35698286, 60433356, 264758, 264369, 264686, 21908769, 264693, 264632
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi 5031865 ref NP_005771.1 pLHFP - lipoma HMGIC fusion partner		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331826, 264908, 265007, 265008, 265009, 60432229, 265017, 265018, 265019, 264448, 264288, 21908768, 21908769, 265020, 18108381, 18108384, 22278000, 22279002, 264567

1820	87769455 (3639, 3640)				264905, 264907, 264594
1821	80431510 (3641, 3642)				264907, 264768, 263978
1822	91221523 (3643, 3644)	Novel Protein sim. GBank gi 4884130 emb CAB43272.1  - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278986, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 35686052, 29331828, 264908, 29331830, 60170831, 264591, 264593, 60433356, 264598, 265017, 265019, 18108351, 264763, 264683, 21906765, 21908787, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 18108364, 18108370, 35695855, 22279000, 22279002, 264488, 264259, 264511, 264288, 264768, 264693, 35696423, 264834, 18108385, 264486
1823	85522330 (3645, 3646)			UNCLASSIFIED	264907, 264908, 264909, 264511, 264631, 264634, 264635, 264637, 264638, 264639, 264758, 264568
1824	86612025 (3647, 3648)	Novel Protein sim. GBank gi 477072 pr A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - immunoglobulin domain	UNCLASSIFIED	60432049, 264910, 264487
1825	87430125 (3649, 3650)	Novel Protein sim. GBank gi 3036803 emb CAA18493  - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gi 4680865 gb AAD27732.1 AF13295 - (AF132957) CGI-23 protein [Homo sapiens]		ATPase-associated	52644507, 52645156, 52646842, 22278994, 22278996, 56994075, 264259, 60432049, 52645080, 35696052, 66712502, 52644045, 265008, 265009, 60432229, 60433356, 60433438, 52646317, 52644296, 265011, 87168559, 264448, 264288, 264369, 264688, 52644229, 264689, 21906785, 21906788, 265020, 60170815, 52644150, 33657023, 27486262, 27486264, 27486265, 35695783, 35696423, 35695855, 83373044, 87168518, 264404, 22279002
1827	81647212 (3653, 3654)				264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gll4503571[ref]NP_001419.1pEN01 - endolase 1, (alpha)	Contains protein domain (PF00113) - Endo-ase	oncogene	264488, 52646842, 56182575, 22278986, 35696288, 22278997, 22278999, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 66712502, 52644045, 56182435, 265006, 264511, 264512, 265007, 265008, 265009, 60170631, 60432228, 264593, 60433356, 60433438, 284738, 33108954, 21906754, 87188474, 265010, 265011, 87188559, 265017, 265019, 264761, 264762, 264448, 264764, 264883, 264288, 264369, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264689, 21906768, 21906769, 35695917, 265021, 60170615, 33657023, 33657349, 263972, 55811576, 35695855, 264635, 264555, 264556, 264638, 264557, 87168518, 22279000, 22279002, 264563, 264482, 264585, 264484, 264567
1829	80187720 (3657, 3658)				264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264810
1830	94312942 (3659, 3660)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52646317, 52644296, 87188559, 265019, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 35695763, 263974, 35896423, 35695655, 52644332
1831	94138063 (3661, 3662)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265019, 265022, 264693, 65274791
1832	84521663 (3663, 3664)	Novel Protein sim. GBank gll1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....			264602

1833	95314184 (3665, 3666)	Novel Protein sim. GBank gi 5174413 ref NP_006026.1 pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	22278994, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 60432289, 29331827, 35696052, 29146499, 264508, 284509, 284908, 264907, 66712502, 284908, 52844045, 284909, 284512, 265008, 264591, 264593, 60433356, 21906754, 33657084, 265011, 265017, 264604, 265018, 265019, 264681, 18108351, 284683, 264288, 264685, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 21905769, 29146829, 265020, 265021, 284690, 284692, 33657023, 65274620, 33657182, 27486264, 33657349, 65274781, 264634, 264635, 264556, 264557, 264558, 264559, 18108385, 56528486, 87168518, 60432113, 22279000, 22279002, 264563
1834	80562790 (3667, 3668)			264259, 264907, 264689, 22279000, 22279002
1835	94135718 (3669, 3670)		UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 264603, 21906768, 263976, 35695855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gi 4759286 ref NP_004288.1 pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	29331825, 264908, 265019, 264764, 264686, 21906765, 264635
1837	94234297 (3673, 3674)	Novel Protein sim. GBank gi 3334400 sp Q24574 UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - ubiquitin Ubiquitin carboxyl-terminal hydrolase family 2	22278995, 29146499, 265006, 265008, 265009, 265010, 264683, 21906765, 29148627, 29148629, 285020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gi 1362599 p J A56154 - Abi substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain	29331822, 265017, 264760, 285020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gi 2117310 emb CAB09116.1  - (Z95620) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264601, 21906765, 21906766, 265021, 33657109, 284556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gi 127560 sp P23249 MOV10_MOUSE - PROTEIN MOV-10	UNCLASSIFIED	264693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gi 4572464 gb AAD23834.1 AF12365 - (AF123653) FEZ1 [Homo sapiens]		56182575, 29331824, 29331826, 60433356, 264764, 264288, 33657023, 283967, 18108370, 18108374, 264631, 264555, 284556, 264639

1842	80982645 (3683, 3684)	Novel Protein sim. GBank gl1326268 (U58728) - C54H2.1 gene product (Caenorhabditis elegans)		UNCLASSIFIED	65274572, 29331822, 29331824, 29331825, 68714117, 29331826, 29331827, 264907, 264909, 52644045, 56182435, 264510, 265006, 265007, 265008, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264686, 264769, 33657023, 264683, 18108364, 33657109, 18108368, 264628, 55810764, 56182323, 18108384, 264563, 264564
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 56182435, 264769, 29331828, 29331828, 264511, 265006, 265007, 264910, 264631, 264508, 264690, 264636, 264584, 264691, 60432229, 60432048, 264259, 264629, 33657023, 264488, 264909, 264587, 264595, 264768
1844	87444764 (3687, 3688)	Novel Protein sim. GBank gl12496887 (sp1Q09232) YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264808, 265022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gl1175494 (sp1Q09819) YAC5_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	transcript factor	264259, 29331824, 264907, 264908, 68712502, 264510, 265007, 265008, 55812038, 265018, 21908765, 52644150, 33657109, 264555, 264556, 264557, 56182323, 18108382, 83373044, 18108385, 264584
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gl13881080 (emb1CAA21739) - (AL032657) similar to EGF-like domain; cDNA EST yk289a12.3 comes from this gene; cDNA EST EMBL:D35388 comes from this gene; cDNA EST yk331h8.5 comes from this gene; cDNA EST yk298a12.5 comes from this gene; cDNA EST yk467g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 264908
1847	87821497 (3693, 3694)	Novel Protein sim. GBank gl15059323 (gb1AAD38967.1) AF151522 - (AF151522) hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcript factor	22278997, 264259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gl15701854 (emb1CAB52191.1) - (AJ245417) G5b protein [Homo sapiens]		tm7	29331825, 29331828, 29331827, 265017, 264883, 264288, 264768, 264768, 21908767, 21908768, 264692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gl14503685 (ref1NP_001989.1) pFBLN - fibulin 2 precursor	Contains protein domain (PF00008) - EGF-like domain	ATPase associated	56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gl14589582 (dbj1BAA76813.1) - (AB023186) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gl1220637 (dbj1BAA01477) - (D10827) zinc finger protein [Mus musculus]	Contains protein domain (PF00008) - Zinc finger, C2H2 type	dna_ma_bind	29331824, 35896052, 264910, 60433438, 264888, 35895917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gil5174629[refNP_006090.1]pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35696286, 22278996, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52644045, 265007, 264910, 60432229, 60433356, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 264448, 264686, 264687, 21906765, 21906767, 21906769, 265021, 265022, 52644150, 264693, 33657109, 18108370, 18108374, 55811576, 35695855, 56182323, 60432113, 22279002, 264563 264687, 264768, 52644507, 264769, 21906765, 21906767, 21906768, 22278995, 56994075, 22278999, 52644150, 264259, 264692, 29331822, 29331824, 52645128, 29331827, 33656970, 33657349, 35695763, 264508, 264906, 264628, 264907, 264629, 264909, 35696423, 35695855, 264510, 265006, 264511, 264512, 264630, 265009, 264631, 264910, 264634, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644296, 87168518, 87168559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264567, 264288, 264389, 264766 264592
1853	91222287 (3705, 3706)	Novel Protein sim. GBank gil854065[emb]CAA563371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gil2072864 (U93569) - putative p150 [Homo sapiens]		nuclease	
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gil4539520[emb]CAB39994.1] - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - nucl_rept Kelch motif		18108392, 52646365, 65274572, 56182575, 22278994, 56994075, 22278996, 35696286, 22278999, 264259, 60432049, 264908, 264510, 265007, 265008, 265009, 264595, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264768, 18108359, 21906764, 21906768, 29148627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264638, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gil3954978[emb]CAA06945] - (AJ008278) acetylglucosaminyltransferase-like protein [Mus musculus]		UNCLASSIFIED	56994075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gil4322670[gb]AAD16120] - (AF094508) dentin phosphoryn [Homo sapiens]	ATPase-associated		22278999, 264259, 264908, 60170831, 264448, 264686, 265020, 265022, 33657109, 60170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gi4981903 gb AAD36415.1 AE001788 ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomal prot	284757
1859	84407464 (3717, 3718)	Novel Protein sim. GBank gi4240317 dbj BAA74937.1  - (AB020721) KIAA0914 protein [Homo sapiens]			22278996, 28331824, 265007, 33109954, 265019, 264369, 21908768, 29148784, 27486261, 52844332, 22279002 265019
1860	17829308 (3719, 3720)	Novel Protein sim. GBank gi4009522 (AF099731) - connexin 31.1 [Homo sapiens]			
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi2143837 pir l84505 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase		264887, 264259, 28331822, 29331824, 29331825, 265007, 285009, 284591, 33109954, 265010, 264369, 264288, 284886, 264691, 264693, 27486284, 18108370, 18108374, 263877, 55811578, 56182323, 264639, 22279000, 22279002, 264482
1862	87372823 (3723, 3724)	Novel Protein sim. GBank gi125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35996288, 264259, 87188474, 264369, 21906768, 264558, 264593
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi3820909 emb CAA09299  - (AJ010842) Dof protein [Drosophila melanogaster]		UNCLASSIFIED	284601, 284768, 29148827, 29148829, 264692, 264629, 264635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi4322263 gb AAD15985  - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	synthase	22278998, 264259, 264907, 265018, 18108370, 264634, 264635, 264555, 264558, 264638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi249572 sp Q93073 Y256_HUMAN - HYPOTHETICAL PROTEIN KIAA0256			22278998, 264490, 29331822, 66714117, 66712502, 265006, 265007, 265008, 265009, 264591, 60433438, 265010, 265018, 264760, 284448, 264768, 29148827, 29148829, 265020, 265022, 18108385, 60432113
1866	87268816 (3731, 3732)	Novel Protein sim. GBank gi5282617 emb CAB45748.1  - (AL080157) hypothetical protein [Homo sapiens]		kinase	18108374, 264769, 18108377, 21906765, 21906766, 35696423, 56182575, 21908769, 29148629, 35696288, 35695917, 265021, 264510, 264511, 264512, 264534, 264535, 60170831, 52644150, 264555, 264691, 284259, 264556, 264692, 264557, 33657023, 60433356, 29331822, 264559, 264595, 29331824, 18108385, 21908754, 33657182, 29331827, 35696052, 33656970, 87168518, 265017, 60431602, 22279000, 264508, 264509, 18108351, 264907, 264682, 264567, 18108372, 264765, 264488 264094
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gi3859930 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]		UNCLASSIFIED	

1868	87357459 (3735, 3736)	Novel Protein sim. GBank gij3881525[embjCAA33884] - (Z70038) cDNA EST EMBL.D32579 comes from this gene; cDNA EST EMBL.D3254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357110.5 comes from this gene [Caenorhabditis elegans]		nuclease	264489, 22278997, 22278999, 29331825, 29331826, 265008, 265009, 33657402, 87168474, 18108351, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 27486264, 264828, 18108374, 264831, 18108385, 87168518, 22279000, 22279002, 264568, 264567
1869	86977292 (3737, 3738)	Novel Protein sim. GBank gij4826772[refjNP_004961.1]p[IGFA - insulin-like growth factor binding protein, acid labile subunit]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264508, 264509, 264906, 264908, 264909, 264910, 264591, 264600, 18108351, 264883, 264766, 264769, 35695855, 264634, 264558, 264639, 18108385, 264583, 264486
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gij1869859[embjCAB06722] - (Z86099) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264686, 264888, 21908768, 21908769, 35695917, 60170815, 264692, 18108368, 35695763, 35698423, 65274791, 264638, 264639, 56526486
1871	80234464 (3741, 3742)			UNCLASSIFIED	264509, 264905, 264595, 264768, 264635, 264636, 264563, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank gij2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	264510, 264594, 264565
1873	80213890 (3745, 3746)				264509, 264512, 265009, 265011, 18108351, 264887, 264691, 18108370, 18108374, 264635
1874	95351136 (3747, 3748)		Contains protein domain (PF00293) - Bacterial mutT protein	UNCLASSIFIED	264488, 35695917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264636, 264637, 264638, 33657402, 264558, 18108385, 264600, 264604, 264764, 264587, 264766
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gij4589520[dbjBAA76782.1] - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	35698286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gij263810[bsj122920] - collagen alpha chain [Riftia pachypila=tube worms, Peptide, 1027 aa]		UNCLASSIFIED	264259, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264556, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gij3983356[gbjAAC63924.1] - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264767, 264686, 264768, 263978, 264693, 264639, 265010, 264563, 264905, 264908, 264907



1878	95351056 (3765, 3766)	Novel Protein sim. GBank gij4510345jgb/AAD21434.1) - (AC008921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - ubiquitin AN1-like Zinc finger	264569, 264488, 35698286, 56994075, 264259, 29331822, 29331824, 29331825, 35698052, 29331828, 29146498, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 33657402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264764, 264369, 264288, 264766, 264687, 264768, 264789, 21808766, 35695917, 265021, 60170615, 33657023, 264692, 264693, 33657109, 27486285, 264628, 18108370, 264629, 18108374, 35696423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526486, 87168518, 264563, 264564, 264566, 264488, 264567, 264905, 264907, 264908, 265007, 264565, 264566
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gij4928643jgb/AAD34082.1)AF15184 - (AF151845) CGI-87 protein [Homo sapiens]	UNCLASSIFIED	264766, 264691, 264692, 83373044
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gij1550785jemb/CAA69283] - (Y08026) immune associated protein 38 [Mus musculus]	UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264687, 33657023, 264632
1881	80214949 (3761, 3762)	Novel Protein sim. GBank gij93144jprj/B40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhouser or Becker)	UNCLASSIFIED	264908, 21806766, 18108370, 263974, 87168518
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gij2384956 (AF022985) - No definition line found [Caenorhabditis elegans]	homeobox	264908, 284910, 87168559, 21806766, 264636
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gij1351218jpl/P47226[TES2_MOUSE : TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gi 4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 56181686, 22278988, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 284512, 265008, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811386, 265010, 265011, 87168559, 284600, 265017, 264604, 265019, 284605, 284780, 55811150, 284761, 284682, 264763, 264683, 264764, 264288, 264369, 264765, 264686, 264768, 264769, 29148784, 33695917, 264890, 264891, 33657023, 264692, 264693, 33657109, 18108370, 284628, 60431528, 264629, 263973, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 80432113, 22279002, 264563, 264564, 264565, 264566, 264486, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gi 2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	58182575, 264259, 264905, 264909, 265008, 264598, 264766, 265020, 264628, 60431528, 284634, 56528486, 284080, 264563
1886	86674062 (3771, 3772)	Novel Protein sim. GBank gi 2834158 gb AAC02577.1  - (AF045641) No definition line found [Caenorhabditis elegans]			22278988, 22278989, 60432049, 264910, 265018, 264766, 21906768, 29148628, 264690, 264693, 264628, 264555, 264486
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gi 5174421 ref NP_006023.1 pCPNE - copine VI (neuronal)	Contains protein domain (PF00188) - C2 domain	ATPase-associated	29331822, 29331824, 29331825, 29331826, 29331827, 264908, 265007, 264681, 264768, 29148627, 264693, 18108364, 35696423, 65274791, 35695855, 264632, 56182323, 264639, 264563
1888	87822804 (3775, 3776)	Novel Protein sim. GBank gi 3319931 emb CAB10841  - (Z88046) dJ1408.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gi 1083308 pir JAS6559 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264908, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21906765, 21906768, 21906769, 265021, 33657023, 33657109, 56182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gi 4240195 dbj BAA74876.1  - (AB020860) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108398, 29147620, 264907, 265009, 284600, 265018, 18108351, 264288, 264689, 21906765, 21906768, 21906769, 264691, 264692, 264693, 264628, 18108370, 264636, 284558, 264404

1891	67013895 (3781, 3782)			UNCLASSIFIED	264686, 264788, 264887, 264892, 264693, 29331822, 29331824, 264508, 264905, 264806, 18108370, 264828, 264907, 264908, 264909, 18108379, 265007, 265008, 264910, 264832, 264591, 264839, 264596, 18108384, 265010, 265011, 264601, 264605, 264583, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gij5688535[dbj][BAA83051.1] - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct	22278995, 264509, 87168559, 18108351, 264448, 264682, 265020, 264683, 18108374, 22278000
1893	88533826 (3785, 3786)			tannin	264369, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 68714117, 29331828, 264806, 265008, 265008, 265009, 264592, 265018, 264881, 264448, 264683, 18108354, 264369, 264884, 264885, 264788, 264887, 264689, 21906768, 265020, 265022, 60170615, 52644150, 264680, 264681, 264682, 33657023, 264893, 33657109, 264628, 18108374, 35695855, 264630, 264832, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22278000
1894	86989120 (3787, 3788)				264508, 264905, 264908, 264907, 264594, 264684, 264680, 264692, 264630, 264635, 264638, 264639, 264583
1895	87631881 (3789, 3790)	Novel Protein sim. GBank gij5282574[pmbl][CAB45729.1] - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		56182575, 264259, 60432289, 29331828, 264107, 264905, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264288, 264768, 33657109, 264628, 55810764, 18108379, 264634, 58182323, 56526488
1896	85673555 (3791, 3792)		Contains protein domain (PF00827) - UBA domain	UNCLASSIFIED	264807, 265008, 264682, 264686, 21906768, 264629, 264631, 264634, 264555, 264259
1897	80565569 (3793, 3794)	Novel Protein sim. GBank gij728836[sp][P39193]ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		cadherin	
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gij127560[sp][P23249]MV10_MOUSE - PROTEIN MOV-10		helicase	22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35696052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644228, 21906765, 21906766, 21906768, 21906769, 60170615, 55810764, 22279000
1899	86673097 (3797, 3798)	Novel Protein sim. GBank gij2909819 (AF031548) - erythrocyte membrane glycoprotein Rhs50 [Homo sapiens]	Contains protein domain (PF00909) - Ammonium Transporter Family	glycoprotein	264259, 264508, 264909, 60432229, 264769, 21906765, 21906769
1900	87841858 (3799, 3800)	Novel Protein sim. GBank gij4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]		UNCLASSIFIED	264683

1901	95196847 (3801, 3802)	Novel Protein sim. GBank gi 585959 sp P38378 S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52644507, 52645156, 18108396, 52646385, 52646842, 18108397, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278998, 264490, 60432049, 264259, 29331822, 52645080, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264906, 264907, 29331830, 264908, 52644045, 264909, 284112, 265006, 264512, 265008, 264910, 265009, 60170831, 60432228, 60433356, 33657402, 60433438, 55812038, 264758, 33109954, 21908754, 33657084, 52644298, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 52644229, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108362, 33657023, 264693, 263987, 33657109, 33657182, 27486264, 33657349, 35695763, 18108370, 18108376, 55811576, 35696423, 35695855, 60431850, 264636, 263981, 52644332, 60170394, 83373044, 18108385, 87168518, 60432113, 264564
1902	80202013 (3803, 3804)	Novel Protein sim. GBank gi 426613 gb AAD20451  - (AF098796) SLM-1 [Mus musculus]		dna_ma_bind	264107, 263976
1903	87778554 (3805, 3806)	Novel Protein sim. GBank gi 3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 29331825, 29331827, 264508, 264907, 265008, 60170831, 60433356, 60433438, 264759, 21906754, 264448, 264288, 265021, 265022, 33657023, 264693, 55811576, 264555, 264556, 22279000
1904	80434213 (3807, 3808)	Novel Protein sim. GBank gi 1352911 sp P47147 YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264509, 264905, 264906, 264907, 264908, 265007, 264910, 264686, 264768, 264687, 264769, 264693, 264628, 18108374, 264634, 264636, 264637, 264565
1905	95351140 (3808, 3810)	Novel Protein sim. GBank gi 3043714 gb BAA25521  - (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial muT protein		264488, 264768, 264769, 264689, 28148629, 35695917, 35696286, 264259, 264692, 18108362, 33657023, 29331824, 33657109, 29146499, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35696423, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264566, 264288, 264766
1908	12763822 (3811, 3812)			UNCLASSIFIED	264937

1907	95351144 (3813, 3814)	Novel Protein sim. GBank gij4929505[gb]AAD34053.1[AF15181] - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278996, 35696286, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 60424269, 29331828, 35696052, 264593, 60433356, 21906754, 55811386, 85658542, 87168559, 265018, 264681, 264682, 264684, 264288, 21906785, 21906788, 21906788, 265020, 265022, 264690, 52644150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313641 (3815, 3816)	Novel Protein sim. GBank gjj3986770 (AF109906) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181686, 22278995, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331826, 29331827, 29331828, 29146499, 264805, 264908, 264907, 264908, 86712502, 264909, 56182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433436, 264596, 55812038, 33109854, 52646317, 265011, 265017, 264604, 265018, 265019, 264805, 55811150, 264681, 264448, 264288, 264886, 264688, 264768, 21906785, 21906766, 21906767, 21906788, 21906769, 55811857, 26148629, 35695917, 265020, 265022, 264691, 264692, 18108364, 85274620, 33657109, 33657349, 35695763, 18108374, 263978, 55810764, 55811576, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22278000, 22278002, 264566, 264486
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gjj224653[dbj]BAA20813] - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264908, 264907, 264908, 264511, 264910, 264593, 264758, 264764, 264766, 18108370, 264634, 264637, 264486
1910	94216821 (3819, 3820)	Novel Protein sim. GBank gij1351218[sp]P47226[TES2_MOUSE - TESTIN 2 (TES2) (CONTAINS: TESTIN 1 (TES1))]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	35696286, 22278996, 22278999, 35696052, 264509, 264905, 264908, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264768, 264768, 264687, 264769, 35695917, 265021, 52644150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486

1911	91725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAD30184.1 AC006530 hypothetical protein [Homo sapiens]	(Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33658970, 264906, 265007, 264591, 55812038, 87168559, 264448, 264369, 21906765, 21906768, 265022, 264691, 264693, 18108365, 55811576, 264556, 18108385, 18108388
1912	95413519 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA83003.1  - (AB028974) KIAA1051 protein [Homo sapiens]	(Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181686, 22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 66714117, 35696052, 264905, 264906, 264907, 264908, 52644045, 56182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264686, 264788, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35696423, 65274791, 264637, 56182323, 83373044, 56526486, 22278002, 264563, 264566
1913	95305546 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_055665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331828, 29331827, 265006, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1914	83423982 (3827, 3828)	Novel Protein sim. GBank gi 4589604 dbj BAA76824.1  - (AB023197) KIAA0980 protein [Homo sapiens]	(Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35696052, 264906, 264908, 264628, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1915	95340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA82991.1  - (AB028962) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 28331826, 29331827, 264508, 264909, 265009, 285017, 265019, 264788, 264769, 264689, 264628, 264635, 264637, 264639, 83373044, 264565
1916	79640761 (3831, 3832)				264693, 264639

1917	87821660 (3833, 3834)	Novel Protein sim. GBank gij5689381[dbj BAA82979.1] - (AB028950) KIAA1027 protein [Homo sapiens]		struct	264769, 264689, 21906765, 21906768, 22278996, 284259, 284691, 284693, 29331824, 29331825, 29331826, 29331828, 264905, 264906, 264628, 264907, 264908, 264909, 264510, 264630, 264910, 264634, 264635, 264638, 264637, 264638, 263981, 264639, 264758, 18108385, 21906754, 265011, 264604, 264583, 18108351, 264762, 264763, 264586, 264764, 264768
1918	95302785 (3835, 3836)	Novel Protein sim. GBank gij5281517[gb AAD41524.1 AF15483 - (AF154831) PV-1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21906765, 21906767, 21906768, 56182575, 21908789, 22278994, 35696286, 35695917, 22278996, 22278997, 265021, 265022, 264534, 264680, 264691, 264692, 33857023, 264693, 29331824, 29331825, 33857108, 29331826, 52845129, 35696052, 29331828, 27486282, 27486284, 35695783, 284508, 264905, 284509, 264906, 264628, 264907, 18108370, 264908, 264628, 264908, 18108372, 18108374, 263978, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264631, 265009, 264910, 264634, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264559, 264596, 83373044, 264758, 52846317, 18108385, 52844286, 56526488, 87168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 264760, 264761, 264482, 264564, 18108351, 264782, 264682, 264565, 264448, 264764, 264566, 264488, 264567, 264369, 264288, 264766, 264487, 264885
1919	94143847 (3837, 3838)	Novel Protein sim. GBank gij3878584[emb CA801237] - (Z77667) cDNA EST EMBL:CO8125 comes from this gene; cDNA EST EMBL:CO9753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 29331822, 265007, 60170831, 60432228, 60433438, 284448, 264682, 264288, 55811957, 33657023, 33657109, 65274791, 56182323, 22279002
1920	91229853 (3839, 3840)	Novel Protein sim. GBank gij1809231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12868 (NID:g877888) [Homo sapiens]		UNCLASSIFIED	264510, 264511, 264512, 264566
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gij4580997[gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264693

1922	87641863 (3843, 3844)	Novel Protein sim. GBank gi 138595 sp P02845 VIT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELIN I (LVI); PHOSVITIN (PV); LIPOVITELIN II (LVI)]; YGP40]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264909, 18108374, 265008, 264557, 264564, 18108351
1923	94323589 (3845, 3846)	Novel Protein sim. GBank gi 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278995, 264094, 264259, 35698052, 264509, 264905, 264908, 264907, 264908, 66712502, 264909, 264511, 264512, 265007, 264910, 265009, 264591, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 55811150, 264681, 264762, 264448, 264764, 264288, 264369, 264766, 264767, 264686, 264687, 264768, 264769, 56181562, 264689, 21908766, 264691, 33657023, 264693, 65274620, 33657109, 18108370, 264628, 264629, 35898423, 264630, 264631, 264632, 264634, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264564, 264565, 264566, 264567, 29331826, 264908, 264908, 264595, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264565
1924	87338925 (3847, 3848)	Novel Protein sim. GBank gi 3877655 emb CAA86657  - (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:C1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gi 4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - ribosomal prot Ribosomal protein S15		22278995, 22278996, 22278997, 264259, 29331824, 66714117, 29146499, 264909, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 60170394
1926	88094739 (3851, 3852)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]	struct		264905, 264908, 264907, 264910, 264593, 265018, 264760, 264764, 264288, 264692, 264693, 263978, 264631, 264634, 264637, 264563
1927	85654857 (3853, 3854)	Novel Protein sim. GBank gi 3043632 dbj BAA25480  - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87798054 (3855, 3856)	Novel Protein sim. GBank gi 1665761 dbj BAA13377  - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Inf Extracellular link domain		264489, 264259, 265017, 265021, 264692
1929	86997236 (3857, 3858)	Novel Protein sim. GBank gi 5001993 gb AAD37247.1 AF13432 - (AF134321) chimeric AFGP/hypsinogen-like serine protease precursor [Dissostichus mawsoni]	UNCLASSIFIED		264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639



1830	87889128 (3859, 3860)	Novel Protein sim. GBank gi 1709230 sp P52863 NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35606236, 28331828, 284805, 264907, 284908, 284909, 284511, 284910, 284758, 284601, 285017, 285019, 284605, 284780, 284784, 284768, 284688, 284789, 285022, 35698423, 284638, 60432113
1831	87797278 (3861, 3862)	Novel Protein sim. GBank gi 404634 (U01840) - serine/threonine kinase [Mus musculus]		kinase	264906, 264908, 60432223, 284758, 284764, 284288, 285020, 284892, 284634, 284637
1832	15030972 (3863, 3864)				284684, 284691, 284635
1833	11813888 (3885, 3886)			UNCLASSIFIED	284595
1834	84426360 (3867, 3868)	Novel Protein sim. GBank gi 4115748 gb BAA36494  - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		struct	56182575, 56182435, 284510, 284757, 284758, 55812038, 55811386, 265016, 55811150, 21906785, 284681, 284631, 284635, 284637
1835	87752511 (3869, 3870)			UNCLASSIFIED	284686, 285011, 284511, 284905, 18108351, 284564, 284681, 284259, 18108370, 284568, 284784, 284389, 284595
1836	85414338 (3871, 3872)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			60432289, 265007, 265010, 265011, 265019, 33657109, 18108374
1837	84847141 (3873, 3874)	Novel Protein sim. GBank gi 543187 pir S37771 - ankyrin, erythrocyte - mouse		kinase	85565842, 21906767, 35695917, 60170615, 284693, 33657109
1838	87403277 (3875, 3876)	Novel Protein sim. GBank gi 4344431 gb AAD22340.1 AC006955 - (AC006955) hypothetical protein [Arabidopsis thaliana]		collagen	284488, 28146488, 284805, 264559
1839	91004978 (3877, 3878)	Novel Protein sim. GBank gi 500858 db BAA03210  - (D14186) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 285017, 21906785, 21906768, 21906768, 55811957, 27488284, 35698423, 60432113, 284584
1840	87348810 (3879, 3880)	Novel Protein sim. GBank gi 1946300 emb CAA73132  - (Y12529) hypothetical protein [Silene latifolia]		struct	284488, 28331822, 264448, 284683, 264288, 285020, 33657023, 284631
1841	94147177 (3881, 3882)	Novel Protein sim. GBank gi 4206386 (AF060570) - rlg-1 protein [Mus musculus]		UNCLASSIFIED	56994075, 22278998, 264259, 29331824, 29331827, 264905, 265008, 33657084, 285017, 265018, 284288, 284897, 21906785, 21906766, 21906767, 265020, 52644150, 27488284, 83373044, 18108387, 60432113, 22279002, 264585
1842	87641870 (3883, 3884)	Novel Protein sim. GBank gi 4927204 gb AAD33049.1 AF133911 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 18108398, 29331825, 27486261, 284509, 18108370, 18108374, 264482
1843	94325298 (3885, 3886)	Novel Protein sim. GBank gi 3122952 sp O15736 TIPO_DICD1 - TIPO PROTEIN		kinase	22278998, 28331822, 29331827, 35696052, 264511, 265009, 264592, 60432228, 265017, 265018, 265019, 284684, 284692, 33657109, 65274791, 284636

1944	94232958 (3887, 3888)	Novel Protein sim. GBank gij1799570dbj BAA13432  - (D87671) TIP-120 [Rattus norvegicus]		UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 58182435, 264512, 264910, 60170831, 60432229, 60433356, 33657402, 60433438, 264596, 33109954, 21906754, 87168474, 87168559, 285017, 265018, 265019, 18108351, 264369, 264686, 264768, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 264692, 33857023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264563
1945	87641672 (3889, 3890)	Novel Protein sim. GBank gij4927204gb AAD33049.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 22278996, 264510, 264511, 18108351, 264683, 264686, 264567
1946	87443990 (3891, 3892)	Novel Protein sim. GBank gij2498104sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN		UNCLASSIFIED	60432289, 29331827, 35696052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21906767, 52644150, 264693, 27486264, 264637, 87168518, 264563
1947	86438862 (3893, 3894)	Novel Protein sim. GBank gij3914801sp Q54888 RPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)		napolymerase	22278998, 264905, 264906, 264908, 264909, 264512, 264758, 264762, 264682, 264683, 264764, 264288, 264768, 264688, 21906768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1948	85199174 (3895, 3896)	Novel Protein sim. GBank gij5420387fembj CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		struct	264909, 60170831, 264591, 264594, 265010, 265011, 264764, 264369, 264689, 264631, 264638
1949	7640129 (3897, 3898)	Novel Protein sim. GBank gij3876766fembj CAA93466.1  - (Z69637) predicted using GeneFinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]		UNCLASSIFIED	264369
1950	87786531 (3899, 3900)	Novel Protein sim. GBank gij3876766fembj CAA93466.1  - (Z69637) predicted using GeneFinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	Contains protein domain (PF00857) - Isochorismatase family	UNCLASSIFIED	264488, 264768, 264688, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264563, 55811150, 18108351, 264369, 264288, 18108354
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gij2626753dbj BAA23424  - (AB008782) sulfate transporter [Arabidopsis thaliana]	Contains protein domain (PF00916) - Sulfate transporter family	transport	56182575, 22278997, 52645080, 29331824, 29331825, 29331827, 55812038, 52646317, 265018, 265019, 264369, 21906765, 21906767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 58182323, 22279002
1952	87069775 (3903, 3904)	Novel Protein sim. GBank gij4929633gb AAD34077.1 AF15184 - (AF15184) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264591, 264593, 264594, 264595, 264555, 264556, 264557, 264558, 264565

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gll1188715sp1P31721C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264259, 264558
1954	91226025 (3907, 3908)	Novel Protein sim. GBank gll4240271dbj[BAA74914.1] - (AB020698) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	264488, 263994, 18108394, 35698288, 22278998, 29331822, 68714117, 29331826, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 265007, 265008, 264910, 265009, 60170831, 60432228, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264768, 264769, 35695917, 265020, 265021, 264691, 33657023, 264692, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264488, 264567
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181686, 22278994, 22278998, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 35698052, 264508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21908765, 21906766, 21906767, 55811957, 265020, 265021, 52645129, 33657109, 27488284, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gll1665821dbj[BAA13407] - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35698052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21908768, 21908769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22278000, 22278002, 264563, 264564

1857	94326510 (3913, 3914)	Novel Protein sim. GBank gij4589674[dbj BAA76586.1] - (AB023229) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52646842, 56182575, 22278997, 22278998, 22278999, 29331824, 66714117, 29331827, 29146498, 264593, 33657402, 33109954, 87168474, 265018, 264448, 264369, 264288, 264766, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 264692, 65274620, 27486284, 33657349, 27486265, 35895855, 22279002, 264482
1858	95313902 (3915, 3916)	Novel Protein sim. GBank gij4240227[dbj BAA74892.1] - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264092, 264094, 264259, 60432049, 29331824, 56182181, 66714117, 264107, 264109, 264909, 264511, 60170831, 60432229, 21906754, 285010, 21806769, 35895917, 265022, 65274620, 263987, 263976, 35896423, 264631, 264632, 264634, 264635, 18108385, 22279000, 22279002, 264593, 265019
1859	85701470 (3917, 3918)	Novel Protein sim. GBank gij2281983[embj CAB10860] - (Z88056) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1860	80308608 (3919, 3920)	Novel Protein sim. GBank gij2274851[dbj BAA21515] - (D64159) 3-7 gene product [Homo sapiens]		struct	264905, 264806, 264907, 264908, 264909, 265008, 265007, 264910, 264595, 265017, 264604, 265018, 18108351, 264764, 264369, 264766, 264768, 21908765, 18108368, 264629, 18108379, 264635, 264636, 264637, 264638, 264486
1861	16292807 (3921, 3922)				264635
1862	91008385 (3923, 3924)			UNCLASSIFIED	65274572, 264592, 264593, 265019, 264691
1863	90936017 (3925, 3926)	Novel Protein sim. GBank gij3721653[dbj BAA33581] - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		eph	65274572, 18108398, 35896286, 29331825, 60432289, 29331827, 264828, 265008, 265009, 60433356, 60433438, 21906754, 265020, 265021, 33657023, 33657109, 27486285, 35895855, 264555
1864	94317605 (3927, 3928)	Novel Protein sim. GBank gij5262638[embj CAB45757.1] - (AL080169) hypothetical protein [Homo sapiens]		cadherin	264488, 264092, 264259, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 265009, 264910, 264592, 264593, 264594, 264595, 264758, 264600, 264603, 264604, 264605, 264760, 264762, 264448, 264764, 264288, 264685, 264766, 264768, 264769, 21906766, 264691, 264692, 264693, 18108370, 264628, 264629, 18108374, 264630, 264631, 264634, 264636, 264637, 264638, 18108382, 83373044, 18108385, 264483, 264564, 264565, 264566, 264486, 264567
1865	94317445 (3929, 3930)	Novel Protein sim. GBank gij4107017[dbj BAA36294] - (AB001773) PEM-6 [Ciona savignyi]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264488, 264510, 264760, 264768, 264486

1866	94192058 (3931, 3932)	Novel Protein sim. GBank gi 4929707 gb AAD34114.1 AF151877 CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331828, 29331828, 29148498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264885, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264486, 264567 29331824, 265010, 265017, 264288, 21906764, 263981, 56526486
1867	87396123 (3933, 3934)	Novel Protein sim. GBank gi 2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	esterase	
1868	88095641 (3935, 3936)	Novel Protein sim. GBank gi 2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35686286, 264905, 264509, 264908, 264807, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264882, 264764, 264685, 264766, 264767, 264889, 264891, 264683, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264564, 264565, 264566, 264567
1869	84328529 (3937, 3938)	Novel Protein sim. GBank gi 2911274 (U20329) - spidroin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35696052, 264908, 264908, 18108351, 264482
1870	80596049 (3939, 3940)	Novel Protein sim. GBank gi 4050087 (AF109907) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 264288, 264766, 264636
1871	94843914 (3941, 3942)	Novel Protein sim. GBank gi 134208 sp P09593 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	264488, 264489, 22278998, 264259, 60432049, 66714117, 29331828, 60432289, 29331827, 35696052, 264508, 264905, 264508, 264906, 264607, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21906765, 33657023, 264692, 18108370, 264628, 35696423, 65274791, 35695855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22279000, 264563, 264564, 264585, 264566, 264488
1872	87645444 (3943, 3944)	Novel Protein sim. GBank gi 4519623 dbj BAA75671.1  - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265006, 264511, 265008, 52644298, 285018, 265019, 264761, 264888, 21906768, 21906769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1873	86395533 (3945, 3946)			UNCLASSIFIED	29331826, 264692, 35696423, 264631, 264555, 264556, 264557, 264558, 264559 264692, 264764, 264563
1874	80396629 (3947, 3948)	Novel Protein sim. GBank gi 3309543 (AF036382) - MLL [Fugu rubripes]		UNCLASSIFIED	

1975	94316478 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 56182435, 265008, 264757, 55812038, 265010, 265017, 264369, 55811957, 65274791, 35695855, 58182323, 80432113, 264259, 35696052, 265018, 265020, 265021, 33657109, 56526486
1976	95358914 (3951, 3952)			UNCLASSIFIED	264908, 264596, 265021, 264566
1977	94852684 (3953, 3954)	Novel Protein sim. GBank gi 2495528 sp Q07782 NASU_RAT - SODIUM/SULFATE COTRANSPOSER (NA(+)/SULFATE COTRANSPOSER)		homeobox	
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gi 4759290 ref NP_004642.1 pUSP1 - Ubiquitin carboxyl- terminal hydrolase, X-linked (AF131848) Unknown [Homo sapiens]		transcript factor	60170831, 264568
1979	87627709 (3957, 3958)	Novel Protein sim. GBank gi 2244815 emb CAB10238.1  - (Z97336) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	29331826, 29146498, 264905, 264907, 265007, 265009, 265010, 265018, 264686, 18108359, 21906768, 35695917, 265020, 60170615, 264693, 18108368, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264555
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gi 4759290 ref NP_004642.1 pUSP1 - Ubiquitin carboxyl- terminal hydrolase, X-linked (AF131848) Unknown [Homo sapiens]		ubiquitin	264489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank gi 4406693 gb AAD20060.1  - (AF131848) Unknown [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331828, 29146498, 29146499, 264107, 264908, 264910, 264595, 21906754, 265010, 265017, 265018, 265019, 264448, 264288, 21906767, 33657023, 27486264, 18108370, 18108374, 18108376, 264630, 264631, 264635, 18108385, 87168518, 22279000, 264482, 264564
1982	90995367 (3963, 3964)	Novel Protein sim. GBank gi 5689523 dbj BAA83045.1  - (AB029016) KIAA1093 protein [Homo sapiens]			65274572, 29331825, 35696052, 33656970, 264909, 265008, 55811366, 264760, 264686, 264691, 27486264
1983	95098668 (3965, 3966)	Novel Protein sim. GBank gi 3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF000086) Zinc finger, C2H2 type	transcript factor	22278996, 35696286, 264259, 29331822, 20281099, 29331824, 60432289, 29331827, 264509, 264905, 264906, 264907, 66712502, 264908, 5284045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433356, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21906765, 55811857, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35698423, 35695855, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373044, 18108385, 22279000, 22279002

1884	85760989 (3967, 3968)	Novel Protein sim. GBank gij2806895[embjCAA17174.1] - (AL021897) fadD14 [Mycobacterium tuberculosis]		synthase	264888, 21908768, 55811957, 56994075, 265020, 265021, 22278999, 265022, 264259, 29331822, 33657182, 29148499, 264628, 18108370, 264908, 264628, 55811576, 35695855, 265008, 265007, 264591, 21908754, 33657084, 265010, 265017, 265019, 264288
1885	85636687 (3969, 3970)	Novel Protein sim. GBank gij5712131[gbjAAD47378.1]AF12049 - (AF12049) DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811578, 264637, 56182323, 18108385, 264584
1886	80200507 (3971, 3972)	Novel Protein sim. GBank gij4686443[gbjAAD31319.1]AF14457 - (AF14457) Mx-interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF000069) - Eukaryotic protein kinase domain	UNCLASSIFIED	264488, 264829
1887	87011117 (3973, 3974)	Novel Protein sim. GBank gij4686443[gbjAAD31319.1]AF14457 - (AF14457) Mx-interacting protein kinase PKM [Mesocricetus auratus]		UNCLASSIFIED	22278999, 29331830, 265007, 265018, 21906768, 33657023, 264682, 264593, 18108377, 264635, 60170394, 22279002
1888	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264910, 264591, 264593, 264758, 264764, 264686, 264768, 265021, 264692, 264628, 264629, 35695855, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1889	91225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein spc97 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52644045, 56182435, 264112, 265007, 33657402, 52644229, 21908765, 21906768, 21906769, 55811957, 33657023, 263967, 33657109, 18108370, 22279000, 22279002
1890	85698888 (3979, 3980)	Novel Protein sim. GBank gij5701727[dbjBAA83074.1] - (AB024729) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1891	85353114 (3981, 3982)	Novel Protein sim. GBank gij4240287[dbjBAA74922.1] - (AB020706) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaplin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35698288, 56994075, 22278997, 22278999, 29331822, 29331824, 29331825, 60432289, 29331828, 264508, 264906, 264907, 264908, 56182435, 264510, 265007, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 264683, 264369, 264288, 264685, 264766, 264687, 264768, 21908765, 21906768, 21906769, 55811857, 265020, 60431528, 263974, 18108379, 35695855, 264555, 264557, 264639, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 264564, 264486
1892	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	struct	29331827, 264906, 264907, 264908, 265007, 264803, 264768, 264686, 264768, 21906768, 264628, 264635, 264636, 18108385, 56528486, 264568, 264567
1893	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - C1G26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264592, 35696423

1994	94329114 (3987, 3988)	Novel Protein sim. GBank gij5830077[gb AAD45822.1 AC00601.1 - (AC00601.1) similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00856) SET domain	mapolymerase	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265008, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 264684, 264388, 264685, 264686, 264768, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 18108362, 264693, 65274620, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56526486, 22279000, 22279002, 264564
1995	95414353 (3989, 3990)	Novel Protein sim. GBank gij4827040[re NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit]	UNCLASSIFIED	UNCLASSIFIED	264488, 18108396, 22278994, 56994075, 22278996, 35686286, 22278997, 22278999, 264259, 29147620, 56182181, 29331824, 60432289, 29331826, 29331827, 35696052, 29146499, 264905, 264907, 66712502, 56182435, 265008, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811388, 85658542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 264693, 27485282, 27486264, 27486265, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87188518, 264404, 60432113, 264567, 264564
1998	80254186 (3991, 3992)	Novel Protein sim. GBank gij791146[emb CAA60020] - (X86028) extensin-like protein [Vigna unguiculata]		UNCLASSIFIED	UNCLASSIFIED
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gij2642034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase	264908, 264809, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gij4589634[dbj BAA76839.1] - (AB023212) KIAA0995 protein [Homo sapiens]		UNCLASSIFIED	264113, 264685, 264555, 264567



1999	94324803 (3997, 3998)	Novel Protein sim. GBank gi 5225312 gb AAD0846.1 AF07244 - (AF072441) calcineurin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35686286, 60424289, 29331827, 29331828, 35686052, 265006, 264512, 55811386, 265010, 265018, 265019, 55811150, 18108351, 264763, 264682, 264369, 264685, 264688, 56181582, 265020, 264691, 33857023, 264693, 33657109, 27486284, 18108370, 18108379, 35695855, 264634, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22278000, 264563, 264564, 264568
2000	95413705 (3999, 4000)	Novel Protein sim. GBank gi 1723232 sp Q10155 YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME 1		UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278996, 35686286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331826, 29331827, 29331828, 35686052, 264106, 29331830, 52644045, 285007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644296, 265017, 265018, 265019, 264761, 264389, 264288, 52644229, 21906768, 21906769, 35695917, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 65274820, 52645129, 27486281, 27486282, 27486284, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526486, 22279002, 264566, 264567
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gi 107550 pir B38637 - Ras inhibitor (clone JC285) - human (fragment)		UNCLASSIFIED	264769, 52644229, 65274572, 21906768, 22278996, 35686286, 35695917, 265020, 22278999, 264534, 264490, 264259, 264692, 60432289, 33657109, 35686052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108365, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gi 729433 sp P38657 ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - isomerase Thioredoxin		264807, 295008, 264910, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074448 (4005, 4006)	Novel Protein sim. GBank gi 86388 pir A27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264905, 264906, 264908, 264910, 264596, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4884249 emb CAB43230.1  - (ALD48986) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	52645156, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35698286, 22278997, 22278998, 22278999, 60432048, 264259, 52645080, 29331824, 29331826, 29331827, 35698052, 29331828, 33656970, 29331830, 264908, 264592, 60433356, 33657402, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264763, 264683, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 18108374, 18108376, 18108377, 35698423, 35695855, 264631, 52644332, 264558, 18108385, 56526486, 87168518, 60432113, 264483, 264488, 264905
2005	87400864 (4009, 4010)	Novel Protein sim. GBank gi 3879501 emb CAA87795  - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi 4106673 emb CAA22813  - (AL035064) queuine tma-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424269, 66714117, 35696052, 264908, 68712502, 264909, 264510, 60433356, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 29148627, 21906769, 29148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810764, 55811578, 35695855, 87168518, 60432113, 264563, 264482, 264488, 263994, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265007, 264910, 264592, 264595, 264758, 265011, 264760, 264762, 264764, 264766, 264685, 264767, 264768, 264769, 55811957, 35695917, 265020, 264691, 264693, 264628, 264629, 65274791, 35695855, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 264566, 264909, 264768, 35695855
2007	94325556 (4013, 4014)	Novel Protein sim. GBank gi 2662161 dbj BAA23712  - (AB007800) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 1550783 emb CAA69257  - (Y07860) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2009	85748240 (4017, 4018)	Novel Protein sim. GBank gij3882305[dbj BAA34512.1] - (AB018335) KIAA0792 protein [Homo sapiens]	UNCLASSIFIED	22278999, 264259, 264910, 264591, 265017, 264881, 264683, 21906788, 264691, 33657182, 33657349, 264631, 87168518, 264404, 22279002, 264583
2010	85422458 (4018, 4020)	Novel Protein sim. GBank gij5262629[emb CAB45753.1] - (AL080164) hypothetical protein [Homo sapiens]	Contains protein domain (PF00057) - eph Low-density lipoprotein receptor domain class A	52644507, 52645156, 52646365, 52646842, 18108397, 65274572, 22278994, 58994075, 3586286, 22278996, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432229, 60433356, 21908754, 52646317, 33108954, 52644298, 87168474, 87168559, 285017, 265018, 265019, 264681, 264885, 264687, 52644229, 264689, 21908785, 21908766, 21908767, 21908788, 35859517, 285020, 52644150, 264691, 264692, 33657023, 263987, 52645129, 35895763, 18108376, 35896423, 65274791, 35695855, 264631, 264634, 60431850, 264637, 264638, 52644332, 60170394, 18108385, 87168518, 22279002, 264564, 264565, 264566, 264567, 56182575, 58994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35896052, 264908, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264681, 264448, 264683, 264389, 264288, 264685, 264768, 264687, 21908785, 21908787, 21908768, 21908789, 285020, 265022, 264691, 33657023, 65274620, 33657109, 264628, 264557, 264559, 83373044, 87168518, 60432113, 22279002, 264259, 29331822, 29331824, 29331825, 28146498, 87168559, 265019, 264682, 264288, 264686, 21908764, 265020, 265022, 33657023, 264693, 33657109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264587
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gij3347953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]	UNCLASSIFIED	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21908767, 265020, 264692, 264488, 29331826, 264807, 264636, 264555, 264639, 264558
2012	8772137 (4023, 4024)	Novel Protein sim. GBank gij1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	22279002, 264587
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gij4507985[ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pZ-17)]	Contains protein domain (PF00069) - dna_rna_bind Zinc finger, C2H2 type	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21908767, 265020, 264692
2014	87347940 (4027, 4028)	Novel Protein sim. GBank gij127720[epi P20938 MYPO_HETFR - MYELIN P0 PROTEIN PRECURSOR]	UNCLASSIFIED	264488, 29331826, 264807, 264636, 264555, 264639, 264558

2015	88094922 (4029, 4030)	Novel Protein sim. GBank gl 81286 pir  S22697 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	56182575, 35698286, 264259, 35698052, 264508, 264908, 264907, 264510, 264512, 87168474, 265010, 264681, 264288, 264689, 264828, 35698423, 35695855, 264639, 264563, 264564
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gl 265046 pir  S26413 - t-complex protein Tc-10 - mouse		struct	264102, 264508, 264110, 265009, 33109954, 21906768, 265021, 33857109, 27486282, 263972, 18108374, 263976, 264555, 264564
2017	79464293 (4033, 4034)			UNCLASSIFIED	264685, 264636
2018	78637067 (4035, 4036)	Novel Protein sim. GBank gl 124735 sp P18175 INVO_PIG - INVOLUCRIN			264693
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gl 2143910 pir  S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat		phosphatase	264107, 264110, 264112, 265017, 263976
2020	94674478 (4039, 4040)	Novel Protein sim. GBank gl 2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	264259, 264508, 264591, 265018, 264682, 264288, 264688, 22279002
2021	86718818 (4041, 4042)	Novel Protein sim. GBank gl 585084 sp Q07803 JEFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 264593, 33109954, 21906764, 21908768, 33657023, 33857109, 27486261, 87168518
2022	95295665 (4043, 4044)	Novel Protein sim. GBank gl 4218005 (AC008135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			264757, 264767, 60170615, 18108385
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gl 5410230 gb AAD42992.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	18108394, 22278999, 264259, 264905, 264906, 264908, 264595, 264762, 264769, 264634, 264636, 87168518, 60432113, 22279000, 264482, 264565
2024	87896443 (4047, 4048)				60433438, 265017, 264688, 264692, 264693, 264636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gl 475318 gb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 264509, 264906, 264909, 55812038, 285017, 265021, 265022, 60170815, 264556
2026	94122114 (4051, 4052)	Novel Protein sim. GBank gl 1655699 emb CAA69032 - (Y07752) perophorin-S [Volvox carteri]		UNCLASSIFIED	56994075, 60432049, 264508, 66712502, 264112, 60170831, 87168559, 264288, 264688, 264689, 21908768, 33657109, 18108370, 264638, 18108385, 60432113, 22279000, 22279002, 264564, 264566, 264567
2027	80249001 (4053, 4054)			UNCLASSIFIED	263978, 264634, 264486

2028	94699884 (4055, 4056)	Novel Protein sim. GBank gji1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - ubiquitin-HECT-domain (ubiquitin-transferase).	ubiquitin	52644507, 52645158, 52646842, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35696052, 264906, 264907, 264908, 29331830, 52644045, 56182435, 265006, 265009, 60432229, 33657402, 264595, 264757, 55812038, 21908754, 52646317, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644229, 21908765, 21906766, 21908767, 21908768, 21908769, 55811857, 35695917, 265020, 265021, 285022, 52644150, 33657023, 65274620, 33657109, 52645129, 18108368, 27486261, 27486262, 27486264, 27486265, 35695763, 264629, 55811576, 35696423, 35695855, 264635, 264636, 52644332, 264558, 83373044, 56526466, 22279000, 22279002, 264563, 265009, 264595, 85658542, 264555, 264556, 264557, 264558, 264559, 83373044
2029	95362032 (4057, 4058)	Novel Protein sim. GBank gji3599940 (AF017368) - faciolgenital dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00821) - RhoGEF domain	UNCLASSIFIED	18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 80432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21908769, 285022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gji5630080 [gbjAAD45825.1] (AC004890) similar to HUB1; similar to BAA24380 (PUD:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 80432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21908769, 285022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2031	80245281 (4061, 4062)				264591, 55811957, 18108385, 264557, 264558, 18108382, 18108394
2032	91232607 (4063, 4064)	Novel Protein sim. GBank gji5688491 [dbjBAA83029.1] - (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase	65274572, 35696286, 29331824, 264908, 265009, 264593, 265018, 264288, 264688, 264769, 21906766, 21908767, 29148627, 264628, 35696423, 264634, 264556, 18108381, 60170394, 264559, 83373044, 18108385, 264482, 264484
2033	95000809 (4065, 4066)	Novel Protein sim. GBank gji2494828 [spQ64886] CAG7_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNAC1II) (STY)		synthase	56181562, 264628, 264632, 264555, 264558
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gji4826984 [refjNP_005147.1] pROD1 - UNKNOWN	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278996, 22278999, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21908767, 21908768, 21908769, 33657109, 83373044, 56526466

2035	83553451 (4069, 4070)				264369, 264686, 265022, 26526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gi2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331826, 29331828, 35696052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264594, 55812038, 33109954, 21906754, 87168559, 265017, 265018, 265019, 264762, 264369, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gi3880625[emb]CAB07858] - (Z93785) predicted using GeneFinder; similar to RNA recognition motif, (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264368, 264766, 264767, 264686, 18108358, 21906765, 21906769, 52644150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108379, 35696423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264563, 264564, 264566
2039	85514626 (4077, 4078)	Novel Protein sim. GBank gi2224653[db][BAA20813] - (AB002354) KIAA0356 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35696423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264488
2040	95308417 (4079, 4080)			UNCLASSIFIED	264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gi2500625[sp]P70700[RPA2_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)]	mapolymerase	UNCLASSIFIED	264488, 22278998, 35696052, 264805, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21906768, 265021, 265022, 264692, 33657109, 264628, 264629, 35696423, 35695855, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gij4406590[gb AAD20040]r (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 264259, 29331826, 35696052, 29331828, 264508, 264509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 264595, 265017, 265019, 264681, 264784, 264389, 264785, 264684, 264288, 264786, 264686, 52644228, 264769, 21908765, 35695917, 264535, 52644150, 264691, 264692, 18108385, 27486261, 27486262, 27486265, 18108374, 35898423, 65274791, 35895855, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264564, 264566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gi15052554[gb AAD38607.1 AF145632] BCDNA.GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52646365, 56994075, 22278997, 22278998, 20281171, 264259, 29331822, 29331824, 66714117, 29331826, 29331828, 33656970, 29146498, 264509, 264908, 52644045, 56182435, 265006, 33657402, 21906754, 52644298, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35895763, 18108374, 55811576, 35895855, 18108380, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264587
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264093, 29331827, 264905, 66712502, 264592, 264689, 21906765, 21906768, 265020, 264692, 264482, 264568
2045	78635532 (4089, 4090)				264692
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gij4406698[gb AAD20062] - (AF131852) Unknown [Homo sapiens]			264259, 264908, 264683, 22279002
2047	84578801 (4093, 4094)	Novel Protein sim. GBank gij4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278999, 29147620, 29331824, 29148498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148629, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2048	84606378 (4095, 4096)			UNCLASSIFIED	264909
2049	88094680 (4097, 4098)	Novel Protein sim. GBank gij4589656[gb BAA78850.1] - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264783, 21906767, 21906768, 264629, 264634, 264637, 22279002, 264564, 264565, 264566, 264567

2050	79633835 (4089, 4100)			UNCLASSIFIED	264693	264488, 264259, 264509, 264906, 264907, 264769, 18108374, 35696423, 264563, 264566, 264486
2051	87780168 (4101, 4102)			UNCLASSIFIED		
2052	88096393 (4103, 4104)	Novel Protein sim. GBank gij4529889[gbjAAD21812.1] - (AF134726) G9A [Homo sapiens]	Contains protein domain (PF00856) - SET domain	kinase		264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264686, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 58526486, 60432113, 264563, 264564, 264566, 264486, 264567
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gij2995449[embjCAA75113] - (Y14848) midline 1 protein [Mus musculus]		UNCLASSIFIED		22278996, 22278997, 264259, 29331822, 264102, 264508, 35695917, 263972, 264482, 60424179, 264094, 264259, 29331825, 60424269, 264906, 60432229, 60433356, 87168559, 265019, 264760, 264288, 264686, 21906769, 33657023, 264693, 55810764, 55811576, 264635, 56182323, 60432113
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gij3876326[embjCAB02090] - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain			
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gij5353745[gbjAAD42226.1] (AF159133) SIR2-like protein [Oryza sativa subsp. indica]		UNCLASSIFIED		264488, 29331826, 60432289, 29331828, 60433358, 265019, 264683, 264684, 265021, 33657109, 18108374, 264637, 18108385, 87168518, 60432113, 22279000, 264564



2056	88177396 (4111, 4112)	Novel Protein sim. GBank gij4826960/ref NP_005042.1 pCARS - glutamine-tRNA synthetase	Contains protein domain (PF00749) - tRNA synthetases class I (E and Q)	synthase	264488, 52645156, 56182575, 22278994, 35696286, 56994075, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 60432289, 28331827, 28331828, 33656970, 264104, 264908, 284808, 265006, 265008, 60170831, 264591, 60432229, 60433438, 18108348, 21906754, 33657084, 52644286, 87168474, 265010, 87168559, 265017, 265018, 264760, 18108351, 264681, 264682, 264448, 264683, 264369, 264288, 264685, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 33695917, 265022, 33657023, 18108362, 33657109, 18108368, 33657182, 27488261, 27486264, 27486265, 33657349, 264626, 18108370, 264629, 18108374, 18108377, 18108379, 35696423, 55811576, 20281152, 264636, 264952, 18108385, 18108388, 87168518, 264482, 264565, 264568, 264567
2057	87877905 (4113, 4114)	Novel Protein sim. GBank gij728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	52646842, 52648365, 56182575, 35696286, 22278996, 22278997, 22278998, 264093, 52645080, 35696052, 29331828, 33656970, 265009, 52646317, 55811386, 52644286, 52644229, 21906769, 35695917, 265021, 60170615, 52644150, 33657109, 33657182, 27486261, 27486262, 35695763, 35696423, 35695955, 52644332
2058	86276896 (4115, 4116)	Novel Protein sim. GBank			265007, 265008, 264591
2059	79666684 (4117, 4118)	gij119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	29331825, 264682, 264686, 264691, 264693, 22278002
2060	83050800 (4119, 4120)	Novel Protein sim. GBank gij2811122 (U87318) - NaDC-2 [Xenopus laevis]		UNCLASSIFIED	56182575, 29331824, 29331826, 264810, 55811957, 18108370, 55811576

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi 2496947 sp Q09298 YQO9_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EEED8.8 IN CHROMOSOME II	Contains protein domain (PF00069) - Kinase Eukaryotic protein kinase domain	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29331828, 264906, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33657402, 21908754, 85658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56526486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Struct Ank repeat	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 283978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264762, 264565, 264764, 264487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gi 4589562 db BAA76803.1  - (AB023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - Oncogene RasGEF domain	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264564, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754515 db BAA13413.1  - (D87515) aminopeptidase-B [Rattus norvegicus]	hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 29331828, 35696052, 264509, 265007, 265008, 60432229, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264781, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33657109, 18108368, 18108374, 35698423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264566, 264486
2065	95092238 (4129, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENS_CHICK - TENSIN	kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433356, 55811388, 85658542, 265018, 55811150, 264681, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002, 56182575, 264259, 264906, 264764, 264288, 56182323, 264567
2066	85783402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58295) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF00096) - UNCLASSIFIED Zinc finger, C2H2 type	

2067	95303892 (4133, 4134)				35696286, 22278997, 22278998, 60432049, 264259, 60432289, 60433438, 264682, 264448, 264369, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35696423, 35695855, 264558, 264404, 264583, 264488
2068	84344754 (4135, 4136)			UNCLASSIFIED	264687
2069	94319177 (4137, 4138)	Novel Protein sim. GBank gij3152862 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	Transcript factor	60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656870, 264509, 264905, 56182435, 265009, 60433358, 87168559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87168518, 60432113, 22278000, 22279002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gij5712131 [gb AAD47379.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264905, 264628, 264908, 264638
2071	86946116 (4141, 4142)	Novel Protein sim. GBank gij3551531 [dbj BAA330161 - (AB017437) avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265006, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 264634, 18108381, 18108385, 18108388, 18108391
2072	91718429 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophysial hormones, C-terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264690, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27925664 (4145, 4146)	Novel Protein sim. GBank gij1504026 [dbj BAA132121 - (D86976) similar to C. elegans protein (Z37093) [Homo sapiens]		UNCLASSIFIED	264556
2074	94324767 (4147, 4148)	Novel Protein sim. GBank gij4240317 [dbj BAA74937.11 - (AB020721) KIAA0914 protein [Homo sapiens]			29331822, 264909, 264511, 265009, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264567

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gij5138930 gb AAD40382.1 - (AF093680) transcription factor IIB (Homo sapiens)			18108394, 22278994, 22278996, 35696286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35696052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265009, 33657084, 264760, 264448, 264288, 264766, 264767, 264689, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27486262, 27486265, 35696423, 35695855, 264631, 264634, 264639, 87188518, 22279002, 264563, 264486, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385, 264592
2077	11389877 (4153, 4154)			UNCLASSIFIED	264592
2078	87539384 (4155, 4156)	Novel Protein sim. GBank gij420500 dbj BAA74579 - (D87908) nuclear protein np95 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	ubiquitin	29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56526486
2079	88095916 (4157, 4158)	Novel Protein sim. GBank gij420255 dbj BAA74906.1 - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264908, 264907, 264628, 20281089, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33108954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2080	94135689 (4159, 4160)	Novel Protein sim. GBank gij240802 femb CAB16219.1 - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gij5524734 gb AAD44360.1 AF16635 - (AF166350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85658542, 265011, 265018, 265019, 21906767, 21906768, 264893, 18108385, 22279000, 22279002
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gij3860558 femb CAA94234 - (Z70271) predicted using Genefinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	264907, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gij2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21906754, 265018, 265019, 264448, 264288, 264685, 21906769, 265020, 265022, 264691, 18108370, 65274791, 264631, 264555, 264563
2084	95189288 (4167, 4168)	Novel Protein sim. GBank gij728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	84989476 (4169, 4170)	Novel Protein sim. GBank gij1655699[embjCAA69032] - (Y07752) pterophorin-S [Volvox carter]	UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264783, 264369, 264686, 264693, 18108370, 56182323
2086	81234404 (4171, 4172)	Novel Protein sim. GBank gij3875032[embjCAA88936] - (Z49125) similarity to Trichostyrax colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 come...	UNCLASSIFIED	35696266, 264259, 35696052, 264908, 264907, 264908, 264809, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35698423, 35698555, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264488
2087	21436337 (4173, 4174)		UNCLASSIFIED	264489
2088	84111527 (4175, 4176)	Novel Protein sim. GBank gij3880930[embjCAA16334.1] - (AL021481) similar to Phosphoglucosylase and phosphomannomutase phosphoserine: cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...		264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21908754, 33109954, 87168474, 265017, 265018, 265019, 264448, 264683, 264369, 264685, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35698423, 35695855, 83373044, 87168518, 22279000, 264567
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gij4758118[ref NP_004623.1 pDAP3 - Death associated protein 3	cadherin	18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 28331822, 20281099, 28331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29148498, 28146499, 284102, 264106, 264107, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264828, 52644045, 264809, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 80433438, 264595, 55812038, 264758, 21906754, 33657084, 55811388, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644228, 264688, 18108358, 56181592, 264769, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 29148629, 29148784, 35695917, 265020, 265021, 265022, 60170815, 264680

2090	88222470 (4179, 4180)				22278995, 22278998, 22278999, 264259, 29331826, 35696052, 264910, 33657402, 60433438, 33108954, 87168474, 87168539, 265018, 265019, 264681, 264684, 264688, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265022, 60170615, 33657023, 35696423, 35695855, 264952, 18108387, 22279000
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gi 4580997 gb AAD24571.1 AF121081 cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	263994, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264288, 264768, 56181562, 21906765, 21906768, 21906769, 265022, 264628, 264563, 264567
2092	88223605 (4183, 4184)			homeobox	22278997, 22278999, 66712502, 87168559, 264683, 265021, 264486
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gi 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Cryptolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2094	91230929 (4187, 4188)	Novel Protein sim. GBank gi 4929551 gb AAD34036.1 AF15179 - (AF151799) CGI-40 protein [Homo sapiens]		MHC	3569286, 52644045, 265008, 265007, 265008, 87168559, 18108351, 21906769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2095	95351526 (4189, 4190)	Novel Protein sim. GBank gi 1363238 pir A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_rna_bind	3569286, 52644045, 265008, 265007, 265008, 87168559, 18108351, 21906769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2096	94119760 (4191, 4192)	Novel Protein sim. GBank gi 3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264488, 264489, 65274572, 56182375, 22278990, 22278997, 22278999, 264259, 60432289, 29331826, 35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 52644150, 264691, 264692, 33657023, 264693, 27486261, 35695763, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264638, 264639, 264563, 264483, 264565, 264566, 264486, 264567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi5174501 refNP_006051.1 pLYF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript/factor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170815, 264692, 33657109, 18108370, 264638, 264483 56994075, 264259, 264288, 265020, 264563
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gi4758208 refNP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
2099	95412827 (4197, 4198)	Novel Protein sim. GBank gi2695659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDPr [Bos taurus]		phosphatase	65274572, 264905, 65274444, 264691, 264636, 264555
2100	95332856 (4199, 4200)	Novel Protein sim. GBank gi3881189 emb CAB15514  - (299281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C08829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nuc_repl	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29146498, 264909, 265008, 285009, 284910, 264591, 60432229, 60433356, 33657402, 264758, 21908754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264782, 264448, 264369, 264288, 18108355, 264686, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108374, 35696423, 264558, 83373044, 87168518, 60432113, 22279000, 22279002 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87762604 (4201, 4202)	Novel Protein sim. GBank gi4589488 dbj BAA76761.1  - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi3874149 emb CAA97423.1  - (Z73103) predicted using GeneFinder (Caenorhabditis elegans)		UNCLASSIFIED	264488, 264489, 35686286, 264259, 35696052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433356, 264758, 264601, 264605, 264780, 18108351, 264448, 264764, 264288, 264767, 264768, 21908769, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gi4240159 dbj BAA74858.1  - (AB020642) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript/factor	65274572, 56994075, 22278998, 264259, 29331824, 29331825, 35686052, 29331828, 66712502, 265008, 60170831, 264595, 33109954, 85658542, 87168559, 265017, 265019, 264448, 21908765, 21908768, 265022, 33657023, 27486262, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264564
2104	85776161 (4207, 4208)			UNCLASSIFIED	284592, 264604, 22279000

2105	94848080 (4209, 4210)	Novel Protein sim. GBank gi 1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g5.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8.....		UNCLASSIFIED	264488, 56182575, 22278994, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 284508, 284905, 284509, 284907, 29331830, 52644045, 284510, 284511, 285007, 284512, 265009, 60170831, 60432229, 33657402, 60433356, 264595, 60433438, 264758, 33657084, 87168474, 265010, 87168559, 265017, 265018, 265019, 264762, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21906785, 21906786, 21808767, 21908768, 21908769, 35695917, 265020, 265022, 60170615, 52644150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274791, 35695855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526486, 87168518, 60432113, 264564, 264566, 264567, 265006, 265019
2106	83365475 (4211, 4212)				
2107	79822662 (4213, 4214)	Novel Protein sim. GBank gi 3881524 emb CAA93883  - (Z70038) ZK1067.4 [Caenorhabditis elegans]			264906, 264639
2108	94233976 (4215, 4216)	Novel Protein sim. GBank gi 3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264764, 264766, 264767, 264768, 264769, 264693, 264629, 35695855, 284632, 264634, 284635, 264638, 264639, 83373044, 264485
2109	80478719 (4217, 4218)			UNCLASSIFIED	18108348, 264769, 18108370, 18108374, 264555, 264556, 264557, 264558
2110	87729075 (4219, 4220)	Novel Protein sim. GBank gi 481043 pir S37671 - ba12 protein - human		UNCLASSIFIED	264564
2111	87818419 (4221, 4222)			UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2112	87283783 (4223, 4224)	Novel Protein sim. GBank gi 2143639 pir J55542 - calmodulin-binding protein - rat	Contains protein domain (PF00009) - struct		264508, 264806, 264591, 264682, 22279002
2113	78941388 (4225, 4226)	Novel Protein sim. GBank gi 4246629 gb AAD20459  - (AF100960) protocadherin [Rattus norvegicus]	cadherin		265006
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gi 3327184 dbj BAA31650  - (AB014585) KIAA0685 protein [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain		66714117, 29331826, 29331827, 60433438, 55812038, 265017, 265019, 264689, 21906769, 55811957, 265020, 265021, 33657109, 60170394, 264558
2115	90993785 (4229, 4230)	Novel Protein sim. GBank gi 4757890 ref NP_004328.1 pC8OR - chromosome 8 open reading frame 1		UNCLASSIFIED	65274572, 264689, 264691, 264692, 60432113



2116	88259387 (4231, 4232)	Novel Protein sim. GBank glj2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35698286, 22278999, 56182181, 29331824, 29331825, 29331827, 35696052, 284907, 56182435, 265008, 284591, 55812038, 55811386, 87168558, 284288, 284389, 21906769, 28148629, 33657023, 35695763, 55811576, 35696423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank glj2330021 (AF019250) - Kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	29331824, 264511, 285009, 33109954, 265017, 265018, 264288, 264689, 265020, 264692, 58526486, 284482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank glj1078307 (p1j)B56573 - nuclear pore complex glycoprotein p62 - African clawed frog		glycoprotein	264259, 264905, 264807, 284808, 284510, 284511, 265009, 264910, 285010, 285010, 284802, 264288, 264768, 264693, 263887, 263972, 284838, 264559
2119	86999317 (4237, 4238)	Novel Protein sim. GBank glj4321407 (gbjAAD15748) - (AF047890) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87788935 (4239, 4240)	Novel Protein sim. GBank glj4885527 (relNP_005480.1) pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - eph Src homology domain 2	eph	264091, 264259, 29331826, 29331828, 265017, 264604, 264288, 264685, 285020, 264691, 18108370, 55810764, 284555, 264636, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank glj475728 (relNP_004886.1) pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	264601, 264768, 263978
2122	91230831 (4243, 4244)	Novel Protein sim. GBank glj4929551 (gbjAAD34036.1) AF15179 - (AF151799) CGI-40 protein [Homo sapiens]			18108394, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 264907, 56182435, 285007, 264910, 265010, 265018, 264686, 265020, 55811578, 284555, 264637, 18108382, 83373044, 18108383, 18108384, 56526486, 284585, 284567
2123	86787898 (4245, 4246)	Novel Protein sim. GBank glj2224551 (dbjBAA20764) - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	struct	18108386, 264757, 265011, 18108351, 264691, 264634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank glj568945 (dbjBAA83011.1) - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	29331822, 264806, 264807, 264591, 264639, 264593
2125	95354041 (4249, 4250)	Novel Protein sim. GBank glj728831 (spjP39188) ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	284593, 284259, 284509, 284907, 264511, 85658542, 264763, 21906765, 35695917, 264636, 264498
2126	95084231 (4251, 4252)	Novel Protein sim. GBank glj4539264 (embjCAB39853.1) - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	284488, 264489, 29331827, 35696052, 264905, 284509, 264908, 264909, 284510, 265009, 284591, 284592, 264593, 33657402, 264594, 284595, 284596, 264758, 264801, 264603, 285018, 264604, 264605, 264760, 264881, 264762, 264683, 264764, 264684, 264288, 264685, 264689, 60170815, 33657023, 33657109, 55810764, 264635, 284636, 264637, 264638, 284639, 83373044, 264564, 264566

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gij4868435[gb AAD31315.1 AF143236] apoptosis related protein APR-2 [Homo sapiens]			35696286, 29331826, 35696052, 284508, 284509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264600, 264601, 264604, 264762, 264763, 264766, 264687, 264768, 264769, 264689, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264567, 56182575, 35696286, 56182181, 29331824, 60432289, 35696052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264764, 264288, 264369, 264687, 264768, 55811957, 264692, 18108368, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2128	87414262 (4255, 4256)				66714117, 264828, 264595, 55812038, 55811150, 55811957, 264693, 18108374, 263978, 65274791, 18108381, 83373044, 22279000
2129	95102089 (4257, 4258)			UNCLASSIFIED	263981
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gjl2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	35696052, 264909, 264768, 35695917
2131	85723065 (4261, 4262)	Novel Protein sim. GBank gjl1086886 (U41276) - Similar to potassium channel protein, [Caenorhabditis elegans]	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	potassium_channel	264488, 22278999, 264259, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 284910, 264591, 264592, 264595, 264758, 21906754, 33109954, 87168474, 265011, 264600, 264601, 264605, 265019, 264760, 18108351, 264681, 264762, 264764, 264288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21906769, 264690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264636, 264555, 264637, 18108380, 264639, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567
2132	95361096 (4263, 4264)	Novel Protein sim. GBank gjl5689373[gb BAA82973.1  - (AB028944) KIAA1021 protein [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gij4220489 (AC008069) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60424179, 52646365, 52646842, 56994075, 35696286, 22278997, 22278998, 80432049, 56182181, 66714117, 60424268, 29331826, 29331828, 35696052, 264805, 264906, 264907, 66712502, 29331830, 56182435, 265008, 264512, 265008, 80431735, 60433356, 33657402, 55812038, 33109954, 21906754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264368, 264288, 52644229, 56181562, 21906765, 21908768, 21806767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 33657023, 33657109, 60431528, 18108374, 35696423, 65274791, 35695855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264563, 264566
2134	95412687 (4267, 4268)	Novel Protein sim. GBank gij3875351[embj(CAB09415) - (Z96047) DY3.6 [Caenorhabditis elegans]			56181686, 35696286, 21806754, 55811386, 265011, 265017, 18108351, 264765, 264766, 264888, 21908768, 35695917, 265020, 33657023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22278902
2135	88079813 (4269, 4270)	Novel Protein sim. GBank gij5689559[dbj(BAA83063.1) - (AB029034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278998, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 87168559, 264601, 18108351, 264448, 264683, 264684, 264689, 18108359, 264691, 33657023, 264692, 35695763, 264629, 35695855, 264831, 264635, 264636, 264637, 56182323, 264639, 22279002, 264564
2136	84346478 (4271, 4272)	Novel Protein sim. GBank gij2662167[dbj(BAA23715) - (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gij4884110[embj(CAB43262.1) - (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264569, 264909, 33109954, 264783, 21908768, 60170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gij5174779[gbj(AAD40696.1) - (U87804) 50 kDa protein [Caulobacter crescentus]		ATPase associated	264259, 29331828, 35696052, 264909, 265008, 265017, 265018, 18108351, 264288, 21908768, 33657023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264556, 264557, 264558, 264559
2139	84843882 (4277, 4278)	Novel Protein sim. GBank gij3850821[embj(CAA77135) - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]			264905, 264910, 264591, 55812038, 55811386, 8569542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33657023, 18108384, 55811576, 83373044, 18108385, 56526486, 264482

2140	87645655 (4278, 4280)	Novel Protein sim. GBank gij4417283jgb AAD20418  - (AC007019) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264509, 265008, 294759, 265018, 264448, 264288, 21906768, 55811957, 265021, 33657023, 27488265, 35696423, 264636, 264556, 264557, 284559, 264566
2141	78623986 (4281, 4282)			UNCLASSIFIED	265020, 284693
2142	80041222 (4283, 4284)			UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank gij2135766jpr IS53362 - mucin 5AC (clone JER47) - human (fragment)		UNCLASSIFIED	22278997, 29331827, 264907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycoprotein precursor [Boreogadus saida]		UNCLASSIFIED	65274572, 264259, 29331824, 29331827, 264908, 264908, 264591, 265011, 87168559, 264600, 265019, 264288, 264768, 21906765, 21906767, 55811576, 35696423, 85274791, 22279002
2145	20564305 (4289, 4290)			UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gij1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR-S28503) [Caenorhabditis elegans]		UNCLASSIFIED	264908, 60433356, 264686
2147	80432911 (4293, 4294)	Novel Protein sim. GBank gij3080398jemb CAA18718.1  - (AL022603) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264907, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank gij118863 sp P20693 FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	Contains protein domain (PF00059) - glycoprotein Lectin C-type domain		29331824, 29331826, 35696052, 264758, 87168474, 265018, 52644150, 33657109
2150	84140059 (4299, 4300)	Novel Protein sim. GBank gij5420387 emb CAB46679.1  - (A1243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278998, 29331822, 29331824, 29331828, 264764, 264769, 21906766, 264486
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gij5689407 dbj BAA82987.1  - (AB028958) KIAA1035 protein [Homo sapiens]			22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 29331828, 264508, 264511, 60433356, 264758, 264596, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264688, 21906765, 21906766, 21906768, 265020, 60170615, 33657109, 33657182, 33657349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000, 18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388
2152	79321640 (4303, 4304)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase		

2153	88313371 (4305, 4306)	Novel Protein sim. GBank gij4758704[re]NP_004216.1pMASL - MIFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 52646842, 22278996, 22278998, 22278999, 264259, 29331822, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265019, 264760, 264288, 264389, 264766, 264687, 264769, 52644229, 21908766, 21908788, 35695917, 33657023, 33657109, 35695855, 264631, 264632, 264635, 264636, 264639, 18108385, 264483, 264564, 264486
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gij225150[pr]j1209265U - chorton protein B11 [Bombyx mori]		UNCLASSIFIED	56984075, 264094, 265009, 265019, 264288, 21908767, 35695917
2155	87424072 (4309, 4310)			UNCLASSIFIED	18108392, 18108398, 22278996, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264686, 265020, 264693, 264628, 56182323
2156	84295205 (4311, 4312)	Novel Protein sim. GBank gij3970966 (AC004974) - spa-1- like; similar to AF026504 (PID:g2555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)	Novel Protein sim. GBank gij1076211[pr]jS50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gij4650844[db]jBAA77027.1]- (AB026190) Kelch motif containing protein [Homo sapiens]		UNCLASSIFIED	264596
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gij2879925[db]jBAA24826]- (AB007897) KIAA0437 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_rna_bind	29331822, 264112, 265009, 264691, 33657023, 264634
2160	16283674 (4319, 4320)				284634
2161	87739131 (4321, 4322)	Novel Protein sim. GBank gij1504006[db]jBAA13202]- (D88966) similar to human ZFY protein. [Homo sapiens]		UNCLASSIFIED	265008
2162	84318526 (4323, 4324)			UNCLASSIFIED	65274572, 264508, 264805, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264596, 264758, 265011, 264600, 264762, 264763, 264693, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264566, 264567
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gij3876537[emb]CAA98270]- (Z73974) cDNA EST yk29115.3 comes from this gene; cDNA EST yk29115.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278996, 264093, 264683, 33657023, 65274620, 60432113
2164	80569456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264565

2165	94329169 (4328, 4330)	Novel Protein sim. GBank gij1086794 (U41107) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	56994075, 22278956, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 29331830, 56182435, 285009, 21906754, 33657084, 265011, 265019, 264448, 264288, 264389, 21906765, 21906768, 21906769, 265020, 265021, 264691, 264692, 33657023, 63274620, 35695855, 264556, 60170394, 83373044, 60432113, 22278002, 264567, 52645156, 22278994, 22278998, 66714117, 29331828, 52644045, 265018, 265019, 264369, 21906765, 21906767, 21906768, 21906769, 265021, 265022, 264693, 27486282, 35695763, 18108376, 56526486, 87168518, 264567
2166	87618934 (4331, 4332)	Novel Protein sim. GBank gij2706522[embjCAA75816] - (Y15895) ubiquitin activating enzyme [Drosophila melanogaster]	ubiquitin	56182575, 35696286, 29331824, 29331826, 29146498, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109954, 265011, 265017, 265018, 18108351, 264369, 21906764, 21906765, 21906768, 29148627, 21906769, 52644150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 264567
2167	87716864 (4333, 4334)	Novel Protein sim. GBank gij2224713[dbjBAA20840] - (AB002384) KIAA0386 [Homo sapiens]	UNCLASSIFIED	66714117, 29331827, 264907, 264511, 264591, 265018, 264764, 264683, 264766, 264768, 264566
2168	86899334 (4335, 4336)	Novel Protein sim. GBank gij4321407[gbjAAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	transport	264629, 264555, 264559
2169	87886937 (4337, 4338)	Novel Protein sim. GBank gij5106521[gbjAAD39741.1]AF10536 - (AF105365) K-CI cotransporter KCC4 [Homo sapiens]	UNCLASSIFIED	65274572, 56182575, 22278997, 22278998, 264259, 29331825, 264509, 264906, 56182435, 60433438, 55812038, 264596, 55811386, 265019, 264762, 264763, 264448, 264764, 264684, 264288, 264766, 264685, 56181562, 264689, 55811957, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35696423, 55811576, 65274791, 264634, 264639, 264558, 87168518, 60432113, 264564
2171	80194050 (4341, 4342)		UNCLASSIFIED	264369, 265020, 264558
2172	85452460 (4343, 4344)		UNCLASSIFIED	264259, 264558
2173	87036740 (4345, 4346)	Novel Protein sim. GBank gij4309681[gbjAAD16478] - (AC006930) R33423_1 [Homo sapiens]	UNCLASSIFIED	264369
2174	95003288 (4347, 4348)	Novel Protein sim. GBank gij2493778[spjQ09456jYQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5]		264906, 35695855, 264555, 264557

2175	84325850 (4348, 4350)	Novel Protein sim. GBank gi 1263287 (U47855) - fibroin-3 (Araneus diadematus)		UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 60432289, 35696032, 264109, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264600, 264603, 264760, 264762, 264448, 264764, 264288, 264768, 264688, 264687, 21906768, 55811957, 35695917, 265020, 265022, 264691, 264692, 33857023, 264693, 264628, 264629, 55811576, 35698423, 65274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00805) - oncogene Pentapeptide repeats (8 copies)	oncogene	52644507, 52646842, 22278994, 35686288, 22278996, 22278998, 28331826, 29331827, 35696052, 28331828, 33858970, 29331830, 284910, 33857402, 264758, 52644296, 87168559, 265018, 264688, 21906765, 21906767, 21906769, 35695917, 52644150, 264690, 33857023, 33857109, 52645129, 33657182, 27486261, 27486262, 33657349, 18108376, 18108377, 35695855, 87168518, 60432113, 264404, 22279000, 264486
2177	84128942 (4353, 4354)	Novel Protein sim. GBank gi 5454072 ref NP_008416.1 pSLU7 - step II splicing factor SLU7		kinase	18108392, 22278997, 22278999, 284093, 33657402, 265019, 264448, 264768, 264689, 21906767, 21906768, 21906769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gi 473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - eph Hsp70 protein	eph	264488, 22278996, 22278999, 28331824, 28331825, 29331826, 28331827, 52644296, 87168474, 18108370, 35695855, 22279002
2179	87316275 (4357, 4358)			UNCLASSIFIED	60424289, 264760, 264628, 264632

2180	95351397 (4359, 4360)	Novel Protein sim. GBank gij3122317 sp P90848 KMB_DICD1 - MYOSIN HEAVY CHAIN KINASE B (MHCK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 264508, 264509, 264906, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264862, 264683, 264684, 264288, 264686, 21906765, 21906768, 21906769, 265020, 265021, 265022, 52644150, 33657023, 33657109, 27486265, 33657349, 18108374, 35696423, 35695855, 263981, 60170394, 18108385, 56526486, 87168518, 60432113, 22279000, 264482, 264566, 264567, 264486, 29331827, 264369, 18108376, 264564
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gij3024689 sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIIID 100 KO SUBUNIT (TAFII-100) (TAFII100)		kinase	
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gij5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278996, 22278997, 22278999, 264259, 29331822, 56182435, 264112, 264764, 264288, 21906767, 21906768, 21906769, 33657109, 18108376, 60170394, 22279000, 22279002
2183	8540649 (4365, 4366)	Novel Protein sim. GBank gij3873408 gb AAC77482.1  - (U17129) unknown [Rhodococcus erythropolis]			264760
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gij3114713 (AF061346) - Edp1 protein [Mus musculus]		inf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264638, 264557
2185	87828463 (4369, 4370)	Novel Protein sim. GBank gij5106958 gb AAD39906.1 AF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			29331824, 264907, 66712502, 264757, 265019, 264288, 264692, 56526486
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gij2664625 emb CAA16972  - (AL021811) putative protein [Arabidopsis thaliana]		ATPase-associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 264768, 55811957, 33657023, 55811576, 56182323, 264563
2187	87388173 (4373, 4374)			UNCLASSIFIED	35696032, 264905, 264906, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264681, 264766, 264769, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264566, 264486
2188	87717708 (4375, 4376)	Novel Protein sim. GBank gij5107816 gb AAD40129.1 AF14941 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	18108398, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264908, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gij3452357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264369, 264288, 263987



2180	87639197 (4378, 4380)	Novel Protein sim. GBank gij132575sp P29315 RINI_RAT - RIBONUCLEASE INHIBITOR		nucleaseinhib	22278996, 22278999, 28331822, 28331824, 29331826, 265008, 264910, 60170831, 55812038, 52844296, 265010, 265018, 264685, 264688, 56181562, 21906769, 35695917, 265022, 60170394, 22279000
2191	95198928 (4381, 4382)	Novel Protein sim. GBank gij5327002 emb CAB46272.1  - (Y18503) XAP-5-like protein [Homo sapiens]			29331825, 28331826, 28331830, 264510, 264511, 264910, 264593, 264594, 264596, 264559, 264558
2182	11126316 (4383, 4384)	Novel Protein sim. GBank gij462600sp P34400 MI10 CAEEL - MIG-10 PROTEIN	Contains protein domain (PF00169) - PH domain		
2183	84140073 (4385, 4386)	Novel Protein sim. GBank gij5420389 emb CAB46880.1  - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181886, 28331825, 28331827, 264508, 264909, 265008, 264592, 60432228, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810784, 55811576, 65274791, 35695855, 60431850, 58192323, 60432113, 264592
2184	21418714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			
2185	88083023 (4389, 4390)	Novel Protein sim. GBank gij2832763 emb CAA15685.1  - (AL009191) /prediction=(method:; /prediction=(method:; /match=(desc:; /match=(desc:; /motif=(desc: [Drosophila melanogaster]		UNCLASSIFIED	22278986, 22278999, 35686052, 265006, 21908754, 285017, 35695917, 265021, 265022, 35695855
2186	85081631 (4381, 4382)	Novel Protein sim. GBank gij5262487 emb CAB45699.1  - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35686286, 22278997, 22278999, 264259, 29331822, 66714117, 60432289, 29331827, 35696052, 28331828, 264508, 52844045, 56182435, 284510, 285007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 284687, 52844229, 21906765, 21906788, 21906767, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 264636, 56182323, 18108385
2187	95073813 (4393, 4394)	Novel Protein sim. GBank gij4929567 gb AAD34044.1 AF151807 CGI-49 protein [Homo sapiens]			264788, 264769, 21906765, 21906768, 21906767, 29148827, 55811957, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 284910, 60432229, 56182323, 33657402, 264758, 83373044, 21808754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264389
2188	88060914 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953_1 [Homo sapiens]		UNCLASSIFIED	

2199	88054355 (4397, 4398)	Novel Protein sim. GBank gl 2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]			264105, 264110, 264112, 264688, 55811957, 33657023, 264692, 263967, 20281071, 56526486
2200	87405385 (4399, 4400)	Novel Protein sim. GBank gl 3043634[db][BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struct		29331824, 264763, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gl 3913470[sp O57314 DHBX_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2	Contains protein domain (PF00106) - short chain dehydrogenase		29331824, 35696052, 264905, 264907, 33657402, 55811386, 265017, 265018, 265019, 264288, 21906768, 35695917, 285020, 265022, 33657023, 33657109, 27486261, 18108370, 35696423, 35695855, 264555, 264556, 83373044, 87168518, 60432113
2202	91672385 (4403, 4404)	Novel Protein sim. GBank gl 5282665[emb CAB45767.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264489, 264259, 29331824, 60432289, 35696052, 264905, 264909, 264592, 265017, 265018, 265019, 18108351, 264762, 264448, 264369, 264288, 264766, 21906765, 21906766, 264690, 264691, 264692, 33657109, 264634, 264636, 264555, 264639, 264558, 264559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank gl 172845[sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25	Contains protein domain (PF00071) - Ras family	glycoprotein	52646355, 56994075, 264259, 29331822, 29331826, 29331827, 29331828, 264910, 265010, 265011, 87168559, 265018, 265019, 264605, 264288, 21906769, 35695917, 33657023, 264692, 33657109, 35695763, 18108376, 264638, 22279000, 264566, 264567
2204	88088671 (4407, 4408)	Novel Protein sim. GBank gl 121036[sp P29346 GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-3 SUBUNIT (GUSTUDUCIN ALPHA-3 CHAIN)	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED	
2205	94147589 (4409, 4410)	Novel Protein sim. GBank gl 4569480[db][BAA76768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00096) - dna_rna_bind Zinc finger, C2H2 type		18108394, 18108397, 56182575, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 265008, 265009, 60432229, 265010, 265011, 265018, 264683, 264288, 264369, 264686, 21906766, 21906768, 21906769, 264690, 264691, 264693, 18108368, 55811576, 65274791, 264634, 18108381, 18108384, 60432113, 22279002, 264583, 264586, 264591
2206	20620008 (4411, 4412)		UNCLASSIFIED		
2207	87787970 (4413, 4414)	Novel Protein sim. GBank gl 4557753[re NP_000372.1 pMID1 - midline 1 protein	Contains protein domain (PF00622) - SPRY domain		29331822, 56182181, 29331827, 35696052, 52644045, 265006, 265019, 56181562, 55811957, 265021, 33657023, 35695763, 35695855, 60170394, 60432113, 264566
2208	86100830 (4415, 4416)				264906, 265019, 18108351, 21906769
2209	87800420 (4417, 4418)	Novel Protein sim. GBank gl 3986746 (AF105228) - tuftsin [Bos taurus]	struct		264112, 265009, 264691, 18108365, 18108374, 264634, 20281166

2210	57152407 (4419, 4420)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	264685, 264686, 18108365, 22279002, 264482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi 3776027 emb CAA09214  - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278998, 264092, 264094, 29331822, 68714117, 29331828, 29331828, 264907, 52644045, 265009, 60170831, 21906754, 87168559, 265017, 265019, 18108351, 264683, 18108354, 264369, 264766, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 33657109, 18108370, 18108374, 264638, 56182323, 18108384, 18108387, 87168518, 264555
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1  - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278996, 22278997, 35696052, 264905, 68712502, 264908, 264826, 56182435, 264112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 18108351, 264765, 21906765, 21906766, 21906769, 265020, 265021, 264693, 264629, 263974, 263976, 18108379, 55811576, 264556, 264637, 264558, 83373044, 22279002, 264482, 264483

2214	95361453 (4427, 4428)	Novel Protein sim. GBank gil4504325[ref]NP_000173.1[pHADH - hydroxyacyl- Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	dehydrogenase	264488, 52644507, 18108394, 56182575, 22278994, 22278995, 35696288, 56994075, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 52645080, 29331822, 29147620, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 20281100, 264509, 264907, 66712502, 264908, 29331830, 52644045, 56182435, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433356, 60433438, 33109954, 33657084, 52644298, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 264532, 60170815, 264690, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 33657182, 27486262, 27486264, 27486265, 35695763, 18108370, 264629, 60431528, 18108374, 18108376, 55810764, 35696423, 35695855, 264634, 264636, 52644332, 264638, 264558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264566, 264909, 265008, 264555, 264558, 87168518
2215	95419206 (4429, 4430)	Novel Protein sim. GBank gil1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]			
2216	87614048 (4431, 4432)	Novel Protein sim. GBank gil1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]		UNCLASSIFIED	264693
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gil5031707[ref]NP_005503.1[pGARP - glycoprotein A repetitions, predominant]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264288, 33657109, 264556
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gil3878636[emb]CAA88953] - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL:TD0719 comes from this gene; cDNA EST yk465db.3 comes from this gene; cDNA EST yk465db.5 comes from this gene; cDNA EST yk49214.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		35696423, 264553
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gil1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family		264682, 264683, 264688, 264689, 264693, 18108370, 18108376

2220	95354165 (4439, 4440)	Novel Protein sim. GBank gi 4507261 ref NP_003145.1 pSTAT - stathefin			264488, 18108394, 18108395, 35696286, 264259, 264097, 60432289, 264509, 264805, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 264593, 264594, 60433356, 264595, 55812038, 264758, 8568542, 265010, 264801, 264603, 265018, 264605, 264760, 264762, 264448, 264764, 264368, 264766, 18108357, 264768, 264687, 18108358, 264769, 55811957, 264690, 264681, 33657023, 264692, 18108362, 18108368, 264628, 264629, 18108374, 263978, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264568, 264486, 264587
2221	88060927 (4441, 4442)	Novel Protein sim. GBank gi 3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425882 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35695855
2223	95091649 (4445, 4446)			UNCLASSIFIED	265010, 264685, 264690, 264693, 264628, 263974, 263976, 55811576, 264555, 264638, 83373044, 264483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gi 3876005 emb CAA84789  - (Z35719) cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES...	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	264259, 264509, 56182435, 265008, 265009, 265009, 264757, 21906754, 18108351, 264693, 18108374, 18108385
2225	85749484 (4449, 4450)	Novel Protein sim. GBank gi 1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans]	transport		22278994, 22278995, 22278999, 52644045, 264600, 285019, 21906765, 21906769
2226	86978953 (4451, 4452)	Novel Protein sim. GBank gi 4826524 emb CA842852.1  - (AL049848) hypothetical protein [Homo sapiens]			264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265007, 264691, 264634, 264486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278998, 265006, 265008, 18108354, 28148629, 28148784, 27486281, 18108374, 264637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gi 806976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	264091, 264092, 264094, 29331822, 29331825, 68714117, 264693, 263972, 264639, 83373044, 264563
2229	88060931 (4457, 4458)	Novel Protein sim. GBank gi 3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342815 (4459, 4460)	Novel Protein sim. GBank gi 226154 pr 1412350A - DNA polymerase [Human adenovirus type 2]		UNCLASSIFIED	264488, 264768, 52644507, 264769, 21908765, 21908766, 21908767, 21908769, 22278995, 35695917, 22278996, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21906754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	88060937 (4461, 4462)	Novel Protein sim. GBank gi 3549154 (AC005625) - R27328_1 [Homo sapiens]		UNCLASSIFIED	
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gi 5281316 gb AAD41476.1 AF13312 - (AF133124) transcription factor IIC63 [Homo sapiens]		transcription factor	18108394, 56182575, 22278995, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264758, 55812038, 264603, 265018, 265019, 18108351, 264882, 264764, 264683, 264369, 264288, 264686, 264687, 264689, 21906765, 21908766, 21906767, 21906769, 29148629, 35695917, 264690, 52644150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264564, 264906, 33657402, 265018, 264288, 264686, 265020, 264635, 18108365
2233	87755292 (4465, 4466)	Novel Protein sim. GBank gi 4248733 gb AAD137801 - (AF109377) IdBP [Mus musculus]			56182435, 264369, 264688, 21906765, 265020, 264693, 264556, 56526486
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gi 1706559 sp P54352 EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)		kinase	
2235	91012316 (4469, 4470)	Novel Protein sim. GBank gi 4972734 gb AAD34762.1  - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278997, 264563
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gi 1082675 pr B53814 - p20 protein - human	Contains protein domain (PF00011) - Hsp20/alpha crystallin family	eph	264569, 264687, 264769, 265022, 264259, 60437049, 264691, 29331826, 60432289, 20281149, 264906, 264907, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264783, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gi 4972734 gb AAD34762.1  - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264488, 264769, 21906765, 21908766, 21908767, 21908768, 21908769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433356, 60433438, 83373044, 18108385, 21906754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288

2238	84998857 (4475, 4476)		Contains protein domain (PF00286) - Viral coat protein	264509, 264907, 264628, 264634, 264564
2239	87798688 (4477, 4478)			29331825, 265009, 264369, 33657109, 18108370, 18108374, 264557, 264559
2240	84121471 (4479, 4480)	Novel Protein sim. GBank gll2982311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]	ubiquitin Ubiquitin-conjugating enzyme	264488, 65274572, 56182575, 35688288, 22278997, 22278998, 264259, 29331827, 3569052, 264508, 52644045, 56182435, 264511, 265007, 265008, 265009, 60433358, 60433438, 55812038, 21906754, 33657084, 55811388, 265018, 265019, 18108351, 284683, 284288, 284768, 264687, 264688, 284769, 21906765, 21906768, 21906769, 35695917, 265021, 265022, 60170815, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35696423, 35695855, 87168518, 22279000
2241	80091951 (4481, 4482)			264583, 264629
2242	91228075 (4483, 4484)	Novel Protein sim. GBank gll2494312 [sp]P70541E2BG. RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)	UNCLASSIFIED synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264598, 21906754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 27486264, 18108374, 35695855, 264634, 264637, 56182323, 83373044, 56526486, 87168518, 264564
2243	78902028 (4485, 4486)			265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gll2291143 (AF018417) - Similar to BZIP transcription factor [Caenorhabditis elegans]	UNCLASSIFIED	264604
2245	95318545 (4489, 4490)	Novel Protein sim. GBank gll470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	UNCLASSIFIED Glycosyl transferases group 1	52845156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21906754, 265011, 264603, 264764, 264687, 21906767, 21906768, 21906769, 55811957, 265022, 284691, 284629, 35696423, 264638, 18108387, 60432113, 22279000, 22279002, 264566

2246	94848710 (4481, 4492)	Novel Protein sim. GBank gll4996096[db][BAA78326.1] - (AB028069) activator of S phase Kinase [Homo sapiens]	(Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 35696052, 264106, 264905, 264907, 265008, 265007, 265008, 60433438, 33109954, 87168559, 265018, 265019, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 27486264, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87862542 (4483, 4494)	Novel Protein sim. GBank gll854065[emb][CAA58337] - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	UNCLASSIFIED	52645156, 52646385, 52645080, 35696052, 33656970, 52646317, 33657084, 265017, 21906768, 21906769, 35695917, 33657109, 52645129, 33657182, 27486261, 27486262, 33657348, 27486265, 18108387
2248	95412896 (4495, 4496)	Novel Protein sim. GBank gll4758502[ref][NP_004123.1]pHABP - hyaluronan-binding protein 2	(Contains protein domain (PF00089) - Trypsin	calhepsin	264488, 264259, 264907, 29331830, 264909, 265007, 265009, 264595, 21906754, 65274444, 264603, 265019, 264762, 264448, 264288, 264688, 21906766, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264486
2249	94685662 (4487, 4488)	Novel Protein sim. GBank gll4038461 (AF107772) - TcST11 [Trypanosoma cruzi]	(Contains protein domain (PF00515) - TPR Domain	eph	264766, 264628, 264636, 264637
2250	79827508 (4489, 4500)	Novel Protein sim. GBank gll3738140[emb][CAA21241] - (AL031852) valyl-trna synthetase, mitochondrial precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gll3218467[emb][CAA07090.1] - (AJ008529) putative phosphatase [Gallus gallus]	UNCLASSIFIED	UNCLASSIFIED	264259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264884, 264288, 264690, 264628, 55811576, 264555, 264556, 264557, 264558, 264559, 264568
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gll4928325[gb][AAD33953.1][AF14531] - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	(Contains protein domain (PF01813) - synthase ATP synthase subunit D	synthase	264092, 264094, 264259, 29331822, 66714117, 29331828, 264102, 264103, 264104, 264105, 264109, 264112, 264511, 265007, 60433356, 265010, 18108351, 21906767, 21906768, 264691, 263974, 263977, 264486, 264567
2253	91010703 (4505, 4506)		UNCLASSIFIED	UNCLASSIFIED	65274572, 265019



2254	95320031 (4507, 4508)	Novel Protein sim. GBank gi 4502847 ref NP_001271.1 pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	264569, 18108394, 18108398, 56182575, 56994075, 35898286, 22278999, 264094, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 35898052, 264106, 264508, 264509, 264806, 264807, 29331830, 66712502, 264908, 284909, 264510, 265006, 264511, 265007, 265008, 265009, 60170831, 60432229, 60433358, 60433438, 264758, 8585842, 265010, 265011, 87188559, 265017, 265018, 265019, 264448, 264764, 264288, 264369, 264768, 264686, 264768, 264769, 21906765, 21906767, 55811857, 264691, 33657023, 264692, 18108362, 65274620, 263969, 264628, 18108370, 60431528, 263972, 264629, 18108372, 18108377, 18108378, 55811576, 35696423, 35695855, 264630, 264634, 264635, 264636, 264556, 263981, 264638, 56182323, 60170394, 264558, 18108381, 18108382, 83373044, 18108385, 87188518, 60432113, 22279002, 264482, 264564, 264565, 264488, 264567, 18108391
2255	91010548 (4509, 4510)	Novel Protein sim. GBank gi 5541865 emb CAB51072.1  - (AL086858) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264508, 264905, 264906, 264907, 66712502, 264908, 56182435, 264510, 264511, 265008, 264593, 264595, 21906754, 33109954, 87168474, 265011, 265017, 265018, 264682, 264784, 264369, 264288, 264768, 264685, 264686, 264768, 21906765, 21906766, 21906768, 21906769, 265020, 60170615, 52844150, 264690, 264692, 264693, 33657109, 33657349, 264632, 264636, 52644332, 56182323, 22279000, 22279002
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gi 3327174 dbj BAA31655  - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	264768, 264689, 18108374
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278996, 22278998, 264681, 21906765, 21906768, 264567
2258	86090516 (4515, 4516)	Novel Protein sim. GBank gi 3025446 (AC004528) - R32184.2 [Homo sapiens]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	284908, 284592, 264784

2259	95364155 (4517, 4518)	Novel Protein sim. GBank gi 4884140 emb CAB43278.1  - (AL050110) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108396, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331827, 264905, 66712502, 284908, 284909, 56182435, 265007, 265008, 60432229, 33657084, 87168559, 18108351, 264448, 264683, 264288, 264369, 56181562, 265021, 60170615, 264690, 33657109, 60431528, 18108374, 52644332, 56182323, 18108385, 22279000, 22279002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gi 3080663 (AC004614) - similar to I-spondin proteins AB006086 (PIDg2529225) [Homo sapiens]	Contains protein domain (PF000090) - oxidase Thrombospondin type 1 domain	oxidase	56182575, 265020, 264905, 264906, 264908, 35698423, 264511, 264635, 55812038, 264758, 265018, 265019, 264605, 264760, 264563
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gi 3334526 emb CAA16138  - (AL021308) predicted using FGENEH [Homo sapiens]		UNCLASSIFIED	
2262	91639292 (4523, 4524)	Novel Protein sim. GBank gi 487759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]			56182575, 22278999, 29331822, 29331825, 60432289, 29331827, 35698052, 264508, 66712502, 52644045, 56182435, 265008, 265008, 265009, 60433356, 55812038, 265010, 265017, 265019, 264288, 264369, 21908765, 21906767, 55811957, 35695917, 52644150, 33657023, 33657109, 55811576, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gi 3341597 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 264907, 264828, 52644150, 18108361, 264693, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gi 1657601 (U66220) - unknown [Nannocystis exedens]		UNCLASSIFIED	264686, 264488, 264768, 264769, 264691, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 35695855, 264510, 264511, 264512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264564, 264565, 264764, 264566, 264486, 264766
2265	86818663 (4529, 4530)	Novel Protein sim. GBank gi 477072 pir J48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264689, 264910, 264764
2266	87773458 (4531, 4532)	Novel Protein sim. GBank gi 3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomalprot	22278995, 22278997, 22278999, 264259, 265006, 265007, 265009, 60433438, 21908754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21906765, 21906768, 35695917, 265021, 18108374, 264638, 22279000, 22279002, 264566, 264487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gij3560229[emb]CAA20697.11 - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	3569286, 264259, 29331824, 29331825, 35698052, 29331828, 264905, 264508, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33657402, 265010, 265018, 264782, 264448, 264288, 264369, 264788, 52644229, 35695917, 264691, 33657023, 18108382, 33657109, 35698423, 264634, 18108381, 87188518, 264588
2268	85693867 (4535, 4538)	Novel Protein sim. GBank gij728832[sp]P39189[ALU2_HUMAN - IIII ALU SUBFAMILY S8 WARNING ENTRY IIII]	cadherin		264488, 264259, 264508, 264595, 265010, 265017, 264788, 18108385, 264488
2269	88177877 (4537, 4538)	Novel Protein sim. GBank gij103418[pir][S17885 - Tcd37 protein - fruit fly (Drosophila melanogaster)]	UNCLASSIFIED		56182575, 60432049, 265007, 265009, 264591, 87168559, 264605, 18108351, 21908764, 265020, 264629, 60431528, 264638, 18108385, 18108387, 60432113
2270	80410327 (4539, 4540)				264763
2271	91010392 (4541, 4542)		cyl6450		264909, 56182435, 285008, 55812038, 55811957, 33657023, 264693, 33657109, 55810764, 55811576, 56182323
2272	84208220 (4543, 4544)		UNCLASSIFIED		264905, 264908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gij4178370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin		52645156, 22278996, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264809, 265008, 264593, 60433438, 21908754, 265018, 264689, 21908765, 21908768, 21908767, 21908769, 265021, 265022, 60170015, 264691, 33657023, 264693, 33657109, 27486264, 18108376, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22279002
2274	91640217 (4547, 4548)	Novel Protein sim. GBank gij1480112[emb]CAA679611 - (X99642) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264591, 21908754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264766, 21908765, 21908768, 21908767, 21908768, 52644150, 264693, 18108364, 35695763, 18108374, 35696423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87188518, 22279002
2275	88082501 (4548, 4550)	Novel Protein sim. GBank gij3165406 (AC004755) - fos37502_2 [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	
2276	11287447 (4551, 4552)		UNCLASSIFIED		264555, 264558

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369006) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	2227899, 35696052, 265008, 265019, 264369, 265020, 265022, 55810764, 264404, 22279002
2278	94133079 (4555, 4556)	Novel Protein sim. GBank gi 2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278997, 29331826, 60433356, 60433438, 21906754, 285018, 33657023, 264639, 83373044, 264565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gi 119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	264766, 264565
2280	94239723 (4559, 4560)				
2281	95283048 (4561, 4562)	Novel Protein sim. GBank gi 4240299 db BAA74928.1  - (AB020712) KIAA0905 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	265008, 33109854, 265010, 265019, 265020, 264092, 264259, 29331822, 29331824, 29331826, 35696052, 264107, 264906, 264909, 52644045, 265008, 33657402, 60433356, 264758, 265011, 265019, 264681, 264683, 264684, 264686, 21908765, 21908767, 21906768, 21906769, 60170615, 264690, 52644150, 18108382, 264692, 18108368, 18108374, 263978, 264631, 18108381, 264559, 18108385, 56528486, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gi 1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264488, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18108351, 21908767, 21908769, 55811957, 33657023, 52645129, 33657109, 33657182, 27466262, 263972, 55811576, 87168518, 20281169
2283	95362386 (4565, 4566)	Novel Protein sim. GBank gi 2495729 sp Q92559 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	60424179, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35696052, 29146499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33109854, 33657084, 55811386, 87168474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264288, 264688, 21906765, 21908767, 21906768, 29148627, 21906769, 55811957, 265020, 265022, 33657182, 27466261, 18108370, 264628, 18108374, 55810764, 18108379, 55811576, 35696423, 35695855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264567

2284	95414855 (4567, 4568)	Novel Protein sim. GBank gi 2498797 sp Q64311 PNAD_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA)			60424178, 52644507, 18108394, 52646842, 22278994, 35696286, 22278998, 22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21906754, 85658542, 87168559, 265018, 265019, 55811150, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 33657023, 33657182, 27486262, 27486264, 27486265, 18108376, 55810764, 35696423, 35695855, 60431850, 87168518, 60432113, 264482, 264564
2285	87781484 (4569, 4570)	Novel Protein sim. GBank gi 3342234 (U93909) - nuclear antigen EBNA-1 [Cercopithecina herpesvirus 15]		collagen	35696052, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264595, 264760, 18108351, 264682, 264783, 264685, 264766, 264686, 264768, 264693, 264629, 35695855, 264631, 264634
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi 3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]		kinase	35696286, 58182435, 60170831, 264591, 60432229, 264592, 264593, 264594, 264595, 55812038, 264596, 87168474, 35695917, 264692, 55811576, 264555, 264557
2287	82866696 (4573, 4574)	Novel Protein sim. GBank gi 630905 pir J542731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	Contains protein domain (PF01391) - collagen Collagen triple helix repeat (20 copies)	UNCLASSIFIED	264682
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		tm7	22278995, 56994075, 22278997, 22278999, 264259, 60432289, 264508, 264512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21906765, 21906766, 21906767, 21906768, 33657023, 264557, 22278900, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gi 2867497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat	kinase	
2280	88084137 (4579, 4580)	Novel Protein sim. GBank gi 2867497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264683
2281	84285281 (4581, 4582)	Novel Protein sim. GBank gi 3253120 (AC005175) - R31449_3 [Homo sapiens]		struct	18108394, 264907, 265006, 265009, 33109954, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2292	94328834 (4583, 4584)	Novel Protein sim. GBank gij4803672[embjCAB42643.1] - (AJ133769) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 56984075, 29331824, 29331825, 35696052, 56182435, 60433438, 55812038, 33109954, 87168474, 87168559, 265018, 18108351, 264763, 264448, 264369, 264288, 56181562, 284789, 21908765, 21906766, 21906767, 21906769, 265021, 265022, 33657023, 264693, 65274620, 33657109, 27486264, 264629, 55810764, 55811576, 35695855, 56182323, 55528486, 87168518, 22279000, 284567
2293	87759213 (4585, 4586)	Novel Protein sim. GBank gij3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - struct Leucine Rich Repeat		264488, 18108397, 35696286, 264092, 264259, 29331822, 29331826, 264906, 264908, 264511, 264512, 265009, 264910, 18108351, 264764, 264369, 264288, 264685, 264766, 265020, 265022, 264534, 35696423, 264631, 264637, 18108381, 56182323, 264639, 18108385, 264404, 264563, 284565
2294	86693580 (4587, 4588)	Novel Protein sim. GBank gij2062680 (U88964) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - nuclease Exonuclease		22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35696052, 265018, 264684, 264288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33657109, 18108376, 35696423, 35695855, 264634, 22279000, 22279002, 264563, 264486
2285	95312200 (4589, 4590)			UNCLASSIFIED	22278996, 60432289, 264682, 264683, 264689, 18108374
2296	80030781 (4591, 4592)				263974, 263978
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gij5689501[dbjBAA83034.1] - (AB029005) KIAA1082 protein [Homo sapiens]		transcriptfactor	264488, 65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 35696052, 264907, 264908, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21906754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21906765, 21906767, 21908768, 21906769, 55811957, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60170394, 83373044, 18108385, 56528486, 264564, 264486

2298	95312207 (4595, 4596)	Novel Protein sim. GBank gij3875051[embjCAB02849] - (Z81050) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D85564 comes from this gene; cDNA EST EMBL:D68046 comes from this gene; cDNA EST yk366b12.3 comes from this gene; cDNA EST yk366b12.5 comes from this gene ...		collagen	60424179, 56181686, 22278995, 35696286, 22278998, 22278998, 22278998, 264480, 264259, 28331822, 28331824, 66714117, 60424268, 35696052, 28331828, 66712502, 56182435, 284510, 265008, 60433438, 21806754, 33109954, 55811386, 265010, 265018, 55811150, 264762, 18108351, 264882, 264683, 264288, 264684, 264688, 264688, 56181562, 264689, 21806766, 21906767, 29148629, 55811957, 29148784, 35695917, 265020, 18108362, 33657023, 18108364, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35696423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22278000, 264482, 264587, 264486
2299	80183720 (4597, 4598)			UNCLASSIFIED	264369
2300	94124348 (4599, 4600)	Novel Protein sim. GBank gij2443886 (AC002284) - Unknown protein [Arabidopsis thaliana]			264488, 22278998, 22278998, 264259, 28331824, 66714117, 35696052, 264508, 264905, 264908, 264907, 264908, 264909, 265008, 264910, 285009, 264758, 285010, 87168559, 264600, 265018, 264760, 264782, 18108351, 264784, 264786, 264788, 264789, 21906768, 21906767, 35695917, 265021, 264691, 33657023, 35695783, 18108370, 18108374, 35696423, 35695855, 264831, 264638, 264638, 18108385, 22279002, 264583
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gij2143637[pirj184505] - calcium-dependent actin-binding protein - rat		struct	264908, 264758, 265017, 21906765, 83373044, 264583
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gij2887497 (AC004144) - R34001.1 [Homo sapiens]		UNCLASSIFIED	52844045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gij4884194[embjCAB43220.1] - (AL049946) hypothetical protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	264259, 60432048, 264907, 264909, 264810, 60432229, 33657402, 265011, 265018, 264782, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gij2494162[spjQ10005]YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR		UNCLASSIFIED	264259, 28331824, 21906767, 33657182, 33657349
2305	90935911 (4608, 4610)	Novel Protein sim. GBank gij4972686[jb AAD34738.1] - (AF132150) unknown [Drosophila melanogaster]			65274572, 22278998, 264908, 265006, 21906769, 264881, 264486

2306	85334040 (4611, 4612)	Novel Protein sim. GBank gi 4929565 gb AAD34043.1 AF15180 - (AF15180) CGI-48 protein (Homo sapiens)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264488, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 284508, 264905, 264907, 29331830, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33657402, 21906754, 85636542, 265010, 265011, 264601, 265017, 265018, 264604, 265019, 18108351, 284448, 264288, 264766, 264768, 21906765, 21906766, 21906767, 21906768, 29148629, 29148784, 35695917, 265020, 265021, 265022, 33657023, 264692, 18108370, 18108374, 18108376, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 284568, 284486 264928
2307	79415283 (4613, 4614)	Novel Protein sim. GBank		UNCLASSIFIED	
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		synthase	35696286, 264259, 29331822, 29331824, 264112, 264512, 264757, 21906754, 264288, 264690, 27486264, 264631, 264634, 264404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi 3878059 emb CAB17070  - (Z99842) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72944 comes from this gene; cDN...		glycoprotein	18108397, 22278996, 22278997, 22278998, 22278999, 60432049, 29331822, 29331826, 60432289, 66712502, 60432229, 60433356, 60433438, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21906766, 21906768, 265020, 284691, 264692, 264693, 65274620, 65274791
2310	79601668 (4619, 4620)	Novel Protein sim. GBank gi 2137337 pir l48281 - gene	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	18108397, 56182575, 22278996, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 284510, 264511, 265008, 284512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264683, 264288, 264369, 264686, 33657023, 20281149, 20281069, 264628, 263972, 55811576, 35696423, 20281071, 264632, 264636, 18108385, 18108387, 87168516, 22279000, 264563, 284486
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gi 2137337 pir l48281 - gene mCBP protein - mouse		transcriptfactor	



2312	87549881 (4623, 4624)	Novel Protein sim. GBank gij2911264 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432229, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264286, 52644228, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 60170815, 33657023, 27486261, 27486264, 35696423, 35695855, 18108385, 22279000, 22279002 263981
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gij3043626 [dbj]BAA254771 - (AB011123) KIAA0551 protein [Homo sapiens]		UNCLASSIFIED	52644507, 52646365, 52646842, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33658970, 52644045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 285017, 265018, 265019, 264288, 264369, 21906765, 21906766, 21906768, 35695917, 52644150, 33657023, 33657109, 52645129, 33657349, 35695763, 18108374, 35696423, 35695855, 52644332, 22279000, 22279002, 264563, 264567
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gij5596714 [emb]CAB51401.1 - (AL035398) dJ796117.2 (CGI-51) [Homo sapiens]		UNCLASSIFIED	55811576, 264635, 56182323, 18108385, 52644507, 52645156, 52646365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264906, 264907, 29331830, 52644045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21908754, 52646317, 33109954, 33657084, 52644286, 87168474, 285010, 87168559, 265017, 285018, 265019, 264681, 264753, 264448, 264683, 264369, 52644228, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264631, 264556, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 264566, 264567
2315	80430119 (4629, 4630)			UNCLASSIFIED	
2316	94312191 (4631, 4632)	Novel Protein sim. GBank gij5531827 [gb]AAD44488.1 - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	glycoprotein	

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 264910, 60432229, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79959879 (4635, 4636)			UNCLASSIFIED	265006, 264910
2319	95101781 (4637, 4638)	Novel Protein sim. GBank gii5262613[emb]CAB45746.1] - (AL080155) hypothetical protein (Homo sapiens)			264488, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 264259, 52645080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21906754, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644229, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486264, 33657349, 35695763, 18108370, 18108376, 18108379, 35696423, 264558, 83373044, 18108385, 56526486, 87168518, 264554, 264555, 264566
2320	91622426 (4638, 4640)	Novel Protein sim. GBank gii728837[sp]P39194[ALU7_SQ WARNING ENTRY IIII]		kinase	22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265019, 21906765, 18108372, 18108387, 22279002
2321	94320377 (4641, 4642)	Novel Protein sim. GBank gii3873837[emb]CAB02700] - (Z81029) Similarity to S.pombe hypothetical protein CTD4.09C (SW:Q10154); cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01062 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com...		UNCLASSIFIED	264488, 264687, 18108394, 264688, 21906765, 18108397, 18108398, 21906767, 21906768, 65274791, 22278995, 35695955, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170615, 264555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264593, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87803165 (4643, 4644)	Novel Protein sim. GBank gii5678957[emb]CAB51685.1] - (AL109630) BACR7A4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264768, 264638

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi 2494162 sp Q10005 YR1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00226) - DnaJ domain	eph	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33656970, 264509, 56182435, 264511, 265008, 60433358, 60433438, 55812038, 33109954, 21906754, 85658542, 87168474, 265011, 87168558, 265017, 265019, 264760, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21906765, 21906767, 21906768, 55811957, 35695917, 265021, 33657023, 18108362, 27486282, 55811576, 264631, 264555, 83373044, 87168518, 60432113, 22278002 264592, 264593, 265020 265020
2324	86633607 (4647, 4648)	Novel Protein sim. GBank gi 5419865 emb CAB46377.1  - (AL098732) hypothetical protein [Homo sapiens]	ATPase-associated		
2325	86165074 (4649, 4650)	Novel Protein sim. GBank gi 231885 sp P29881 CP4C_BLA1 - CYTOCHROME P450 4C1 (CYP1VC1)	Contains protein domain (PF00067) - Cytochrome P450	Cyt450	265006, 284759, 35695855, 56182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi 231885 sp P29881 CP4C_BLA1 - CYTOCHROME P450 4C1 (CYP1VC1)		UNCLASSIFIED	
2327	88081848 (4653, 4654)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1  - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 265007, 264512, 264810, 264758, 265010, 264768, 264788, 264789, 33657023, 264693, 264628, 264631, 264634, 264638, 264639, 264488
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi 1245105 (U46463) - glutamine repeat protein-1 [Mus musculus]		UNCLASSIFIED	60433436, 264595, 265017, 264766, 264692, 264629, 264635, 264638, 264638, 56182323, 60432113, 264566
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi 1169343 sp P42209 DIF6_MOUSE - DIFF6 PROTEIN	Contains protein domain (PF00735) - Cell division protein	UNCLASSIFIED	265017, 264685, 60432113, 264088 265009
2330	87335396 (4659, 4660)	Novel Protein sim. GBank gi 5679136 gb AA046874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	
2331	86890463 (4661, 4662)	Novel Protein sim. GBank gi 5679136 gb AA046874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		ATPase-associated	35695285, 22278998, 29331824, 60424289, 265006, 265008, 265018, 264448, 264764, 21906765, 35695917, 35695855, 264636, 22279000, 264566
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi 2104452 emb CAB08779  - (Z85387) unknown [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 29331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263978
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi 3879895 emb CAA92691.1  - (Z88318) cDNA EST CEMSD82F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C09493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST...		UNCLASSIFIED	
2334	94319788 (4667, 4668)	Novel Protein sim. GBank gi 4966270 gb AA052261.2  - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E- value=1e-13, N=1 [C...	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044

2335	80046103 (4668, 4670)	Novel Protein sim. GBank gll3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00612) - IQ, calmodulin-binding motif	- struct	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gll1929056[emb]CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	264907, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gll4495063[emb]CAB39181.1] - (Z85986) dJ108K11.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]		UNCLASSIFIED	35696286, 22278999, 56182181, 29331825, 60424269, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 265019, 21906768, 35695917, 264691, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gll2224689[dbj]BAA20829] - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	UNCLASSIFIED	18108394, 29331822, 66714117, 60432289, 264908, 56182435, 265009, 60433438, 264596, 265010, 265019, 18108354, 264288, 264369, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gll3873550[emb]CAA22127] - (AL033534) serine-rich protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264592, 264369, 264691, 264558
2340	90937716 (4679, 4680)				65274572, 22278994, 35696286, 22278997, 22278999, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264768, 284685, 21906769, 35695917, 264691, 264692, 35696423, 87168518, 22279000
2341	87775281 (4681, 4682)	Novel Protein sim. GBank gll3874563[emb]CAB02797] - (Z81042) similar to Yeast hypothetical protein YEE6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264259, 264908, 264909, 264682, 22279000
2342	95334988 (4683, 4684)				264488, 63274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 264905, 264509, 29331830, 265006, 60170831, 60432229, 60433356, 87168474, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810764, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 284567
2343	87775448 (4685, 4686)	Novel Protein sim. GBank gll4929741[gb]AAD34131.1[AF15189] CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264907, 264512, 265011, 264683
2344	79953198 (4687, 4688)	Novel Protein sim. GBank gll2506307[sp]P13944[CA1C_CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)]	Contains protein domain (PF00092) - von Willebrand factor type A domain	UNCLASSIFIED	264758
2345	94319789 (4689, 4690)			collagen	264488, 264259, 66712502, 264759, 83373044, 264566

2346	94131820 (4691, 4692)	Novel Protein sim. GBank gl 125411 (U53153) - one short region of weak similarity to S. cerevisiae protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP:P14922) [Caenorhabditis elegans]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35696052, 29331828, 33657402, 6043356, 33108954, 87188559, 264603, 265019, 18108351, 264881, 264885, 21908766, 265021, 33657109, 55811576, 35895855, 264637, 52844332, 264557, 83373044, 22278000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264684, 264768, 264687, 264688, 264691, 264692, 55811576
2348	95196133 (4695, 4696)	Novel Protein sim. GBank gl 1928056[emb CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopodium obscurum]		kinase	18108394, 35696286, 264259, 35696052, 264508, 264509, 264905, 284908, 284907, 264908, 264909, 264510, 264511, 265008, 265007, 264512, 265008, 265009, 284910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264782, 18108351, 264764, 264288, 264766, 264768, 264689, 35695917, 264693, 264628, 18108370, 264628, 18108374, 35898423, 284631, 264635, 264636, 284637, 264638, 264639, 83373044, 18108385, 264567, 264486
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gl 4884106[emb CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]			35696052, 28146489, 284909, 264369
2350	88260594 (4698, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21908754, 265010, 87188559, 265018, 265019, 264761, 264681, 264288, 18108357, 21908766, 21908767, 264681, 264692, 35695855, 87168518, 22279000, 22279002, 264482
2351	88968042 (4701, 4702)	Novel Protein sim. GBank gl 726832[sp P39189 ALU2_HUMAN - III] ALU SUBFAMILY SB WARNING ENTRY IIII		kinase	56182575, 264809, 265006, 264558
2352	87337196 (4703, 4704)	Novel Protein sim. GBank gl 731637[sp P38760 YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	81638784 (4705, 4706)	Novel Protein sim. GBank gl 1346955[sp P48809 RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264636
2354	87337199 (4707, 4708)	Novel Protein sim. GBank gl 731637[sp P38760 YHH5_YEAST - HYPOTHETICAL 75.8 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265008, 265008

2355	91638786 (4709, 4710)	Novel Protein sim. GBank gi 4938503 emb CAB43861.1  - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56994075, 22278996, 35696286, 22278999, 264259, 29331825, 29331826, 29331828, 29146498, 264905, 264908, 265008, 264758, 87168474, 265010, 265017, 264687, 21906765, 21906767, 21906769, 264691, 264692, 263967, 18108370, 87168518, 22279000
2356	95327688 (4711, 4712)	Novel Protein sim. GBank gi 5138920 gb AAD40377.1  - (AF092135) PTD014 [Homo sapiens]			52644507, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 284259, 29331824, 66714117, 29331825, 60432289, 35696052, 29331828, 264908, 66712502, 264512, 265007, 265008, 60170831, 60432229, 60433356, 60433438, 264758, 52646317, 33109954, 21906754, 55811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264369, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170815, 33657109, 27486264, 35695763, 55810764, 18108378, 35696423, 55811576, 35695855, 60170394, 56182323, 83373044, 18108385, 56526486, 264404, 60432113, 22279000, 264482, 264563, 264566, 264486, 264567
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gi 4929741 gb AAD34131.1 AF15189 - (AF15189) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264488, 264769, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264566, 284369, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gi 4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755858 (4717, 4718)	Novel Protein sim. GBank gi 1086830 (U41264) - coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g6.5; coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk18g12.....		UNCLASSIFIED	35696286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21906769, 265020, 264692, 35695855, 264558, 56526486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gi 3881545 emb CAA93779  - (Z69904) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22279000
2361	84232191 (4721, 4722)	Novel Protein sim. GBank gi 746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 264512, 265009, 264757, 21906765, 65274620, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank gll1171093[sp]P19706[MYSB_ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)]		UNCLASSIFIED	22278998, 264259, 29331822, 29331824, 60432289, 264509, 264512, 60432229, 60433356, 264448, 264682, 264683, 264369, 21906765, 21906768, 21906768, 60432113, 22279000, 22279002 264907, 264628, 264635
2363	95006635 (4725, 4726)	Novel Protein sim. GBank gll654065[emb]CAA58337] - (X83413) U88 [Human Herpesvirus 6]		UNCLASSIFIED	
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gll5639830[gb]AAD45886.1[AF14601 - (AF146018) hydroxypyruvate reductase (Homo sapiens)]	Contains protein domain (PF00308) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 264887, 18108398, 22278998, 56994075, 35698288, 22278997, 22278998, 264259, 66714117, 29331825, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 265006, 264512, 265007, 265008, 33657402, 264758, 21906754, 87168474, 265010, 87168559, 264603, 265017, 265018, 265019, 264760, 264762, 18108351, 264448, 264764, 264683, 264684, 264288, 18108355, 264768, 18108358, 264689, 18108359, 21906765, 21906766, 21906767, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 18108368, 18108370, 18108374, 35696423, 35695855, 264635, 264556, 264557, 264639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56526486, 264482, 264564, 264486 22278998, 22278999, 22278999, 264907, 264909, 264910, 33657402, 264758, 264600, 264766, 264887, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 83373044, 264566 52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264768, 264689, 21906766, 21906769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264568
2365	94140746 (4729, 4730)	Novel Protein sim. GBank gll1840045 (U48082) - transporter protein [Homo sapiens]		transport	
2366	94312388 (4731, 4732)			UNCLASSIFIED	
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gll1065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35698286, 21906768, 55810764, 65274791, 264587 264628
2368	94322190 (4735, 4736)				

2369	94314334 (4737, 4738)	Novel Protein sim. GBank gij5360901[dbj BAA52158.1] - (AB029343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52644507, 52646842, 35696286, 264092, 264094, 52645080, 35698052, 264107, 29331830, 52644045, 265006, 265007, 265009, 52644298, 52644229, 264689, 21906765, 21906766, 35695917, 265020, 52644150, 263967, 33657109, 27486265, 35695763, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385
2370	79804120 (4739, 4740)			UNCLASSIFIED	264508, 264909, 264596
2371	57280406 (4741, 4742)				264369
2372	87642413 (4743, 4744)			UNCLASSIFIED	263967, 263981
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gij4589582[dbj BAA76813.1] - (AB023186) KIAA0989 protein [Homo sapiens]		UNCLASSIFIED	29331826, 285010, 285019, 35695917, 264634, 60432113
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gij5105131[dbj BAA80445.1] - (AP000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - 3' exoribonuclease family	UNCLASSIFIED	265006, 265007, 265008, 265009, 265011, 264766, 35695917, 35695855, 263981, 264557, 264565
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gij1351115[sp P47758 SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)]		UNCLASSIFIED	60432049, 29331824, 264807, 52644045, 264512, 60433356, 21908754, 52644298, 87168559, 264448, 21908765, 21908768, 21908769, 33657023, 18108368, 55811576, 52644332
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gij2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	ATPase_associated	264259, 29331830, 264909, 264910, 265009, 60433438, 21906754, 265017, 265018, 265019, 264682, 264288, 264685, 21906767, 263972, 35695855, 87168518, 60432113
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gij5257005[gb AAD41239.1] - (AF083248) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	18108394, 65274572, 22278997, 22278999, 264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 29331828, 33656970, 29146498, 29146489, 264509, 265006, 265007, 265008, 265009, 60170831, 265010, 265011, 265018, 55811150, 18108351, 264764, 264288, 21906767, 21906768, 29148627, 29148629, 265021, 33657023, 33657109, 18108370, 18108374, 18108379, 35696423, 264556, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gij1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 56714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21906765, 33657023, 264557, 56182323, 83373044, 18108385, 22279002, 264482
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gij3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - Kinase WD domain, G-beta repeat	Kinase	265017, 264288, 21906768



2380	86823062 (4759, 4760)	Novel Protein sim. GBank gi4502939[ref]NP_001845.1[pcol1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264810, 265011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gi4455609[emb]CAB36555] - (AL031846) dJ742C18.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHRomain Organization Modifier) domain	helicase	56182575, 264091, 264093, 264259, 29331825, 264105, 264906, 60433356, 21906754, 265017, 265018, 264683, 264288, 264685, 264686, 264887, 264891, 264892, 264693, 55811576, 264636, 264567
2382	81225982 (4763, 4764)	Novel Protein sim. GBank gi4325130[gb]AAD17276] - (AF119716) dmi-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	29331824, 60432228, 264905, 264598, 21906754, 264769, 265022, 264693, 263887, 33657109, 264629, 264631, 264558, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi1902882[dbj]BAA19005] - (D89049) lectin-like oxidized LDL receptor [Bos laurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	265009, 21906765, 21906768
2384	95354768 (4767, 4768)	Novel Protein sim. GBank gi2462851 (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	struct	264488, 52644507, 52645156, 52646365, 35698286, 22278999, 52645080, 29331824, 29331826, 35696052, 29331828, 264906, 264828, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644296, 265011, 265017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 285020, 52644150, 33657023, 264693, 65274620, 52645128, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486285, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2385	95419485 (4769, 4770)		UNCLASSIFIED		264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278996, 22278997, 22278998, 264259, 52645080, 29331822, 29331826, 35696052, 52644045, 285008, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22278002, 264563, 264565, 264567
2386	94742849 (4771, 4772)	Novel Protein sim. GBank gi492869[gb]AAD34110.1[AF151873] CGI-115 protein [Homo sapiens]		glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 29148498, 264112, 264511, 60170831, 60432228, 264595, 60433438, 87188474, 87188559, 264682, 21908765, 21906766, 21906767, 21906769, 29148829, 35695917, 265021, 264690, 33657109, 264828, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14957990 (4773, 4774)			UNCLASSIFIED	264634	
2388	11424604 (4775, 4776)			UNCLASSIFIED	264595	
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gij4758058[ref]NP_004372.1pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor		264488, 22278998, 22278999, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264511, 264512, 264910, 264591, 21908754, 264601, 264604, 264761, 18108351, 264764, 264288, 264766, 264768, 264769, 21906765, 21906768, 264692, 264693, 35696423, 264635, 264636, 264555, 83373044, 22279000, 264486	
2390	94320912 (4778, 4780)	Novel Protein sim. GBank gj1644239[dbj]BAA12223] - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	52644507, 56182575, 22278995, 35696286, 22278996, 22278997, 22278999, 28331822, 29331825, 29331826, 35696052, 264905, 52844045, 265009, 264758, 264759, 33109954, 52644296, 85658542, 265011, 265017, 265018, 264605, 52644229, 21906765, 21906787, 21906768, 21906769, 35695917, 52644150, 33657023, 33657109, 33657349, 35695763, 18108370, 18108374, 18108376, 35696423, 35695855, 264555, 52644332, 56182323, 60170394, 83373044, 56526486	
2391	80036194 (4781, 4782)			UNCLASSIFIED	263976	
2392	94245016 (4783, 4784)	Novel Protein sim. GBank gj4240169[dbj]BAA74863.1] - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	35696286, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 265009, 264591, 264758, 264800, 264604, 264762, 264448, 264764, 264369, 264766, 264768, 264769, 264689, 35695917, 264629, 18108374, 263978, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 60170394, 264639, 264565, 264486	

2393	95302633 (4785, 4786)	Novel Protein sim. GBank gi 4506667 ref NP_000993.1 pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00468) - Ribosomal protein L10	ribosomalprot	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 56994075, 35689286, 22278996, 22278997, 22278998, 264093, 60432049, 264259, 29331822, 29147620, 20281099, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35686052, 29146499, 264508, 264509, 264905, 264907, 264908, 66712502, 52844045, 264828, 264809, 56182435, 264112, 264113, 264510, 265006, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52646317, 33109954, 21906754, 55811386, 265010, 265011, 265017, 265018, 265019, 264881, 264762, 18108351, 264763, 264682, 264764, 264683, 264389, 264286, 18108354, 264766, 264688, 264687, 264688, 264689, 18108359, 21906765, 21906766, 21908787, 21906768, 21906769, 55811957, 29148629, 29148784, 35685917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108368, 27486261, 27486262, 33657349, 35685763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810764, 35686423, 35685855, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394, 35686286, 22278997, 22278998, 58182181, 35686052, 265006, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21906765, 21906768, 21906769, 55811957, 35685917, 33657023, 65274620, 33657182, 33657349, 35685763, 18108374, 18108376, 55810764, 55811576, 35686423, 60170394, 18108385, 264584, 264566, 264567
2394	94323266 (4787, 4788)	Novel Protein sim. GBank gi 4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q99876 (PID:g302533) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi 5712756 gb AAD47636.1 AF16079 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]		dna_ma_bind	264259, 29331824, 264910, 264288, 265021, 83373044, 18108387, 264563, 264568

2396	85086700 (4791, 4792)	Novel Protein sim. GBank g 106322 pir B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - nuclease Leucine Rich Repeat	52646355, 18108397, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264106, 264907, 29331830, 66712502, 264110, 60170831, 264591, 33657402, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264766, 52644229, 21906766, 21906767, 265020, 265021, 60170515, 264692, 33657023, 65274620, 52645129, 33657182, 27486262, 27486264, 27486265, 264629, 18108374, 35696423, 35695855, 264631, 264556, 52644332, 264558, 83373044, 18108388, 87168518, 22279002, 264482
2397	87280854 (4783, 4784)			52644507, 52645156, 56182575, 264259, 29147620, 264805, 264907, 264908, 264909, 264910, 264758, 52644296, 264803, 264804, 264762, 264681, 264764, 18108357, 264769, 21908768, 264693, 264628, 264635, 264638, 264639, 264564
2398	88047689 (4795, 4796)	Novel Protein sim. GBank g 3258609 (AC005178) - H53_GS1 [Homo sapiens]	UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank g 786117 (L41834) - nuclear protein [Ensis minor]	UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 60432289, 264906, 29331830, 56182435, 264112, 264910, 33109954, 21906754, 87168474, 264600, 265017, 265018, 265019, 264764, 264765, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265022, 60170615, 33657023, 18108370, 18108374, 264556, 60170394, 264558, 87168518, 22279000, 22279002, 264564, 264566, 264487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank g 2352822 gb AA669285.1 - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]	phosphatase	21908766, 52646842, 56994075, 33657182, 27486262, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gij2352822[gib AAB69285.1] - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	52644507, 52645156, 52644229, 264688, 21908784, 21908785, 52646385, 52646842, 21908786, 21908787, 21908788, 22278995, 35695917, 35694075, 35696286, 22278996, 22278997, 265020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 29331824, 33657109, 52645129, 29331826, 33657182, 29331827, 35696052, 27486281, 27486282, 33656870, 33657349, 27486285, 35695783, 264106, 264905, 35696423, 35695855, 265006, 265007, 265008, 265009, 264637, 52644332, 55812038, 52646317, 18108385, 52644286, 87168474, 265010, 87168559, 60432113, 265017, 265018, 265019, 264583, 264288, 264907, 264908, 264909, 264568
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gij4689258[gib AAD27832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]			
2403	84135432 (4805, 4806)	Novel Protein sim. GBank gij4928575[gib AAD34048.1 AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF000062) - C-type lysozyme/alpha-lactalbumin family		22278999, 35696052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gij2315796 (AF016685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	35695286, 29331826, 35696052, 265008, 265018, 21908769, 264564
2405	94311851 (4808, 4810)	Novel Protein sim. GBank gij464178[gib BAA03581] - (D14853) polyprotein [Hepatitis C virus]		UNCLASSIFIED	35696286, 29331822, 265007, 21908754, 265017, 265018, 265019, 264763, 264369, 21908765, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	98094501 (4811, 4812)	Novel Protein sim. GBank gij2773363 (AF041382) - microtubule binding protein D-CLP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	struct	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264106, 264906, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33108954, 265010, 265011, 265018, 265019, 264369, 264685, 264686, 21908768, 21908769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 58182323, 264639, 22279000, 22279002, 264583, 264685, 264686
2407	79465005 (4813, 4814)			UNCLASSIFIED	
2408	87391503 (4815, 4816)	Novel Protein sim. GBank gij423442[pil S33513 - gene Fil protein - mouse		UNCLASSIFIED	264910, 265010, 264448, 264557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gi1176601 sp P45966 YNZ6_CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T09A5.6 IN CHROMOSOME III		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29146498, 52644045, 60433438, 33657084, 87168474, 264760, 21906767, 29146627, 29146629, 52644150, 33657023, 263967, 20281069, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gi14966262 gb AAC48052.2  - (UB4849) Contains similarity to P1am domain: PF00646 (F- box), Score=28.7, E-value=4.3e-05, N=1  Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gi13114713 (AF051348) - Edp 1 protein [Mus musculus]	Inf		29331824, 29331827, 29331828, 264764, 264369, 33657109, 56182323
2412	87776332 (4823, 4824)	Novel Protein sim. GBank gi15410336 gb AAD43038.1  - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278998, 29331827, 264907, 264908, 264510, 265017, 265018, 265019, 18108351, 21906766, 265020, 33657109, 264559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank gi15262705 emb CAB45778.1  - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264488, 264259, 29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264682, 264764, 264766, 264686, 264768, 264689, 265021, 33657023 18108370, 264628, 35695855, 264632, 264634, 264635, 264636, 83373044, 264563, 264564, 264565, 264566, 264567, 264486, 52645156, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 264909, 60433356, 33657402, 264594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170615, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 18108370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52644332, 264638, 264558, 56182323, 83373044, 18108385, 87168518, 22279002
2414	94312590 (4827, 4828)	Novel Protein sim. GBank gi1082340 pir S52863 - DNA- binding protein R kappa B - human		ubiquitin	

2415	88088002 (4829, 4830)	Novel Protein sim. GBank gij423915 pir A45439 - myosin I heavy chain - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	264259, 264908, 60433356, 33657402, 21906754, 265018, 264687, 264689, 21906769, 55811957, 265021, 264690, 264691, 33657023, 264693, 35696423, 56182323, 56526486, 264636
2416	84118356 (4831, 4832)	Novel Protein sim. GBank gij3025445 (AC004528) - R321B4_1 [Homo sapiens]			
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gij1084944 pir S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins		264094, 29331822, 29331824, 29331827, 264369
2418	84234349 (4835, 4836)	Novel Protein sim. GBank gij1176572 sp P45895 YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 284091, 264259, 29331824, 29331825, 60432289, 29331828, 264805, 264907, 264511, 265009, 60432228, 21906754, 87168559, 265019, 264682, 21906768, 21906769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264568
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gij284006 pir S18732 - autoantigen, 64K - human		struct	264569, 264762, 264448, 264691, 264631, 264634, 264555, 264558, 264638, 264558
2420	8484244 (4839, 4840)	Novel Protein sim. GBank gij107621 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264564
2421	87805345 (4841, 4842)			UNCLASSIFIED	264909, 264768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gij2224567 dbj BAA20772  - (AB002311) KIAA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	transport	18108392, 18108394, 18108398, 264906, 265006, 265010, 18108351, 18108374, 18108385
2423	88058380 (4845, 4846)	Novel Protein sim. GBank gij4505153 ref NP_002392.1 pMEKK - MAP/ERK kinase kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 60432049, 29331822, 29331826, 60432289, 29331828, 265008, 265008, 60433356, 21906754, 265017, 265018, 265019, 21906766, 21906768, 21906769, 265020, 265021, 20281148, 263971, 60432113
2424	84854047 (4847, 4848)	Novel Protein sim. GBank gij2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35686286, 22278997, 60432049, 264259, 29331826, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265019, 264766, 21906768, 55811957, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22279000, 264634
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gij2077932 dbj BAA19879  - (D86556) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	
2426	87813945 (4851, 4852)	Novel Protein sim. GBank gij2039368 gb AA853003.1  - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278996, 22278998, 264259, 264102, 264512, 265008, 21906767, 18108370, 18108374, 263976

2427	87022693 (4853, 4854)	Novel Protein sim. GBank gij4680695[gib]/AAD27737.1[AF13296] CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	264259, 20281099, 35696052, 265008, 264594, 265011, 264760, 18108351, 264682, 264683, 264369, 264684, 264686, 264687, 264689, 21908766, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gij1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		22278998, 22278999, 35696052, 21908754, 264288, 21908765, 21908768, 21908769, 35695917, 265020, 263972, 22278002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gij601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	UNCLASSIFIED Beta defensins	22278999, 29331824, 264906, 264909, 264511, 265009, 21908754, 265017, 265018, 265019, 264448, 264683, 264288, 21908765, 21908768, 265021, 264693, 18108381
2430	86948827 (4859, 4860)		UNCLASSIFIED	264112, 264691
2431	87849884 (4861, 4862)	Novel Protein sim. GBank gij3860729[emb]CAA14630] - (AJ235270) CELL DIVISION PROTEIN FTSJ (ftsJ) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein	29331826, 29331827, 35696052, 29146499, 264905, 264908, 264681, 264288, 264689, 21908765, 264692, 35696423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gij3876367[emb]CAA93287] - (Z69360) Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]	protease	264634, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gij2224593[dbj]BAA20784] - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264569, 264905, 265018, 264762, 264683, 264691, 264558, 264557, 264639, 264558 264563
2434	19520148 (4867, 4868)		UNCLASSIFIED	264555
2435	20759044 (4869, 4870)		UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2436	88044008 (4871, 4872)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		29331828, 265007, 265009, 265017, 264760, 264685, 264693, 264565
2437	83363424 (4873, 4874)	Novel Protein sim. GBank gij3641352 (AF091234) - putative transcription factor [Mus musculus]	UNCLASSIFIED	29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 265009, 264591, 33657402, 21906754, 265011, 264760, 264764, 264685, 264686, 264768, 35695917, 33657023, 264693, 264631, 264632, 56182323, 264558, 83373044, 264563, 264564, 264565, 264566, 284567
2438	94143473 (4875, 4876)	Novel Protein sim. GBank gij3860014 (AF091088) - unknown [Homo sapiens]	UNCLASSIFIED Uncharacterized protein family UPF0031	



2439	84850650 (4877, 4878)	Novel Protein sim. GBank gi 4263519 gb AAD15345  - (AC004044) small nuclear riboprotein Sm-D1 (Arabidopsis thaliana)	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108387, 56182575, 56181686, 56994075, 22278998, 35698286, 22278997, 22278999, 264259, 52845080, 29331822, 56182181, 29331824, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35698032, 28148498, 264509, 264905, 264908, 52844045, 60431735, 33109954, 21806754, 33857084, 55811386, 52844296, 87188474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52844229, 56181562, 21806764, 21806765, 21806766, 21806767, 21806768, 21806769, 35695917, 33857023, 33857109, 33857182, 27486262, 27486264, 33657349, 27486285, 35695763, 18108370, 60431528, 263977, 55810764, 35698423, 65274791, 35695855, 60431850, 56182323, 60432113, 22278900, 22279002, 264567
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 284508, 264907, 264510, 285018, 265019, 264448, 264369, 265020, 265021, 58182323, 264539, 222789002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gi 3024889 sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIA0288 (HA6116)		UNCLASSIFIED	264488, 264629, 18108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gi 4506013 ref NP_002703.1 pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278996, 22278999, 29331822, 264768, 264693
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gi 1170658 sp Q02875 KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - KRAB box	transcription factor	264806
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gi 4758824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	264259, 18108382, 18108383, 18108385, 22278900
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gi 2135950 pir J58222 - PQ-rich protein - human			264259, 35696052, 264369, 18108361
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gi 4753887 emb CAA05409.2  - (A-J002424) p65 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhib	265011, 264689, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gi 4885613 ref NP_005409.1 pST5 - suppression of tumorigenicity 5		cadherin	56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 265018, 264692, 65274820, 60431528, 65274791, 56182323

2448	87749680 (4895, 4896)			UNCLASSIFIED	22278996, 22278997, 22278999, 29331826, 35698052, 264107, 264110, 87168474, 87168559, 18108351, 21906767, 21906768, 27486282, 263976
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		cadherin	264259, 264828, 265007, 264595, 265021, 56526486
2450	86597784 (4899, 4900)	Novel Protein sim. GBank		UNCLASSIFIED	264906
2451	91014563 (4901, 4902)	gi 1710021 sp P35290 RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) Ras family	glycoprotein	264093, 29331822, 29331824, 29331825, 66714117, 29331826, 29331828, 35698052, 264907, 66712502, 29331830, 264910, 265009, 264758, 265017, 265018, 264762, 264448, 264288, 21906767, 265021, 33657023, 264693, 33657109, 263969, 83373044, 18108385
2452	91230509 (4903, 4904)	Novel Protein sim. GBank gi 1504034 dbj BAA13216  - (D86980) KIAA0227 [Homo sapiens]		isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264563
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID.g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	ngf/recep	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gi 1076802 pir I549915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263994, 66714117, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264686, 264768, 264769, 264534, 264691, 264692, 33657023, 264693, 33657109, 264628, 263978, 35695855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264583, 264584, 264486
2455	95288301 (4909, 4910)	Novel Protein sim. GBank gi 543817 sp P35585 AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264488, 22278996, 264259, 35698052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264689, 21906766, 21906767, 21906769, 29148629, 35695917, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264566, 264567
2456	88166700 (4911, 4912)	Novel Protein sim. GBank gi 2588630 (AC003079) - Ankyrin- like; 54% similar to 2022340A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	84118375 (4913, 4914)	Novel Protein sim. GBank gij3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	55181686, 264805, 264807, 264511, 264596, 55811388, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 56526488, 264563
2458	85875304 (4915, 4916)	Novel Protein sim. GBank gij2384942 (AF022985) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264691, 264693, 264634, 264559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gij5441942 [gb]AAD43187.1 [AC004997] supported by mouse EST AAS38043 (NID:g2284036) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gij4929701 [gb]AAD34111.1 [AF15187] - (AF151874) CGI-116 protein [Homo sapiens]		kinase	65274572, 35698286, 22278996, 22278997, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35658970, 29146489, 264102, 264109, 60433438, 265017, 285018, 285019, 264288, 21806765, 21806766, 21806769, 35695917, 285020, 284691, 33657023, 27486261, 18108374, 35695855, 87168518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gij4426962 [gb]AAD20633] - (AF126062) Art-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 264910, 18108351, 18108370, 18108374
2462	86998002 (4923, 4924)	Novel Protein sim. GBank gij5420387 [emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			264809, 264758, 264684, 18108374, 264637, 18108385
2463	84388543 (4925, 4926)	Novel Protein sim. GBank gij5052516 [gb]AAD38588.1 [AF14561] - (AF145613) BcDNA.GH03108 [Drosophila melanogaster]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264566
2464	91218957 (4927, 4928)	Novel Protein sim. GBank gij5410300 [gb]AAD43021.1] - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01398) - PCI domain	protease	264489, 52646842, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52646317, 33109954, 33657084, 265017, 265018, 265019, 264762, 264448, 264764, 264288, 264766, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22279002, 264486

2465	85357483 (4929, 4930)	Novel Protein sim. GBank gi 4506401 ref NP_002871.1 pRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - oncogene Eukaryotic protein kinase domain	18108392, 52644507, 52645156, 52646365, 22278994, 22278995, 3569288, 22278996, 22278998, 264259, 29331822, 29331824, 29331825, 60424269, 60432289, 29331827, 35696052, 29331828, 264907, 29331830, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264910, 33657402, 60433438, 55812038, 21906754, 33108954, 265010, 265011, 87168559, 264600, 285017, 265018, 265019, 18108351, 264369, 264288, 264685, 264767, 21908765, 21906767, 21808768, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 52645129, 33657109, 27486261, 27486264, 35695763, 264628, 263972, 18108374, 35695855, 264636, 264637, 60170394, 56526488, 87168518, 60432113, 264563, 264564, 264566, 264487 264369
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gi 4321619 gb AAD15788.1  - (AF051098) seven transmembrane domain orphan receptor (Mus musculus)		
2467	88059465 (4933, 4934)	Novel Protein sim. GBank gi 3513300 (AC005595) - F16601.1, partial CDS [Homo sapiens]	UNCLASSIFIED	56994075, 264908, 21906768, 33657023
2468	87614696 (4935, 4936)	Novel Protein sim. GBank gi 2143455 pir j158106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	29331824, 52644045, 265008, 264910, 265019, 21906765, 21906789, 265021 264288, 264628
2469	86294397 (4937, 4938)	Novel Protein sim. GBank gi 5470389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264592, 264692, 264555, 264556, 264557, 264558, 264559, 18108385, 264482
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gi 5419882 emb CAB46424.1  - (AL096749).DKFZp434G153 [Homo sapiens]	UNCLASSIFIED	65274572, 35696286, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 56182323
2472	85060811 (4943, 4944)	Novel Protein sim. GBank gi 4929747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]	UNCLASSIFIED	284092, 60432049, 29331825, 60433356, 265010, 265011, 18108351, 264784, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gi 4539009 emb CAB39630.1  - (AL049481) putative protein [Arabidopsis thaliana]		60424179, 65274572, 22278999, 60424269, 29331826, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi 3252827 (AC004382) - Unknown gene product [Homo sapiens]		65274572, 56994075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 264369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gij1216488 (U48852) - HT protein [Cricetulus griseus]	Contains protein domain (PF000008) - Igl EGF-like domain	284259, 29331822, 265006, 265007, 265010, 265011, 264448, 264288, 264369, 264885, 264866, 18108337, 264768, 18108362, 264693, 18108370, 18108374, 18108379, 35698423, 83373044, 18108383, 18108385, 264564, 264565, 264567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gij3252827 (AC004382) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	264259, 60424268, 66714117, 264905, 265006, 264511, 265008, 265009, 264758, 265010, 265011, 18108351, 264681, 264369, 264288, 264889, 21908767, 265020, 18108374, 264638, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)		UNCLASSIFIED	283978
2478	17659163 (4955, 4956)		UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gij1644232[dbj]BAA11082[ - (D67066) N-WASP [Bos taurus]	im7	56994075, 22278998, 21906754, 264682, 21906765
2480	95295605 (4959, 4960)		UNCLASSIFIED	264905, 264907, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gij5689469[dbj]BAA83018.1[ - (AB028989) KIAA1066 protein [Homo sapiens]	collagen	65274572, 56182575, 22278997, 264094, 264259, 29331822, 29331824, 66714117, 29331827, 35696032, 264508, 264905, 264906, 264907, 264908, 264908, 52644045, 264909, 56182435, 265008, 264910, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264764, 264288, 264766, 264886, 264768, 21906768, 55811957, 265020, 264691, 264692, 264693, 264629, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22278002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gij321249[pip]S28407 - guanine nucleotide-exchange activator CDC25 homolog - mouse	UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264768, 264693, 264631, 264632, 264636, 264638, 264639, 264563
2483	87731583 (4965, 4966)		UNCLASSIFIED	264488, 22278995, 264083, 264095, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_HUMAN - III] ALU SUBFAMILY J WARNING ENTRY IIII	kinase	264563
2485	87766556 (4969, 4970)	Novel Protein sim. GBank gij1165397 (U25281) - SH3 domain binding protein [Rattus norvegicus]	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265019, 264448, 264288, 264685, 264686, 264769, 264689, 35695917, 265022, 264692, 264693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gi 2662167 dbj BAZ3715  - (AB007903) KIAA0443 [Homo sapiens]			265017, 264555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi 464559 sp P35287 RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331822, 35696052, 264106, 264905, 264907, 29331830, 264909, 265006, 264511, 265008, 265009, 60433438, 21906754, 33109954, 87168559, 265018, 264681, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 18108377, 35696423, 35695855, 60170394, 18108385, 56526486, 22278000, 22279002, 264563, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	264910, 264448, 264288, 264694, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gi 4886439 emb CAB43355.1  - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	284686, 264693, 55811576, 22279002
2490	88069609 (4979, 4980)	Novel Protein sim. GBank gi 2586624 (AC003083) - Rap2 interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	264907, 265008, 22279002
2491	91242116 (4981, 4982)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - III! ALU SUBFAMILY SB WARNING ENTRY III!		Im7	264259, 29331826, 265008, 264762, 18108370, 18108376, 18108379
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gi 3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21906764, 21906768, 264692, 60431528, 87168518, 60432113, 22279000

2493	95422415 (4985, 4988)	Novel Protein sim. GBank gi 4240307 dbj BAA74932.1  - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - struct R3H domain	18108394, 264887, 65274572, 56182575, 22278995, 56994075, 60432049, 29331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264905, 264508, 264906, 264907, 29331830, 264909, 264510, 265008, 264511, 265007, 264512, 265008, 265009, 264910, 21906754, 265011, 264600, 265017, 265018, 264604, 264605, 265019, 55811150, 264762, 18108351, 264681, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 264692, 33657023, 33657349, 18108370, 18108374, 18108376, 55810764, 18108379, 65274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22278000, 22279002, 264482, 264588, 264488
2494	30783118 (4987, 4988)			264907, 264601
2495	94234551 (4989, 4990)	Novel Protein sim. GBank gi 5420389 emb CAB46660.1  - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED collagen
2496	80018765 (4991, 4992)	Novel Protein sim. GBank gi 4808220 emb CAB42832.1  - (AL022315) dJ117715.1 (PUTATIVE novel protein) [Homo sapiens]		263994, 22278997, 35696052, 264509, 264905, 264908, 264907, 264808, 264909, 265008, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264768, 264769, 264689, 265020, 264692, 65274620, 264629, 55810764, 35696423, 55811576, 264636, 264637, 18108385, 22278000, 264564, 264567, 264486
2497	91723554 (4993, 4994)			28147620, 264805, 265006, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264558, 18108381, 18108383, 18108388
2498	87724633 (4995, 4996)	Novel Protein sim. GBank gi 1200503 (U47924) - B [Homo sapiens]		UNCLASSIFIED
2499	94685125 (4997, 4998)	Novel Protein sim. GBank gi 3510234 (AC005581) - R31237.1, partial CDS [Homo sapiens]		52644507, 22278996, 22278999, 29331824, 29331828, 33657402, 21906754, 87168474, 265019, 264369, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 33657023, 18108376, 18108387
				29331827, 264512, 264910, 264286, 18108374, 35695855
			Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	264909, 55812038, 264631, 264637, 264558

2500	94648324 (4989, 5000)	Novel Protein sim. GBank gj3881275[emb]CAA21725] - (AL032655) predicted using GeneFinder, similar to Inositol monophosphatase family, cDNA EST yk255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52845507, 52845158, 22278995, 56994075, 35698286, 22278998, 264259, 52845080, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52644286, 87168474, 87168559, 264603, 264681, 264448, 264683, 264288, 264369, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 33657182, 35695763, 35696423, 35695855, 52644332, 83373044, 18108387, 87168518, 22278002
2501	94303896 (5001, 5002)	Novel Protein sim. GBank gj14929615[g]AAD34088.1[AF15183] - (AF151831) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	65274572, 56182575, 35696286, 22278996, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264591, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 264598, 87168474, 87168559, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 284369, 264288, 264766, 18108357, 21908765, 21908766, 21908767, 21908768, 29148629, 35695917, 264692, 33657023, 264629, 35696423, 55811576, 35695855, 264630, 264834, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 60432113, 22278002, 264566
2502	90993716 (5003, 5004)	Novel Protein sim. GBank gj3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308) [Homo sapiens]	Contains protein domain (PF01237) - Oxysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 284369, 264288, 264684, 264686, 55811957, 265021, 264692, 33657109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gj2196874[emb]CAA72638] - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385



2504	87668708 (5007, 5008)	Novel Protein sim. GBank gij550420[embjCAA48220] - (X68101) trg [Rattus norvegicus]			264488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264908, 264908, 52644045, 265009, 60433356, 33657402, 60433438, 264585, 33109854, 87168474, 285017, 265019, 264448, 264288, 264768, 52644229, 21908765, 21906766, 21906767, 21906768, 52644150, 264892, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108387, 87168518, 60432113, 22279002, 264584, 264605
2505	8760559 (5009, 5010)			UNCLASSIFIED	
2506	91232326 (5011, 5012)	Novel Protein sim. GBank gij2137562[pirjI49635] - mouse Dhm1 protein - mouse		nuclease	264488, 52644507, 52645156, 52646365, 65274572, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264258, 60432049, 29331822, 29331825, 29331826, 29331828, 264509, 56182435, 264112, 264593, 60433356, 55812038, 21906754, 265011, 265017, 265018, 265019, 284605, 264762, 18108351, 264448, 264288, 264768, 21908765, 21906766, 21906767, 21906768, 21908769, 35695917, 265020, 265021, 265022, 60170615, 33657023, 27486264, 18108379, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264565
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gij5174489[refINP_006035.1]pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - histone deacetylase family		264488, 263994, 264592, 264595, 264369, 264686, 264768, 35695917, 35696423, 264563
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gij4826433[embjCAB42889.1] - (AL031447) dJ126A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 60432049, 264259, 29331828, 265006, 265007, 60433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21908765, 21906769, 55811957, 265020, 265022, 27486261, 33657349, 18108377, 35695855, 60432113, 22279002, 264563, 264585
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264556, 264567

2510	95421379 (5019, 5020)	Novel Protein sim. GBank gjl3293537igb/AAC25762.1] - (AF071059) zinc finger RNA binding protein [Mus musculus]		dna_ma_bind	65274572, 22278994, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 33656970, 264908, 66712502, 265007, 264910, 60170831, 60432229, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 264681, 33657023, 264683, 65274620, 33657109, 33657182, 27486282, 33657349, 18108370, 35695855, 264555, 58182323, 83373044, 60432113, 22279002, 265017, 21906764, 265020, 264692
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gjl4323152igb/AAD16228.1] - (AF098863) Ets-protein Spl-C [Mus musculus]			
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gjl4502075jeflNP_001135.1pAMFR - autocrine motility factor receptor	Contains protein domain (PF000087) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 264259, 29331825, 29331826, 29146499, 264907, 264909, 265008, 265008, 264591, 60432229, 21906754, 264763, 264683, 264766, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gjl3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED	60424179, 52845156, 18108394, 22278994, 35699286, 56994075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264369, 56181562, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108366, 33657109, 27486261, 27486282, 33657349, 18108374, 55810764, 35696423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gjl2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87994509 (5029, 5030)	Novel Protein sim. GBank gjl3757727jemb/CAA18783] - (AL022727) dJ80119.7 (olfactory receptor-like protein (hs6M1-3)) [Homo sapiens]	Contains protein domain (PF000001) - 7 transmembrane receptor (rhodopsin family)	Im7	
2516	87786908 (5031, 5032)			UNCLASSIFIED	264259, 29146498, 264905, 264288, 29148629, 35695917, 27486261, 264634
2517	87784966 (5033, 5034)	Novel Protein sim. GBank gjl4220527jemb/CAA23000] - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5036)	Novel Protein sim. GBank gi4928591 gb AAD34058.1 AF15181 - (AF15181) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 284907, 284909, 284511, 265007, 60432228, 60433358, 60433438, 55812038, 285010, 285017, 284448, 284288, 284889, 21906768, 21906769, 265022, 52644150, 264693, 18108370, 263972, 284555, 56182323, 83373044, 18108385, 60432113, 264088
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gi4283748 gb AAD15420  - (AC004883) similar to KIAA0766; similar to PID:g3882253 [Homo sapiens]		kinase	264259, 66714117, 29331828, 29331827, 29331828, 284907, 66712502, 265008, 265008, 264594, 265010, 265011, 265018, 264288, 21906768, 265020, 60431528, 55811578, 65274791, 264632, 284555, 284638, 22279002, 264584
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gi4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4		transport	264259, 264908, 264910, 264682, 21906769, 265020, 264563
2521	85316244 (5041, 5042)	Novel Protein sim. GBank gi5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 264489, 263984, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 264907, 66712502, 284511, 265008, 285007, 264591, 284592, 264593, 264594, 284595, 284596, 264681, 284448, 264763, 284682, 264764, 264684, 264369, 284288, 264685, 264686, 21906768, 55811957, 264682, 264693, 27486281, 18108370, 284628, 264629, 18108374, 55811578, 35696423, 35695855, 284632, 264558, 18108385, 65274727, 60432113, 264583, 284564, 264585, 284566, 284587
2522	87754032 (5043, 5044)	Novel Protein sim. GBank gi4580011 gb AAD24201.1 U81002 - (U81002) TRAF4 associated factor 1 [Homo sapiens]		transport	264489, 22278997, 20281171, 21906754, 35695917, 263987, 263978, 263981, 20281169
2523	95340467 (5045, 5046)				263969
2524	85340469 (5047, 5048)	Novel Protein sim. GBank gi1809327 (U76374) - skm- BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87168559, 265019, 284288, 21906765, 21906769, 35695917, 265020, 265021, 265022, 52644150, 284691, 33657023, 33657109, 27486281, 35696423, 65274791, 264559, 83373044, 56528486, 87168518, 284587

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gi 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]			kinase	264488, 22278997, 22278999, 60432049, 60432289, 29331828, 264905, 265008, 55812038, 21906754, 265019, 264369, 21908765, 21906766, 21908767, 21908769, 35695917, 265020, 265021, 33657109, 60431528, 83373044, 60432113, 22279000, 22279002, 264565
2526	95289404 (5051, 5052)	Novel Protein sim. GBank gi 4589628 dbj BAA76836.1  - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14		ribosomal prot	60424179, 264768, 264687, 264769, 264689, 65274572, 21906767, 56182575, 21906768, 21908769, 55811957, 22278994, 22278995, 35695917, 265020, 265021, 22278999, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264690, 264691, 60432049, 264259, 264097, 33657023, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 27486262, 264508, 264509, 264905, 264907, 18108370, 66712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810764, 55811576, 35696423, 35695855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52646317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526488, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264564, 18108351, 264448, 264586, 264288, 264488, 264587, 264766, 264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354
2527	88084580 (5053, 5054)	Novel Protein sim. GBank gi 2258437 (AF008197) - syncollin [Rattus norvegicus]			UNCLASSIFIED	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gi 2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:gi399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain		dna_rna_bind	
2529	86670926 (5057, 5058)	Novel Protein sim. GBank gi 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:008891) [Caenorhabditis elegans]			synthase	
2530	80259878 (5059, 5060)					264369, 264556
2531	87768931 (5061, 5062)				UNCLASSIFIED	29331822, 29331824, 60432289, 264508, 264509, 264906, 265011, 264769, 21908768, 33657023, 87168518, 22279000
2532	87419778 (5063, 5064)	Novel Protein sim. GBank gi 2864625 emb CAA16972  - (AL021811) putative protein [Arabidopsis thaliana]				264593
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gi 437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]			UNCLASSIFIED	264555

2534	87332322 (5067, 5068)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35698052, 264905, 265017, 21906769, 265020, 265022, 33657109, 22279000
2535	81225056 (5069, 5070)	Novel Protein sim. GBank gi 4468311 (emb CAB37992) - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35698286, 60432289, 29331828, 66712502, 265008, 60432229, 265017, 265018, 265019, 264288, 264389, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	kinase		18108398, 56182575, 35698286, 22278997, 22278999, 60432049, 264259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264789, 264689, 21906765, 21906768, 21906787, 265021, 52645128, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22278900, 22279002, 264587, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gi 4557026 ref NP_003913.1 pHERC - guanine nucleotide exchange factor p532	ubiquitin		65274572, 35698286, 29331822, 29331825, 29331827, 29331828, 35698052, 264908, 66712502, 264909, 265008, 265011, 264780, 264288, 264685, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 18108374, 35698423, 35695855, 264636, 264558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5078)			UNCLASSIFIED	
2539	94144918 (5077, 5078)			UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 29146499, 264908, 264112, 60170831, 87168559, 264604, 265019, 264685, 264768, 87168518, 22278900, 264565, 264566
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gi 1362647 pir J53876 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gi 1711658 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264768

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gij5225320igb AAD40850.1 AF083107  siruin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophysial hormones, N- terminal Domain	UNCLASSIFIED	264488, 18108394, 52646365, 52646842, 65274572, 22278994, 35986286, 22278996, 264259, 52645080, 29331822, 29331824, 29331827, 35696052, 33656970, 264907, 264909, 52644045, 264510, 265006, 264512, 265007, 265008, 265009, 264910, 60431735, 52646317, 52644296, 265010, 265011, 265018, 265019, 18108351, 264683, 264288, 264685, 264687, 52644229, 264769, 21906766, 21906767, 21906769, 52644150, 33657023, 33657109, 52645129, 33657182, 27486261, 27486264, 33657349, 35695763, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264558, 83373044, 18108385, 18108387, 87168518, 264563, 264564
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gij5419857 emb CAB46374.1  - (AL096723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)		65274572, 56182575, 22278999, 264259, 29331826, 264907, 264510, 264511, 264592, 264595, 264764, 264369, 264288, 264684, 264766, 264689, 21906765, 21906767, 21906769, 60170615, 264692, 264693, 55811576, 65274791, 264636, 264556, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218549 (5087, 5088)	Novel Protein sim. GBank gij2498110 sp Q83191 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52646365, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 264448, 264686, 264687, 264689, 21906765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526486, 22279000, 264482, 264563, 264567
2545	87742845 (5089, 5090)	Novel Protein sim. GBank gij3327046 dbj BAA31591  - (AB014516) KIAA0616 protein [Homo sapiens]			29331825, 264906, 265009, 60170831, 265017, 264369, 21906767, 60170815, 264692, 33657109
2546	88093861 (5091, 5092)	Novel Protein sim. GBank gij2996032 (AF054566) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	94143869 (5093, 5094)	Novel Protein sim. GBank gi 4928607 gb AAD34064.1 AF15182 - (AF15182) CGI-69 protein (Homo sapiens)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264488, 18108394, 52646842, 18108397, 58182575, 22278995, 56984075, 22278998, 22278999, 264259, 29331822, 29331824, 29331828, 60432289, 29331827, 35696052, 29331828, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432228, 60431735, 264594, 80433438, 21908754, 52648317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21906765, 21906768, 21908767, 21906768, 29148627, 21908769, 55811957, 265020, 265021, 265022, 264690, 264691, 18108382, 264692, 264693, 27488261, 18108370, 18108374, 55810764, 55811576, 35698423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108360, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87188518, 22279002, 264584, 264568, 264486
2548	88179079 (5085, 5086)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35696286, 56984075, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87188559, 264684, 264369, 52644229, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22279000, 22279002, 264563, 264567
2549	94196883 (5097, 5098)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00412) - LIM domain containing proteins	struct	56182575, 22278998, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21906764, 21906765, 21906766, 21906767, 21906769, 265020, 265021, 52644150, 264691, 18108368, 60431602, 18108376, 35698423, 56182323, 18108387, 264567, 56182575, 29331822, 264105, 264512, 18108351, 35695817, 264637, 264638
2550	87778584 (5099, 5100)	Novel Protein sim. GBank gi 2143886 pir j152323 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gl 4337103 gb AAD18079  - (AF129756) NG26 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 265018, 264605, 265019, 264288, 21906766, 21906768, 21906769, 265020, 60170615, 264693, 33657109, 35696423, 264638, 56182323, 83373044, 22279000
2552	95332620 (5103, 5104)			UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 35696052, 29331828, 264508, 264907, 56182435, 265008, 264591, 33109954, 264760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811576, 35696423, 35695855, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gl 1711658 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DSCR REGION		UNCLASSIFIED	264866, 264488, 263976, 264768, 29331826, 35696052, 35696423, 264601, 264511, 264602, 264910, 264634, 264760, 264555, 264762, 264906, 264592, 264691, 264566, 264908, 264684, 264567, 264909, 264768
2554	87761620 (5107, 5108)	Novel Protein sim. GBank gl 728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII		cadherin	22278997, 29331822, 264508, 21906769, 33657023, 33657109, 56182323
2555	87627651 (5109, 5110)	Novel Protein sim. GBank gl 4884319 emb CAB43260.1  - (AL050084) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gl 4106984 (AC003038) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695855, 264558, 264567, 264595
2557	78437803 (5113, 5114)	Novel Protein sim. GBank gl 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264906, 264511, 265018, 264448
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gl 4539998 emb CAB39619.1  - (AL049481) AIG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 264288, 264765, 264766, 264769, 21906765, 21906766, 60432113, 264482
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gl 5051399 emb CAB44995.1  - (AL078630) 573K1.3 (nm17M1-4) (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE) protein)) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gl 5326825 gb AAD42056.1 AF044953 - (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]		UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432229, 87168559, 265017, 265018, 265019, 264689, 21906766, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264559, 18108385, 87168518, 22279002



2562	87645539 (5123, 5124)	Novel Protein sim. GBank gl 4106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	5694075, 22278986, 22278987, 22278988, 264259, 29331822, 60432289, 33657402, 60433356, 21908765, 55811957, 60170615, 33657023, 264693, 35695855, 87168518, 264488, 35696286, 22278989, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21908767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486
2563	88085497 (5125, 5126)	Novel Protein sim. GBank gl 4886447 [emb CAB43371.1] - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21908767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486
2564	80502763 (5127, 5128)	Novel Protein sim. GBank gl 1352844 [sp P47179] YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR		sulfotransferase	29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2565	85530906 (5129, 5130)			UNCLASSIFIED	68714117, 264909, 283978, 264632
2566	80224958 (5131, 5132)	Novel Protein sim. GBank gl 628012 [pir JAS3933 - myosin I myr 4 - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	UNCLASSIFIED - struct	18108370, 35695855, 264556, 264558, 18108383
2567	86143590 (5133, 5134)				265020, 60170615
2568	91233099 (5135, 5136)	Novel Protein sim. GBank gl 468009 [sp P34548] YNJ4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	60424179, 16108394, 56181686, 56984075, 22278989, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21908766, 21908767, 35695917, 265021, 33657023, 18108382, 33657109, 33657182, 35695763, 60431528, 55810764, 18108379, 83373044, 18108385, 60432113, 264482

2568	95313764 (5137, 5138)	Novel Protein sim. GBank gij2595560 gb AAB84166.1  - (AF029874) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - Transcription factor bZIP transcription factor	18108394, 56182575, 56181586, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264906, 56182435, 265008, 265009, 264910, 60432229, 284592, 60433356, 60433438, 21908754, 87168559, 265017, 265018, 265019, 264682, 264448, 264288, 21908765, 21908766, 21908767, 21908768, 29148627, 21908769, 35695917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263967, 35695763, 20281069, 263974, 18108374, 55810764, 35696423, 35695855, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264556
2570	84136754 (5139, 5140)	Novel Protein sim. GBank gij4758954 ref NP_004567.1 pPPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	22278998, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35696052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264686, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35695855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gij732218 sp P34609 YO60_CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III	struct	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim. GBank gij4884319 emb CAB43260.1  - (AL050084) hypothetical protein [Homo sapiens]	UNCLASSIFIED	35696286, 29331827, 35696052, 264100, 264104, 264110, 264592, 21906754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35695855, 60170394, 264559, 18108385

2573	95313928 (5145, 5146)	Novel Protein sim. GBank gi 399138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - complement C1q domain	264488, 60424179, 65274572, 56182575, 56181698, 22278995, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432229, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 58181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 265020, 265021, 265022, 60170615, 264690, 52644150, 264691, 264692, 33657023, 85274620, 18108365, 18108368, 27486265, 60431602, 264629, 60431528, 263978, 85274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 58182323, 60170394, 83373044, 18108384, 87168518, 60432113, 264482, 264564, 264585, 264566, 264567, 22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 265008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21906765, 21906766, 21906768, 55811957, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 83373044, 18108385, 264482
2574	94746814 (5147, 5148)	Novel Protein sim. GBank gi 3334982 (AC005306) - R27218_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi 4680681 gb AAD27730.1 AF13295 - (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi 4337103 gb AAD18079 - (AF129756) NG25 [Homo sapiens]		UNCLASSIFIED
2578	87786941 (5155, 5156)			UNCLASSIFIED
2579	87202879 (5157, 5158)			UNCLASSIFIED

2580	88166788 (5159, 5160)	Novel Protein sim. GBank gij2588628 (AC003080) - Similar to KIAA0299; 60% similarity to AB002297 (PID:g2224539) [Homo sapiens]			265007, 265018, 264762
2581	87899048 (5181, 5182)	Novel Protein sim. GBank gij4406642(gb)AAD20048] - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00595) - POZ domain (Also known as DHR or GLGF).	collagen	56994075, 29331824, 29331826, 29331828, 264905, 60433356, 60433438, 264758, 87188559, 21906769, 265022, 35695855, 263981
2582	87786789 (5183, 5184)	Novel Protein sim. GBank gij2739367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph	264488, 264907, 264908, 264910, 264764, 264684, 264766, 264638, 264555, 264565
2583	91220950 (5165, 5166)	Novel Protein sim. GBank gij4378112(emb)CAA16521.1] - (AL021578) dJ453C12.2 (similar to transcription factor RBP-L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcription factor	56181686, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430941 (5167, 5168)			UNCLASSIFIED	264908, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436128 (5169, 5170)	Novel Protein sim. GBank gij2736151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase	264768
2586	91226136 (5171, 5172)				22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264908, 265007, 265009, 264591, 60433356, 33657402, 265018, 264762, 264288, 21906766, 21906767, 21906769, 265022, 264691, 83373044, 56526486, 22278002
2587	80430943 (5173, 5174)				264908, 265019, 264768, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)			UNCLASSIFIED	264564
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gij3021598(emb)CAA71415] - (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264769, 35696423, 264636
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gij2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucoamylase	22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank gij5702202(gb)AAD47199.1]AF12916 - (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph	264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	185332648 (5183, 5184)	Novel Protein sim. GBank gi 3024998 sp Q60936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331828, 60432289, 29331827, 29331828, 264906, 264909, 265007, 265008, 264910, 60432229, 264594, 60433356, 60433438, 55812038, 18108348, 21908754, 265011, 87168559, 265017, 265019, 264764, 264369, 264288, 264766, 265021, 60170815, 33657023, 33657109, 264629, 35696423, 35695855, 264557, 264638, 60170394, 56182323, 83373044, 56526486, 87168518, 264563, 264482, 264565
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]		Im7	22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 264389, 21908768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi 4929587 gb AAD34054.1 AF15181 - (AF15181) CGI-59 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108398, 56182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264905, 264909, 52644045, 56182435, 264510, 264512, 285007, 264757, 21908754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21908768, 33657109, 263975, 263977, 264634, 264558, 60170394, 56182323, 56526486, 264482, 264563, 264564, 264566, 264567, 264692
2595	79581676 (5189, 5190)	Novel Protein sim. GBank gi 4309681 gb AAD15476  - [AC006930] R33423_1 [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 265018, 264448, 265021, 60431528
2596	87538637 (5191, 5192)			UNCLASSIFIED	264905, 264509, 264908, 264762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264488
2597	94784089 (5193, 5194)			UNCLASSIFIED	22278998, 264259, 29331824, 87168474, 264683, 21908766, 35695917, 264691, 33657023, 33657109, 18108370, 18108374, 264564, 264585
2598	88094948 (5195, 5196)	Novel Protein sim. GBank gi 1001351 dbj BAA10838  - (D64006) hypothetical protein [Synchocystis sp.]		UNCLASSIFIED	264766, 264769, 21906768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526486, 22279000, 264586, 35696286, 264093, 264288, 21906769, 35696423, 35695855
2599	87642889 (5197, 5198)	Novel Protein sim. GBank gi 3941737  (AF108719) - BAT2 [Mus musculus]		MHC	
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gi 4263521 gb AAD15347  - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	Kinase receptor	

2601	81243070 (5201, 5202)	Novel Protein sim. GBank gj 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	55182575, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264908, 265007, 265008, 264591, 60433356, 33657402, 60433438, 21906754, 265011, 265018, 265018, 18108351, 264448, 264369, 21906769, 265020, 60170615, 264693, 33657109, 18108370, 18108370, 56182323, 18108381, 18108385, 22279002, 264563, 60433438, 21906754, 87168559, 264601, 264359, 264288, 21906767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gj 4406832 gb AAD200471 - (AF131801) Unknown [Homo sapiens]			
2603	94325821 (5205, 5206)	Novel Protein sim. GBank gj 3122367 sp Q61211 LIGA_MOUSE - LIGATIN		UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432288, 29331826, 29331827, 29331828, 35696052, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33657084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170815, 264691, 33657023, 264693, 33657109, 27486262, 18108374, 35696423, 65274791, 35695855, 264555, 264636, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000
2604	94676601 (5207, 5208)	Novel Protein sim. GBank gj 5454030 ref NP_006468.1 pRRP2 - RAS-related on chromosome 22		oncogene	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35696423, 264831, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2605	94316756 (5209, 5210)	Novel Protein sim. GBank gj 3628745 db BAA33366  - (AB013721) mltisugumin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	22278998, 264490, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264758, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21906765, 21906766, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636
2606	87746406 (5211, 5212)				22278996, 264510, 264512, 265009, 264768, 22279002, 264566

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gll4826626[gb AAD30202.1] - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264908, 264907, 284908, 66712502, 264828, 56182435, 55812038, 265010, 265017, 285018, 285019, 284788, 264689, 21906765, 55811957, 265020, 265022, 264692, 33657023, 284693, 33657109, 18108370, 264639, 56182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	81734786 (5215, 5216)	Novel Protein sim. GBank gll2226005 (U49973) - ORF2: function unknown [Homo sapiens]			
2609	94843791 (5217, 5218)	Novel Protein sim. GBank gll3024889[sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)]	Contains protein domain (PF00850) - histone Histone deacetylase family		284488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 285018, 284448, 284765, 264288, 264766, 264689, 21806765, 21906767, 21906769, 265020, 265021, 264691, 264692, 33657109, 27486261, 18108370, 65274791, 264638, 264558, 56182323, 18108385, 5628486
2610	88177654 (5219, 5220)	Novel Protein sim. GBank gll4336855[gb AAD17989] - (AF106473) leucine-rich-domain Inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]	transcript factor		18108394, 22278994, 56994075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263987, 33657182, 27486261, 18108374, 263978, 55811576, 264638, 87168518, 60432113, 22278999, 265017, 264684, 21906768, 22279000
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gll387876[emb CAA92984] - (Z68760) predicted using GeneFinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases		
2612	87771198 (5223, 5224)	Novel Protein sim. GBank gll5679138[gb AAD46874.1 AF160934] BCDNA.LD14189 [Drosophila melanogaster]	isomerase		
2613	79481496 (5225, 5226)		transport		285009, 264910, 264759, 265017, 21906767, 18108365, 18108388, 60432113
2614	87643948 (5227, 5228)	Novel Protein sim. GBank gll5533081[gb AAD45009.1 AF16118] P55T protein [Mus musculus]	UNCLASSIFIED		264685 22278998, 22278999, 29331825, 264508, 264906, 21906754, 264602, 264766, 284769, 52644229, 21906765, 33657109, 27488264, 18108370, 263972, 264555, 60432113
2615	87381996 (5229, 5230)		UNCLASSIFIED		264768, 18108394, 264692, 264693, 284508, 264509, 264807, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264768

2616	87428895 (5231, 5232)	Novel Protein sim. GBank glj3876761[emb](CAA92894) - (Z68760) predicted using GeneFinder; Similarity to Mouse FKBP-type peptidyl-prolyl cis-trans isomerases	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278995, 22278997, 22278998, 60432049, 60432289, 264828, 60433356, 264594, 60433438, 33109954, 87168474, 265011, 265017, 265018, 264288, 264766, 21906765, 21908767, 265020, 265021, 18108376, 18108377, 18108387, 87168518, 264482, 264567
2617	86976888 (5233, 5234)	Novel Protein sim. GBank glj728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]		kinase	265010, 265019, 264369, 264693, 55811576, 22279002
2618	91231662 (5235, 5236)	Novel Protein sim. GBank glj3319282 (AF049103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264806, 264907, 68712502, 29331830, 285008, 264910, 265009, 60433356, 60433438, 264758, 21808754, 265011, 87168539, 265017, 265018, 264369, 264288, 264766, 264768, 264688, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 33657023, 264692, 33657109, 264628, 18108374, 35695855, 18108381, 83373044, 18108385, 18108388, 56526486, 264563
2619	87694000 (5237, 5238)	Novel Protein sim. GBank glj2431772 (U66411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - iron-containing alcohol dehydrogenases	dehydrogenase	284259, 60432289, 60433438, 21906754, 264369, 60432113, 264566
2620	95314841 (5239, 5240)	Novel Protein sim. GBank glj4322567[gb]AAD160971 - (AF090436) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	52644507, 52645156, 52645842, 65274572, 22278995, 56994075, 35698286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35698032, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264446, 264369, 264288, 264687, 264768, 52644229, 264688, 264689, 21906765, 21906768, 35695917, 52644150, 264692, 33657109, 35695763, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002, 264594, 264636
2621	80253495 (5241, 5242)	Novel Protein sim. GBank glj4557341[ref]NP_001174.1pATP6 - ATPase, H <sup>+</sup> transporting, lysosomal subunit 1; vacuolar proton pump; H-ATPase subunit			264488, 264908, 264907, 264908, 264512, 265007, 264758, 35695917, 264634, 264636, 264563, 264482
2622	81780390 (5243, 5244)				
2623	91639306 (5245, 5246)	Novel Protein sim. GBank glj3880355[emb](CAB05299) - (Z62285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148629



2624	81638308 (5247, 5248)	Novel Protein sim. GBank gjl3880355[emb]CAB05299] - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	56181686, 22278998, 22278997, 22278998, 22278998, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35698052, 29146499, 68712502, 52644045, 285007, 285008, 60433356, 33109854, 21906754, 265010, 265011, 265018, 264448, 264288, 21906765, 21906766, 21906767, 29148629, 35695917, 265021, 265022, 27486285, 18108370, 60431528, 55811576, 35695855, 58182323, 18108385, 87168518, 22279002, 18108391
2625	86452068 (5249, 5250)	Novel Protein sim. GBank gjl2887429[dbj]BAA24857] - (AB007887) KIAA0427 [Homo sapiens]		UNCLASSIFIED	264091, 264511, 263981
2626	16533797 (5251, 5252)	Novel Protein sim. GBank gjl487416 (L20302) - actin filament protein [Gallus gallus]		struct	265008
2627	87836823 (5253, 5254)	Novel Protein sim. GBank gjl88462[pir]J127307 - proline-rich phosphoprotein (gene PRH1, Db allele) - human		UNCLASSIFIED	22278998, 265007, 265009, 264448, 21906767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gjl3123552[emb]CAA18609] - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) (Homo sapiens)		UNCLASSIFIED	22278997, 22278998, 264259, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264907, 264909, 265008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264389, 264288, 18108357, 21906765, 21906768, 265022, 65274781, 264638, 18108387, 87168518, 22279002
2629	87376490 (5257, 5258)	Novel Protein sim. GBank gjl4929595[gb]AAD34058.1(AF15182 - (AF151821) CGI-63 protein [Homo sapiens]		synthase	29331825, 29331826, 264102, 265006, 264766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	78188384 (5259, 5260)			UNCLASSIFIED	264638, 18108385
2631	94845809 (5261, 5262)	Novel Protein sim. GBank gjl321605[pir]JQ1161 - Gag protein - Visna virus (strain EV1)	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	52644507, 52645156, 52646385, 52846842, 22278994, 22278995, 35698286, 56994075, 22278997, 22278998, 264259, 52645080, 29331822, 29331824, 29331825, 29331828, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 264910, 52646317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 264288, 264369, 264768, 264768, 52644229, 21906764, 21906765, 21908768, 21908767, 21908769, 35695917, 265020, 52844150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486282, 27486285, 33657349, 35695763, 35698423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 264566, 264486, 264685
2632	38730414 (5263, 5264)				

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gj1139548[dbj BAA10889] - (D64009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265008, 265007, 265008, 265009, 55812038, 33657084, 55811388, 265010, 265011, 87168559, 265018, 265019, 264683, 264288, 264686, 29148629, 33657023, 264693, 33657182, 35695763, 55811576, 264639, 58182323, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264585
2634	87330921 (5267, 5268)	Novel Protein sim. GBank gj15441611[emb CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]	UNCLASSIFIED	29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gj14680663[gb AAD27721.1]AF132946 - (AF132946) CGI-12 protein [Homo sapiens]		22278997, 264259, 29331824, 66714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148629, 18108376, 55811576, 35695855, 87168518, 22279000, 264569, 29331822, 29331828, 265006, 60170831, 264681, 264765, 264685, 29148627, 21906769, 29148784, 265022, 60170615, 264635, 18108385, 56526488, 22279002, 264567
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gj13879146[emb CAB07846] - (Z83386) Similarity to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40	
2637	95011299 (5273, 5274)	Novel Protein sim. GBank gj14758208[ref NP_004081.1]pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278996, 22278999, 20281171, 264259, 29331822, 52645080, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52644296, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264687, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 65274620, 27486264, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264564, 264565, 264566, 264488, 264567

2638	94326733 (5275, 5276)	Novel Protein sim. GBank gjl4929889jgb/AAD34105.1 AF15186 - (AF151868) CGI-110 protein (Homo sapiens)	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52844507, 52846842, 18108398, 56182575, 22278995, 22278996, 35696286, 22278987, 22278999, 264259, 60432049, 29331822, 60424269, 29331826, 35696052, 29146498, 284805, 52844045, 56182435, 60433358, 33657402, 55812038, 55811386, 265019, 264288, 264768, 52844229, 56181562, 29148827, 29148829, 55811957, 29148784, 35695917, 265021, 52644150, 33657023, 65274620, 33657109, 35895763, 18108374, 55810764, 35896423, 55811576, 35895855, 60431850, 56182323, 60432113, 264404
2639	95361346 (5277, 5278)	Novel Protein sim. GBank gjl2190007jgb BAA20355  - (AB004109) phosphatidylserine synthase II (Citellus griseus)		synthase	284488, 29331825, 35696052, 264508, 264509, 284909, 264512, 33657402, 60433438, 264758, 85658542, 284600, 265020, 265021, 33657109, 264628, 35896423, 264555, 264639, 264563, 264584, 264565, 264566, 264486
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gjl3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm, score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm, score: 67.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 264908, 33109954, 265017, 265019, 21906768, 35695763, 264636, 264637, 18108387
2641	11669834 (5281, 5282)	Novel Protein sim. GBank gjl2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gjl4490304jemb CAB38795.1  - (AL035678) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264259, 29331822, 33657402, 265019, 264359, 284691, 264634, 56526486, 22279002
2643	87643981 (5285, 5286)	Novel Protein sim. GBank gjl3789797jgb AAC67502.1  - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278987, 264259, 29148499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264389, 264684, 264885, 264886, 29148827, 264690, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264556, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gjl3789797jgb AAC67502.1  - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	nucl_recpt	264107, 264687
2645	17277228 (5289, 5290)	Novel Protein sim. GBank gjl1708722jgsp P49749 EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	265007
2646	84148542 (5291, 5292)	Novel Protein sim. GBank gjl1708722jgsp P49749 EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	264908, 264687, 284632, 83373044

2647	91212978 (5293, 5294)			UNCLASSIFIED	56182575, 22278996, 35696286, 22278998, 264259, 29331822, 56182181, 29331825, 60424289, 60432289, 35696052, 66712502, 264908, 265007, 55812038, 33109954, 21906754, 33857084, 265019, 264448, 264288, 56181562, 21906765, 21906766, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264564
2648	87600587 (5295, 5296)				29146498, 56182435, 33109954, 265011, 264682, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113
2649	94128783 (5297, 5298)	Novel Protein sim. GBank gjl3041852 (AC004539) - unknown function; similar to Y09105 (P1D:gl666171) [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331826, 60432289, 66712502, 56182435, 60170831, 60432229, 33657402, 33109954, 21906754, 265017, 264688, 264688, 21908765, 21908768, 60170815, 264693, 263967, 18108370, 263976, 60170394, 60432113, 22279002, 264563, 264685
2650	87297533 (5299, 5300)	Novel Protein sim. GBank gjl5360271 [dbj BAA81908.1] - (AB029335) HRPET-3 [Halicynthia torezii]			
2651	88088745 (5301, 5302)	Novel Protein sim. GBank gjl4240225 [dbj BAA74891.1] - (AB020675) KIAA0868 protein [Homo sapiens]	Contains protein domain (PF000054) - Laminin G domain	synthase	29331824, 29331826, 29331827, 265007, 55812038, 21906754, 18108366, 18108384, 22279002, 264567
2652	10343125 (5303, 5304)	Novel Protein sim. GBank gjl4493956 [emb CAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28		UNCLASSIFIED	264692
2653	87798735 (5305, 5306)	(PFC0845c), Hypothetical protein, len: 167 aa. Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR:...		UNCLASSIFIED	265018, 18108370, 18108387, 264566
2654	85103240 (5307, 5308)				60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727
2655	91228018 (5309, 5310)	Novel Protein sim. GBank gjl3875272 [emb CAB02861] - (Z81051) predicted using GeneFINDER; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	Transcription factor	56182575, 56181686, 264092, 264259, 56182181, 60432289, 264907, 33657402, 55812038, 21906754, 87168559, 265017, 264448, 264369, 264288, 21806765, 21908766, 21908767, 21908768, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526486, 264404, 60432113
2656	84582601 (5311, 5312)	Novel Protein sim. GBank gjl3043718 [dbj BAA25523] - (AB011169) KIAA0597 protein [Homo sapiens]			264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank gl 5689509 dbj BAA83038.1  - (AB029009) KIAA1086 protein [Homo sapiens]			dna_rna_bind	264693
2658	80062454 (5315, 5316)	Novel Protein sim. GBank gl 3688089 (AC005757) - R32811_1 [Homo sapiens]		Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35686286, 264259, 29331822, 29331824, 29331826, 29331828, 265019, 264683, 21908766, 35695917, 264693, 35695855, 264637, 87168518, 264486, 264567
2659	87800755 (5317, 5318)	Novel Protein sim. GBank gl 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	264909, 264910, 265018, 264369, 264769, 21908769, 264693, 263972, 18108388
2660	91718472 (5319, 5320)	Novel Protein sim. GBank gl 728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		Contains protein domain (PF00036) - Kinase EF hand	kinase	264488, 65274572, 35696286, 22278996, 22278998, 264259, 29331822, 29331824, 60432289, 29331828, 35696052, 264908, 56182435, 265008, 265009, 60433356, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264368, 264288, 264667, 21908765, 28148784, 35695817, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22279000, 22279002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank gl 4758048 ref NP_004739.1 pCPR8 - cell cycle progression 8 protein			glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 264909, 264593, 33109954, 265010, 265017, 265018, 265019, 264760, 264448, 264369, 264288, 21908765, 21906768, 265022, 264691, 33657023, 27486262, 60431528, 18108374, 35695855, 18108388, 264482
2662	80228739 (5323, 5324)	Novel Protein sim. GBank gl 3874714 emb CAA91263  - (Z66494) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]			dehydrogenase	264555, 264556, 264558, 264486, 264906, 264908, 264757, 264758, 264767, 264691, 33657023, 264638
2663	87780823 (5325, 5326)	Novel Protein sim. GBank gl 1389670 (U59977) - Notch homolog Scalloped wings [Lucilia cuprina]		Contains protein domain (PF00008) - EGF-like domain	oncogene	35686286, 264509, 264595, 264288, 264685, 264686
2664	85518329 (5327, 5328)	Novel Protein sim. GBank gl 4884406 emb CAB43311.1  - (AL050190) hypothetical protein [Homo sapiens]			UNCLASSIFIED	35686286, 22278998, 29331822, 35696052, 264906, 264907, 264809, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21908765, 21908766, 21908767, 21908768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264488
2665	87770662 (5329, 5330)	Novel Protein sim. GBank gl 5106956 gb AAD39908.1 AF11381 - (AF113815) FH1/FH2 domain-containing protein FHO5 [Homo sapiens]			UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21908767, 264558, 22279002
2666	87828472 (5331, 5332)	Novel Protein sim. GBank gl 2500370 sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1		Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264559, 264559, 264563, 264565, 264567

2668	81216716 (5335, 5336)	Novel Protein sim. GBank gi15454186[ref][NP_006327.1]pZYG1 - ZYG homolog		UNCLASSIFIED	56181888, 35696286, 22278998, 22278999, 56182181, 29331824, 60424269, 29331825, 35696052, 29331828, 66712502, 56182435, 60433356, 264758, 21906754, 55811388, 265011, 87188559, 265017, 265019, 55811150, 264448, 264369, 264288, 21906765, 21906766, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 264692, 33657109, 35695763, 60431528, 18108374, 35696423, 55811576, 264634, 60431850, 83373044, 18108385, 87168518, 22279000, 264563, 264564
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi12147012[pir][JC4889 - proline rich protein - rat			264489, 264689, 21906767, 65274572, 56182575, 21906768, 29148627, 21906769, 29148629, 35696286, 35695917, 22278998, 22278999, 265021, 265022, 60170615, 52644150, 60432049, 264259, 264691, 33657023, 264692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331826, 29331827, 35696052, 29331828, 29146488, 29146499, 264905, 264908, 52644045, 264909, 56182435, 35696423, 65274781, 35695855, 265006, 264910, 264635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi1723523[sp][Q10362]YDBB_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger		18108370, 263974
2671	91214836 (5341, 5342)	Novel Protein sim. GBank gi14768277[gb][AAD29444.1]AF06425 - (AF064255) very long-chain acyl-CoA synthetase homolog 2: VLCS-H2 [Homo sapiens]		transport	52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21906754, 264682, 264288, 265021, 33657023, 33657109, 33657182, 27486261, 27486262, 27486285, 18108376, 18108385
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gi14966346[gb][AAD34677.1]AC00634 - (AC006341) Contains two PF01344 Kelch motif domains. [Arabidopsis thaliana]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264767

2673	87430749 (5345, 5346)	Novel Protein sim. GBank gll5457337[emb]CAB41505.2] - (AJ236876) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00864) - Poly(ADP-ribose) polymerase catalytic region.	polymerase	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 35695763, 60431850, 60170394, 87168518, 264563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank gll4758824[ref]NP_004280.1[pNRF3 - nuclear factor (erythroid-derived 2)-like 3]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	264488, 22278996, 35696286, 264091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 85686542, 264766, 21906765, 35695917, 264628, 35696423, 18108383, 87168518
2675	79563835 (5349, 5350)			UNCLASSIFIED	264691
2676	79628393 (5351, 5352)			UNCLASSIFIED	264906, 265008
2677	84328600 (5353, 5354)	Novel Protein sim. GBank gll1079042[pir][S52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278999, 284480, 264259, 52845080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 29146489, 29331830, 284908, 52844045, 265006, 265007, 265008, 265009, 60432229, 60433358, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 284448, 264683, 284288, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 60170615, 52844150, 264691, 33657023, 263987, 33657109, 27486264, 27486265, 33657349, 35695763, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 83373044, 18108387, 22279000, 22279002, 264564

2678	95001694 (5355, 5356)	Novel Protein sim. GBank gl 66760 pir A40465 - alanine transaminase (EC 2.6.1.2), cytosolic - human	UNCLASSIFIED	264488, 263994, 264489, 18108394, 5264842, 35696286, 22278999, 264259, 29331825, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109954, 52646317, 21905754, 265010, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108364, 18108365, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264486, 264567
2679	93361544 (5357, 5358)	Novel Protein sim. GBank gl 1709233 sp P07514 NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	264488, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 264909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85636542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810784, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264566, 264259, 264102, 264905, 264908, 265007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gl 4589604 db BAA76824.1  - (AB023197) KIAA0980 protein (Homo sapiens)	Contains protein domain (PF00038) - EF hand	264488, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2681	80933844 (5361, 5362)	Novel Protein sim. GBank gl 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase	35696286, 264908, 55811388, 265017, 55811150, 55811957, 35695917, 60431528, 55810784, 55811576, 35696423, 65274791, 56526486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gl 423468 pir JQ1974 - HTF9-C protein - mouse	UNCLASSIFIED	264909, 264769, 264635, 264636
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gl 5114351 gb AAD40286.1  - (AF158271) RING finger protein terf (Homo sapiens)	Contains protein domain (PF00622) - SPRY domain	



2684	65787151 (5367, 5368)	Novel Protein sim. GBank gl[486469]emb[CAB43385.1] - (AL050284) hypothetical protein [Homo sapiens]			264593	
2685	88054289 (5369, 5370)	Novel Protein sim. GBank gl[3342729 (AC005331)] - R31341_2 [Homo sapiens]		UNCLASSIFIED		
2686	87628680 (5371, 5372)	Novel Protein sim. GBank gl[4650844]dbj[BAA77027.1] - (AB028150) Keich motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - Keich motif	struct	264259, 29331822, 60432289, 29331827, 29331830, 284909, 284512, 264596, 264769, 284534, 264555, 264556, 264557, 264558, 60170394, 284559, 284486	
2687	87898183 (5373, 5374)	Novel Protein sim. GBank gl[5281314]gb/AAD41475.1[AF133123] transcription factor IIC102 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor	18108394, 18108398, 22278996, 35696286, 22278997, 29331828, 29331828, 68712502, 21906754, 265011, 264760, 264761, 284763, 264689, 21906765, 35696423, 264559, 18108385, 264563	
2688	79959584 (5375, 5376)				264908, 264760	
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gl[3880023]emb[CAA97339] - (Z73098) Similarity to yeast hypothetical protein (Swiss Prot accession number Q09685); cDNA EST EMBL:D72882 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat		22278997, 22278998, 22278999, 29331824, 35696052, 264908, 264908, 56182435, 264512, 264910, 285009, 60433438, 21906754, 18108351, 264682, 264683, 264767, 21906765, 21906768, 33657023, 33657182, 27486262, 27486284, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002	
2690	88003055 (5378, 5380)	Novel Protein sim. GBank gl[2477513 (AC002398)] - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct		
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gl[4107276]emb[CAA67130] - (X98506) acetyl-CoA synthetase [Solanum tuberosum]		synthase	65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264369, 284684, 21906769, 60170815, 60431528, 55810784, 284634, 284636, 264558, 264637, 22279002, 264584, 264566	
2692	94111914 (5383, 5384)	Novel Protein sim. GBank gl[3513303 (AC005584)] - R26984_1 [Homo sapiens]	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase		
2693	20438807 (5385, 5386)			UNCLASSIFIED	264592	
2694	94111918 (5387, 5388)	Novel Protein sim. GBank gl[3122400]sp Q35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN			264559	
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gl[4972740]gb AAD34765.1] - (AF132177) unknown [Drosophila melanogaster]		collagen	35696286, 56994075, 22278998, 264259, 35696052, 29331830, 285011, 264288, 56181582, 284690, 264692, 33657023, 27486282, 263976, 18108376, 35696423, 35695855, 60170394, 83373044, 56528486, 22279000, 22279002, 264566	
2696	87874040 (5391, 5392)	Novel Protein sim. GBank gl[728831]sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		synthase	264594, 21906766, 18108370, 18108372	

2697	91638472 (5393, 5394)	Novel Protein sim. GBank gij5689473dbj BAA83020.1  - (AB028991) KIAA1068 protein [Homo sapiens]	UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 264761, 18108351, 284448, 264288, 264766, 264688, 264689, 21906765, 21906768, 265020, 265021, 60170615, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87168518, 22279002, 264553, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank gij841318 (U22818) - mutant sterol regulatory element binding protein-2 [Cricetulus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 29331830, 284909, 52844045, 264910, 60433356, 33657402, 33109854, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 265021, 265022, 52844150, 33657023, 33657182, 27486261, 35696423, 65274791, 284638, 60432113, 22279000
2699	87780650 (5397, 5398)	Novel Protein sim. GBank	UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139836 (5399, 5400)	Novel Protein sim. GBank gij5174395 ref NP_006006.1 pB120 - Brain protein 120	UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181562, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gij1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]		18108394, 52845158, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29148499, 265006, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57295368 (5403, 5404)	Novel Protein sim. GBank gij2605967 (AF030027) - 24 [Equine herpesvirus 4]	UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87648514 (5405, 5406)	Novel Protein sim. GBank gij5689399 dbj BAA82983.1  - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar).	60432289, 265007, 21906765, 21906768, 265021, 264563

2704	87849515 (5407, 5408)	Novel Protein sim. GBank gi 4335694 gb AA63294  - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29148499, 264905, 264908, 264807, 52644045, 264511, 33657402, 264600, 264602, 265017, 264605, 264781, 18108351, 264764, 264687, 264769, 265021, 264681, 264682, 18108382, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5409, 5410)				264488, 264509, 264511, 264512, 264910, 264593, 87188474, 264604, 264288, 264687, 264769, 264638, 264566, 264486
2706	94326789 (5411, 5412)	Novel Protein sim. GBank gi 3255852 emb CAA16821.1  - (AL021728) /prediction=(method:./match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 65274572, 22278994, 56894075, 22278997, 264258, 29331824, 29331825, 29331828, 29331828, 33858970, 264907, 264908, 264909, 52844045, 56182435, 265006, 265007, 60433438, 55812038, 21908754, 52844286, 265010, 264601, 265017, 265019, 264681, 264448, 264682, 264288, 264686, 264687, 264688, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 264690, 264691, 33637023, 264692, 264693, 65274620, 27486264, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170384, 83373044, 65274727, 87188518, 22278900
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gi 3417294 (AC004381) - Unknown gene product [Homo sapiens]			22278995, 22278998, 56182435, 21908754, 87188559, 265017, 264448, 52845129
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gi 545790 bbs 147178 - DARPP-32-dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]	UNCLASSIFIED		65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264369, 264288, 264765, 264693, 264565
2709	94853888 (5417, 5418)	Novel Protein sim. GBank gi 3169705 (AC004780) - F17127_1 [Homo sapiens]	UNCLASSIFIED		29331822, 18108370, 18108374, 83373044
2710	87627979 (5419, 5420)	Novel Protein sim. GBank gi 46831 emb CAB37892  - (AL031432) dJ46SN24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			29331824, 264759, 264693, 18108382, 18108388

2711	94111920 (5421, 5422)	Novel Protein sim. GBank gi 3122400 sp O35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264769, 21906764, 21906765, 21906767, 21906768, 21906769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264259, 264691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27486262, 33657349, 264508, 264905, 264907, 60431528, 264908, 264909, 55810764, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33108954, 18108385, 21906754, 33657084, 87168518, 87168474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264565, 264764, 264568, 264288, 264766 264488, 35696286, 22278998, 264259, 29331824, 60432289, 35696052, 264508, 264908, 66712502, 52844045, 265006, 60432229, 33657402, 60433356, 265010, 265019, 18108351, 264681, 264288, 264685, 21906765, 21906766, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 56182323, 87168518, 60432113 56714117, 264906, 264563
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gi 5081315 gb AAD39343.1 AF07660 - (AF076607) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	
2713	88003064 (5425, 5426)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5429, 5430)	Novel Protein sim. GBank gi 432198 gb AAD15897  - (AF067430) Smarce1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264636
2716	88003068 (5431, 5432)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]		glycoprotein	264091, 264259, 29331822, 66714117, 264908, 264369, 264693, 264556, 264563 264593, 264558
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gi 3327046 db BAA31591  - (AB014516) KIAA0616 protein [Homo sapiens]			
2718	78604062 (5435, 5436)				264693
2719	88180423 (5437, 5438)	Novel Protein sim. GBank gi 746495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87168559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gij1335873 (U46690) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108374, 60424178, 264489, 56182435, 21906765, 21906766, 35698423, 22278997, 265020, 265022, 285008, 265008, 264082, 264636, 60432229, 264691, 264692, 33657023, 264693, 33857402, 83373044, 29331824, 18108368, 60424269, 29331826, 18108385, 52645129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22278002, 264905, 264482, 264563, 264906, 18108351, 264681, 18108370, 29331830, 264908, 66712502, 52644045, 264909, 264828, 18108354, 22278995, 35696286, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21906768, 265021, 33657109, 263969, 60431528, 264629, 55811576, 65274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000, 35696286, 22278999, 21906754, 265017, 264762, 264288, 21906765, 21906767, 21906768, 35695917, 18108362, 27466282, 35695855, 264558, 264559
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gij4829663 (gb)AAD34092.1 (AF15185 - (AF151855) CGI-97 protein [Homo sapiens])	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023		264508, 264509, 264906, 264908, 264910, 55812038, 264766, 264687, 264628, 264636, 264488, 18108396, 22278999, 20281099, 29331824, 29331826, 60432229, 29331828, 60170831, 60432229, 60433438, 18108351, 264682, 21906766, 21906767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002, 264488, 52644507, 264259, 29331827, 21906754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27466261, 18108370, 18108374, 35696423, 18108385, 22279000, 264488, 264828, 264685
2722	91638807 (5443, 5444)	Novel Protein sim. GBank gij3212997 (gb)AAC23434.1 - (AC004997) match to ESTs AA687999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g12314); similar to various tre-like proteins including: AF040654 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00556) - TBC domain	oncogene	
2723	87387732 (5445, 5446)			UNCLASSIFIED	
2724	87639563 (5447, 5448)	Novel Protein sim. GBank gij4680681 (gb)AAD27730.1 (AF13295 - (AF132955) CGI-21 protein [Homo sapiens])		ubiquitin	
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gij3169705 (AC004760) - F17127_1 [Homo sapiens]		UNCLASSIFIED	
2726	86880599 (5451, 5452)	Novel Protein sim. GBank gij3342738 (AC005328) - R26860_1, partial CDS [Homo sapiens]		MHC	

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gi 731267 sp P39219 RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLASE)	Contains protein domain (PF00849) - synthase RNA pseudouridylate synthase	65274572, 56182575, 22278994, 56994075, 22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 264508, 66712502, 264910, 33657402, 60433438, 264758, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 264767, 21906765, 21906767, 21906769, 55811957, 35695917, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 55811576, 35696423, 35695855, 264630, 60431850, 264636, 56182323, 87168518, 60432113, 22279000, 264584, 264565
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gi 3880433 emb CAA91399  - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	18108394, 56182435, 21906767, 55811957, 35695855, 265021, 264690, 264556, 264259, 264557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gi 2408095 emb CAB16300  - (Z99168) putative RNA splicing protein [Schistosoma mansoni]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	65274572, 264259, 60432289, 66712502, 56182435, 264448, 264288, 264369, 55811957, 265021, 284557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gi 3880433 emb CAA91399  - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	264887, 29331824, 29331826, 35696052, 264107, 56182435, 265008, 265009, 264592, 60431735, 265011, 264601, 265017, 18108351, 264288, 29148627, 55811957, 265021, 264690, 18108368, 18108374, 264557, 264558, 264559, 18108387, 55828486, 264566, 264486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gi 1723239 sp Q10166 YAUB_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME 1	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase	264259, 35696052, 265008, 264758, 264762, 264448, 264288, 29148627, 21906769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gi 3880433 emb CAA91399  - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED Mitochondrial carrier proteins	264687, 264489, 18108358, 56182435, 264689, 35696423, 55811957, 265021, 265006, 265008, 264910, 265009, 264690, 264555, 264259, 264556, 264557, 264559, 264559, 18108383, 33657109, 87168518, 265010, 264601, 60432113, 265017, 264905, 264448, 263972, 264369, 264567
2733	87363060 (5465, 5466)	Novel Protein sim. GBank gi 4519621 dbj BAA75670.1  - (AB017614) OASIS protein [Mus musculus]	UNCLASSIFIED	29331825, 264509, 264909
2734	94140286 (5467, 5468)	Novel Protein sim. GBank gi 4519621 dbj BAA75670.1  - (AB017614) OASIS protein [Mus musculus]	transcription factor bZIP transcription factor	60424178, 52844507, 56182575, 264259, 29331828, 264907, 264510, 264910, 60433356, 265019, 55811150, 264681, 264763, 264687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712336 (5469, 5470)	Novel Protein sim. GBank gij3850569 (AC005278) - ESTs gb T21276, gb T45403, and gb AA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	2278996, 60432289, 29331827, 29146498, 264108, 264909, 264112, 33657402, 87168474, 265017, 264762, 264448, 264764, 264684, 21906765, 264693, 33657109, 263976, 264638, 264638, 264537, 22278000, 22278002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264629, 263978, 264632, 264564
2737	87604526 (5473, 5474)	Novel Protein sim. GBank gij2558501[jdb BAA22886] - [DB3850] hepaloma-derived growth factor [Mus musculus]			264690
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gij8420387[jemb CAB48679.1] - [AJ243459] proteophosphoglycan [Leishmania major]			264488, 265008, 264768, 264691
2739	94318834 (5477, 5478)	Novel Protein sim. GBank gij3417386[jemb CAA75495] - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5478, 5480)			UNCLASSIFIED	264488, 56182575, 22278995, 35698286, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265006, 265007, 265009, 60432229, 33657402, 55812038, 87168474, 265010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 60431850, 264639, 56182323, 18108382, 18108385, 65274727, 22279002, 264564
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gij3242764 (AC005154) - similar to protein U28928 (PID:g861306) [Homo sapiens]		UNCLASSIFIED	22278996, 52644045, 52644229, 21906768, 21906769, 265020, 60170915, 264691
2742	87648644 (5483, 5484)	Novel Protein sim. GBank gij4758412[re NP_004472.1]pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 2 (GaiNAC-T2)	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264805, 264758, 55812038, 264369, 29148627
2743	87627891 (5485, 5486)	Novel Protein sim. GBank gij4468311[jemb CAB37892] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35686286, 264259, 264906, 264908, 265006, 60433438, 265017, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264690, 264691, 264693, 263969, 263971, 35695855, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gij3880433[jemb CAA91399] - (Z66521) similar to mitochondrial RNA splicing MSF4 like protein; cDNA EST EMBL.C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35686423, 35695917, 35695855, 265020, 265021, 264511, 265009, 264490, 264556, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331828, 21906754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 264482, 264448, 264488, 264369, 264288

2745	87740125 (5489, 5490)	Novel Protein sim. GBank gij4405795[gjb]AAD198261 - (AF038983) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	3598286, 264509, 264905, 264907, 264908, 264909, 264510, 264512, 265008, 264758, 264601, 265017, 264804, 264763, 264288, 264686, 264769, 264693, 35898423, 35895855, 264634, 264638, 264563, 264564, 264565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gij4758738[ref]NP_004680.1[pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	UNCLASSIFIED	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35896052, 29331828, 264905, 264906, 264907, 264908, 264909, 52644045, 265008, 60170831, 264598, 55812038, 265018, 264683, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 264890, 33657023, 264693, 33657109, 18108368, 18108374, 264558, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank gij4557803[ref]NP_000262.1[pNPC1 - Niemann-Pick disease, type C1		glycoprotein	264569, 52644507, 18108394, 22278995, 35898286, 22278997, 22278998, 52645080, 29331824, 56182181, 29331826, 29331827, 35896052, 264907, 264908, 264909, 265009, 33109954, 55811386, 87168474, 265010, 87168559, 264603, 265019, 264760, 264686, 264788, 21908769, 35895917, 60170815, 264692, 33657023, 52645129, 27486264, 60431528, 18108374, 35898423, 35895855, 264556, 56182323, 18108385, 264482
2748	91214983 (5495, 5496)	Novel Protein sim. GBank gij4191272[emb]CAA099841 - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00646) - F-box domain.		65274572, 29331828, 264112, 264511, 265019, 264760, 264767, 264768, 264769, 21906768, 21906769, 265020, 27486262, 56528486, 87168518, 22279000
2749	87346307 (5497, 5498)				264259, 264908, 264510, 265008, 265009, 264760, 264369, 264768, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gij1872498 (U74297) - PIUS [Oryctolagus cuniculus]	UNCLASSIFIED	UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33657084, 265011, 265019, 18108351, 264288, 264686, 264769, 264689, 55811957, 264693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)			UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88082675 (5503, 5504)	Novel Protein sim. GBank gij3041859 (AC004534) - OG-2 homeodomain protein-like; similar to U65087 (PID:g1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	UNCLASSIFIED - homeobox	



2753	94138972 (5505, 5508)	Novel Protein sim. GBank gj3851648 (AF098301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	56182575, 56994075, 22278998, 29331822, 29331824, 29331825, 29331828, 285007, 264593, 55812038, 33109954, 18108351, 264288, 58181562, 21906767, 21906788, 285021, 284693, 18108374, 65274781, 284632, 56182323, 22279002, 264563, 264567
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gj535428 (U13738) - calmodulin-like protein [Plum sativum]	Contains protein domain (PF00036) - EF hand	struct	22278999, 66714117, 29331827, 35696052, 29331828, 284808, 264908, 264909, 285011, 265017, 265018, 265019, 264288, 21906785, 21906787, 265022, 33657023, 264693, 56182323, 18108382, 22279000
2755	88001472 (5508, 5510)	Novel Protein sim. GBank gj2996853 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465808 (5511, 5512)			UNCLASSIFIED	264594
2757	95381590 (5513, 5514)	Novel Protein sim. GBank gj1173539 (U30473) - putative src-like adapter protein, non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	eph	85658542, 264693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank gj3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		struct	264693
2759	81005312 (5517, 5518)	Novel Protein sim. GBank gj2072200 (U94863) - p40 [Borna disease virus]			65274572, 35696286, 66714117, 29331828, 264508, 56182435, 21906754, 55811957, 264629, 264636, 56182323, 22279002
2760	79824798 (5519, 5520)			UNCLASSIFIED	264908
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gj4914573 (emb) CAB3885.1 - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	nuclease	22278998, 29331822, 29331830, 285010, 265019, 264288, 21906785, 21906788, 21906789, 265020, 56182323, 22279002, 264563
2762	87592699 (5523, 5524)	Novel Protein sim. GBank gj3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	struct	18108394, 22278998, 264906, 264909, 265006, 285007, 264757, 265010, 285011, 265017, 265019, 18108351, 264448, 264683, 264686, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108365, 33657109, 18108368, 18108370, 18108381, 18108382, 18108384, 18108388, 87168518
2763	87539968 (5525, 5526)	Novel Protein sim. GBank gj3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264369, 35696423
2764	84305140 (5527, 5528)	Novel Protein sim. GBank gj2905843 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases		52646842, 264259, 29331822, 29331825, 29331826, 29331828, 33656970, 264905, 264907, 29331830, 265006, 265009, 21906754, 265019, 264448, 21906769, 27486262, 56182323, 56528488, 87168518, 264487

2765	84315105 (5529, 5530)	Novel Protein sim. GBank gij4686672[emb CAA17688.2] - (AL022018) /prediction=(method:: /prediction=(method:: /match=(desc: [Drosophila melanogaster])		264488, 65274572, 22278995, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 264595, 264758, 55812038, 33109954, 265010, 87168559, 264600, 265018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264768, 264767, 264768, 56181562, 21906764, 21906765, 21906768, 35695917, 265021, 264691, 264692, 33657023, 33657109, 264628, 18108370, 264829, 18108374, 55811576, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168516, 22279000, 22279002, 264563, 264482
2766	94315109 (5531, 5532)	Novel Protein sim. GBank gij5441611[emb CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 60433356, 264288, 264685, 264689, 35695917, 265022, 264693, 264628, 65274791, 264635, 264555, 264556, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gij1079451[pir A55463 - tropomodulin, skeletal muscle - chicken]	struct	264112, 263974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gij5441322[emb CAB46721.1] - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]	UNCLASSIFIED	264488, 263994, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264686, 264768, 18108357, 264769, 264689, 21906766, 21906768, 21906769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264488, 264567

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gi 5419859 emb CAB46375.1  - (AL086725) hypothetical protein [Homo sapiens]		tubulin	264488, 56182575, 264259, 29331822, 29331824, 68714117, 29331825, 60432289, 29331828, 264908, 29331830, 56182435, 264592, 33857402, 264448, 264369, 264288, 60170615, 264691, 33857023, 264892, 33857109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113, 18108398, 22278995, 22278996, 22278999, 284105, 265006, 265019, 18108351, 264687, 21906765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gi 5701965 emb CAB52157.1  - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264636, 56182323, 83373044, 60432113, 18108398, 22278995, 22278996, 22278999, 284105, 265006, 265019, 18108351, 264687, 21906765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2771	88084071 (5541, 5542)	Novel Protein sim. GBank gi 3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 264369
2772	95357308 (5543, 5544)	Novel Protein sim. GBank gi 4885531 ref NP_005465.1 pNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	264259, 29331822, 29331824, 66714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 65274444, 264768, 21908769, 33657109, 263978, 264555, 264638, 264557, 83373044, 264563, 264564, 264486
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gi 3288888 (AC005253) - R26445_1 [Homo sapiens]		UNCLASSIFIED	18108374, 264686, 264687, 263978, 56182435, 264889, 55810764, 21908768, 35896423, 55811578, 65274791, 56181886, 55811957, 35895855, 284110, 265021, 264112, 265022, 265008, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424289, 18108385, 29331828, 29331827, 27486261, 29331828, 35896052, 55811386, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264908, 18108370, 264484, 264682, 20281069, 264448, 68712502, 264683, 264784, 264288, 264684, 264768, 263974, 22278995, 35896286, 22278996, 22278999, 264259, 29331826, 60432289, 35896052, 264112, 33657402, 21906754, 87168559, 265017, 265018, 264288, 21906766, 21908767, 21906788, 35895917, 265020, 265021, 33657023, 33657109, 18108370, 263978, 35896423, 35895855, 87168518, 22279000, 264482
2774	87819908 (5547, 5548)	Novel Protein sim. GBank gi 465852 sp P34388 YLS3 CAEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomalprot	264259, 29331826, 60432289, 35896052, 264112, 33657402, 21906754, 87168559, 265017, 265018, 264288, 21906766, 21908767, 21906788, 35895917, 265020, 265021, 33657023, 33657109, 18108370, 263978, 35896423, 35895855, 87168518, 22279000, 264482

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gi 4689132 gb AAD27775.1 AF07704 - (AF077042) 30S ribosomal protein S7 homolog (Homo sapiens)	Contains protein domain (PF00177) - Ribosomal protein S7p/S5e	264488, 22278995, 5694075, 22278998, 35998286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35998052, 265007, 21908754, 265017, 265019, 264448, 264682, 264369, 264288, 18108354, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 60170615, 264691, 18108370, 35696423, 65274791, 35695955, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 264563, 264565, 264488, 264567
2776	87791557 (5551, 5552)			56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21908754, 55811386, 265017, 265019, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 55810764, 55811576, 264555, 56526486, 22279000
2777	79818728 (5553, 5554)		UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)		UNCLASSIFIED	264907, 264593, 264760, 264628
2779	87849728 (5557, 5558)	Novel Protein sim. GBank gi 4680711 gb AAD27745.1 AF13297 - (AF132970) CGI-36 protein [Homo sapiens]	UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35696052, 265008, 264512, 264448, 264288, 29148627, 18108364, 20281149, 18108370, 264629
2780	94679397 (5559, 5560)	Novel Protein sim. GBank gi 4758524 ref NP_004825.1 phGK] - HPK/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	29146499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi 4469352 gb AAD21222] - (AF069502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	60424179, 29331824, 60424269, 66714117, 29331826, 56182435, 87168474, 265017, 264784, 56181562, 21908785, 21908786, 21906768, 35695917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN] - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	65274572, 22278996, 22278998, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 52644045, 265009, 265017, 265018, 264604, 265019, 264760, 264683, 264288, 264766, 264685, 264688, 264788, 52644229, 264689, 21906768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016828 (5565, 5566)	Novel Protein sim. GBank gil728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]		tm7	264909, 264628, 263878, 263981
2784	87614360 (5567, 5568)				264259, 26331822, 26331824, 26331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gil2134933[pir]S58890 - collapsin response mediator protein - human		UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21906765, 21906768, 21906768, 265020, 264564
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gil2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00009) - Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87901286 (5573, 5574)	Novel Protein sim. GBank gil5174507[ref]NP_006020.1[pMA1] - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21906765, 21906768, 55811957, 22278999, 264093, 60170815, 264259, 29331822, 18108365, 29331824, 33657109, 29331827, 35696052, 264100, 264105, 264908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22278002, 55811150, 264369, 264288
2788	88090644 (5575, 5576)	Novel Protein sim. GBank gil3252826 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gil2495729[sp]Q92556[Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA8725)]		UNCLASSIFIED	264103, 21906769, 264693
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gil5101772[emb]CAB45135.1]- (A)242978) p821 [Homo sapiens]		struct	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264259, 264638, 29331824, 264508, 264509, 264905, 264563, 264908, 264628, 18108370, 264907, 264764, 264908, 264288, 264909
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gil2911266 (AC002550) - Unknown gene product [Homo sapiens]			21906764, 18108368
2792	95083783 (5583, 5584)	Novel Protein sim. GBank gil2854163[gb]AAC02581.1]- (AF045842) No definition line found [Caenorhabditis elegans]			22278996, 22278997, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264908, 66712502, 29331830, 264909, 60432228, 60433356, 60433438, 33109854, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 264288, 264369, 264768, 52844229, 21906765, 21906768, 265020, 265021, 33657023, 293974, 18108374, 65274791, 35695855, 264638, 264556, 264558, 56182323, 83373044, 18108385, 56526486, 60432113, 22278000, 264587
2793	87425476 (5585, 5586)			UNCLASSIFIED	264259, 60432289, 86712502, 265009, 264636
2794	85794830 (5587, 5588)			UNCLASSIFIED	264689, 265022, 264691, 18108388, 264567

2795	95334888 (5589, 5590)	Novel Protein sim. GBank glj5454146 ref NP_008348.1 pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	55274572, 56182575, 35896286, 22278998, 22278999, 60432049, 264259, 29331822, 29331825, 66714117, 60432289, 29331826, 29331827, 35698052, 29331828, 264907, 66712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 52844150, 33657023, 264693, 65274620, 33657109, 35596423, 55811576, 65274791, 56182323, 56526486, 60432113, 22279002, 264482, 264563, 264484, 264567
2796	94848857 (5581, 5582)	Novel Protein sim. GBank glj4680651 gb AAD27715.1 AF13294 - (AF132940) CGI-06 protein [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35896052, 264509, 264908, 264907, 264908, 66712502, 56182435, 264510, 265006, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433358, 264594, 264595, 55812038, 264596, 21906754, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 264448, 264682, 264389, 264288, 264685, 264766, 264687, 56181562, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 52644150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486265, 33657349, 18108374, 35696423, 65274791, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22279000, 264563, 264564, 264565, 264566, 264567
2797	95110780 (5593, 5594)	Novel Protein sim. GBank glj4838557 gb AAD31040.1  - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278995, 22278996, 22278997, 29331827, 29148499, 264509, 264906, 56182435, 264757, 21906754, 265010, 265017, 265019, 264681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 29148628, 265020, 52844150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2798	86198005 (5595, 5598)	Novel Protein sim. GBank glj2852645 (AF007160) - unknown [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	264488, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264493, 264486, 264567

2799	88080651 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331828, 35696052, 29331828, 264909, 60433356, 33657402, 33109954, 87168474, 264448, 52844229, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 52644150, 35695955, 264634, 60432113, 22279000, 264488, 56994075, 264259, 20281099, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 264288, 264788, 264688, 60170815, 264691, 264692, 27486265, 264628, 264628, 264636, 264557, 264558, 264559, 87168518, 264564, 264566, 264567, 265007, 264687
2800	88318481 (5599, 5600)	Novel Protein sim. GBank gi 4240301 (dbj BAA74929.1) - (AB020713) KIAA0908 protein [Homo sapiens]		glycoprotein	
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (PID:g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter	transport	264448, 35695855
2803	78577446 (5605, 5606)	Novel Protein sim. GBank gi 4559368 (gb AAD23029.1) (AC006585) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED - peptidase	264639, 264566
2804	57111131 (5607, 5608)				
2805	87398486 (5609, 5610)				264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21908754, 264369, 264288, 264632, 60170394, 264563, 264482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gi 1168973 (sp P44403) CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29146488, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 29148828, 265022, 52644150, 56182323

2807	91720702 (5613, 5614)	Novel Protein sim. GBank gi 468310 emb CAB37991  - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]	UNCLASSIFIED	5264507, 52645156, 52645642, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 35696052, 29331828, 33656970, 264100, 264105, 264907, 52644045, 60433356, 264594, 60433438, 52646317, 21906754, 33109954, 33657084, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264763, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486285, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gi 5541863 emb CAB51071.1  - (AL096857) hypothetical protein [Homo sapiens]	MHC	60432289, 264510, 265010, 265017, 265018, 264681, 264686, 265021, 264690, 22279000, 264566
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gi 2772561 (AC004002) - similar to ciliary dynein beta heavy chain; 78% Similarity to P23098 (PID:g118965) [Homo sapiens]	ATPase_associated	18108351
2810	87259032 (5619, 5620)		UNCLASSIFIED	264559, 22278996, 264091, 264259, 29331828, 29146499, 29148629, 29148784, 264693
2811	91235845 (5621, 5622)	Novel Protein sim. GBank gi 3264583 (AC005189) - match to ESTs H97758 (NID:g118643) and AA085546 (NID:g1628773) [Homo sapiens]	UNCLASSIFIED	264106
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gi 4240273 dbj BAAT4915.1  - (AB020699) KIAA0892 protein [Homo sapiens]	UNCLASSIFIED	22278999, 264259, 66712502, 264693
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gi 3548791 (AC005620) - R33590_1 [Homo sapiens]	UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87168518, 60432113
2814	90960906 (5627, 5628)	Novel Protein sim. GBank gi 3548791 (AC005620) - R33590_1 [Homo sapiens]	transcriptfactor	65274572
2815	79774521 (5629, 5630)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264907, 264909
2816	95358229 (5631, 5632)		UNCLASSIFIED	264488, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264780, 264681, 264766, 264769, 264689, 21906765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486



2817	87749542 (5633, 5634)	Novel Protein sim. GBank gij1293846 (U56966) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 58182435, 264510, 265008, 264511, 264512, 264593, 264758, 265010, 264760, 264761, 264764, 264288, 264687, 264769, 55811957, 33695917, 33657109, 263978, 264634, 264636, 264638, 264584, 264565, 264566, 264488, 264587, 66712502
2818	86073578 (5635, 5638)	Novel Protein sim. GBank gij549988 (U13149) - possible prospory-associated protein [Perlmsetum ciliare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	
2819	87793527 (5637, 5638)			UNCLASSIFIED	264909, 264511
2820	87765744 (5639, 5640)	Novel Protein sim. GBank gij4929773 [gbjAAD34147.1] (AF15209) CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21908754, 265017, 18108351, 264683, 264369, 264886, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385, 264638
2821	95320511 (5841, 5842)	Novel Protein sim. GBank gij399144 [spjP02747] C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	
2822	94260221 (5843, 5844)	Novel Protein sim. GBank gij2224671 [dbj] BAA20820 (AB002363) KIAA0365 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21908765, 80170615, 264638, 264766
2823	95320513 (5845, 5846)	Novel Protein sim. GBank gij399144 [spjP02747] C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	
2824	95320515 (5847, 5848)	Novel Protein sim. GBank gij399144 [spjP02747] C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5849, 5850)				264760
2826	94311905 (5851, 5852)	Novel Protein sim. GBank gij3856683 [emb] CAA22020 (AL033503) conserved hypothetical protein [Candida albicans]			52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906768, 21906767, 21906769, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35696423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320518 (5653, 5654)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 263994, 264489, 65274572, 29331822, 66714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 60432229, 264592, 264593, 264595, 264596, 21906754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264690, 264691, 264692, 264693, 263972, 264629, 35695855, 264631, 264634, 264635, 264555, 264638, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264567, 264486, 18108391
2828	91228815 (5655, 5656)	Novel Protein sim. GBank gi 3598974 AF077000 - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	phosphatase	29331822, 35695052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264766, 264686, 55811957, 18108370, 18108374, 55810764, 35698423, 55811576, 56182323, 83373044, 87168518
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi 4680689 gb AAD27734.1 AF13295 - (AF13295) CGI-25 protein [Homo sapiens]			22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 66712502, 264510, 264511, 264593, 60433438, 21906754, 265011, 264603, 18108351, 264288, 21806765, 21906768, 21906769, 29148629, 52644150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264565, 264486
2830	88087109 (5659, 5660)	Novel Protein sim. GBank gi 2498667 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1			265008, 265019, 264639, 22279002
2831	87614717 (5661, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21906767, 60431528, 264636, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1  - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi 2224567 dbj BAA20772  - (AB002311) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi 4589532 dbj BAA76788.1  - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase-associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi 2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcription factor	264259, 264112, 265010, 264762, 264764, 263974, 264555, 264558, 264559

2837	87766482 (5673, 5674)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 264907, 264909, 265006, 265007, 265018, 265019, 264682, 264288, 21908766, 21908767, 55811957, 35695917, 18108374, 56182323, 22279000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gij973378 (U31263) - core protein [Hepatitis C virus]	UNCLASSIFIED	18108394, 18108397, 264259, 29331828, 265007, 265019, 264448, 18108388, 20281149, 264565, 264567
2839	85799317 (5677, 5678)	Novel Protein sim. GBank gij1575515 (U64899) - (thrombospondin-related anonymous protein [Plasmodium gallinaceum])	UNCLASSIFIED	264555
2840	87774665 (5679, 5680)	Novel Protein sim. GBank gij2224605[dbj]BAA20790] - (AB002330) KIAA0332 [Homo sapiens]		264509, 264511, 265011, 264288, 264769, 265020, 264634, 264636, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gij2224605[dbj]BAA20790] - (AB002330) KIAA0332 [Homo sapiens]	dna_rna_bind	56182575, 35696052, 264907, 264908, 264909, 264910, 264593, 264595, 264786, 265022, 264691, 33657182, 35695763, 18108370, 35695955, 264631, 264558, 264593, 264587
2842	80080086 (5683, 5684)	Novel Protein sim. GBank gij5578957[emb]CAB51350.1] - (AL050306) dJ475B7.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]	UNCLASSIFIED	264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gij5578957[emb]CAB51350.1] - (AL050306) dJ475B7.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]	UNCLASSIFIED	264908, 264907, 264908, 264909, 264910, 264784, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gij585123[sp]Q08876[FBL C, MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)]	Contains protein domain (PF00008) - EGF-like domain	264685
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	homeobox	26148488, 87168474, 264686, 35696423, 83373044, 264564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gij5306263[gb]AAD41995.1[AC00623] - (AC006233) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	26331830, 264909, 265008, 265011, 87168559, 264629, 264558
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gij3399676 (AC005390) - R31180.1 [Homo sapiens]	UNCLASSIFIED	264908, 264768, 264769, 264629, 264637, 264566
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gij5262615[emb]CAB45747.1] - (AL080156) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264490, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264763, 264764, 264765, 264766, 264686, 264628, 264629, 264555, 264638, 264556, 264557, 264638, 264558, 264559, 264563, 264566, 264567
2849	88084283 (5697, 5698)	Novel Protein sim. GBank gij3342218 (AC004131) - Unknown gene product [Homo sapiens]		29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35696423, 18108384, 56526486, 18108390
2850	87623636 (5699, 5700)		UNCLASSIFIED	35696286, 265008, 265009, 265018, 264288, 35695917, 264693, 18108374, 35695855, 22279000

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gi 4321619 gb AAD15788.1  - (AF051098) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264759, 55811386, 265010, 18108351, 264448, 264369, 21906765, 264691, 264692, 264693, 35695855, 264556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gi 1825729 (U88306) - similar to drosophila membrane protein PATCHED SP:P18502 (PID:g129645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gi 2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF00397) - Kinase WW domain		56182575, 55811150, 264690, 27486262, 27488265, 264632, 56182323, 56526486, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gi 2795825 (AC004021) - kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079096) [Homo sapiens]	Contains protein domain (PF01344) - dna_rna_bind Kelch motif		35698286, 29331824, 29331825, 29331826, 264908, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gi 1504040 dbj BAA13219  - (D86983) similar to D.melanogaster peroxidase(U11052) [Homo sapiens]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat		22278994, 29331822, 29331824, 29331825, 264906, 264908, 265009, 33109954, 265018, 265019, 264448, 21906765, 265020, 264690, 27486265, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gi 3264583 (AC005189) - match to ESTs H97758 (NID:g1118643) and AA085546 (NID:g1628773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27488262, 285007, 265009, 265017, 264482, 264563, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank gi 3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - struct PHD-finger		22278995, 35696286, 29331824, 29331825, 35696032, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35695763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gi 462585 sp P35227 ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)	Contains protein domain (PF00097) - zinc finger, C3HC4 type (RING finger)		264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264908, 29331830, 264908, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769, 21906766, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264829, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264584, 264556, 264486, 264567, 60424179, 65274572, 29331828, 264905, 264511, 264758, 265011, 21906767, 21908769, 55811957, 265021, 56182323
2859	90937875 (5717, 5718)	Novel Protein sim. GBank gi 4323320 gb AAD1733.1  - (AF124427) claudin-15 [Mus musculus]	UNCLASSIFIED		

2860	87532589 (5718, 5720)	Novel Protein sim. GBank gi 469186 emb CAB38414.1  - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridyate)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	284259, 28331822, 29331824, 29331825, 29331826, 28331827, 29331828, 284510, 284511, 33109954, 18108351, 284883, 284785, 284369, 284886, 21906765, 284691, 284692, 284693, 18108368, 22278002, 284482
2861	86698507 (5721, 5722)	Novel Protein sim. GBank gi 3941730 (AF108003) - BS4 [Homo sapiens]			284369, 284692
2862	87569585 (5723, 5724)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN  - leucine-rich neuronal protein		UNCLASSIFIED	284691, 284638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gi 3249088 (AC004473) - Contains similarity to goliath protein gb M97204 from D. melanogaster. [Arabidopsis thaliana]	Contains protein domain (PF00009) - struct Zinc finger, C2H2 type		56994075, 35696286, 22278998, 29331822, 29331824, 35686052, 29331828, 284106, 284511, 55812038, 33657084, 55811386, 285018, 265019, 21906765, 21906766, 21906768, 35695917, 265020, 265022, 33657023, 33657109, 33657348, 284628, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22278002
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gi 1079451 pir J35463 - tropomodulin, skeletal muscle - chicken	struct		284259, 284910
2865	95312191 (5729, 5730)	Novel Protein sim. GBank gi 438840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 284482
2866	95105480 (5731, 5732)	Novel Protein sim. GBank gi 585703 sp Q07066 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN	glycoprotein		55274572, 22278996, 22278998, 22278999, 284259, 29331824, 29331827, 29331828, 60433438, 21906754, 265018, 284448, 284764, 52844150, 83373044
2867	86980001 (5733, 5734)	Novel Protein sim. GBank gi 4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED		284488, 284768, 21906768, 22278998, 265022, 284259, 284508, 284805, 284907, 284511, 284910, 284635, 284636, 284637, 265011, 265017, 265018, 265019, 284583, 284088, 264566, 284764, 284369, 284587, 284486, 264288, 284766

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gi 1282868 emb CAA63923  - (X94232) l-Cell activation protein [Homo sapiens]		18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 52844045, 264828, 285006, 285007, 265008, 265009, 264591, 60432228, 264593, 60433356, 264595, 21906754, 265017, 265019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108388, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35698423, 35695855, 264632, 56182323, 87168518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88094412 (5737, 5738)		UNCLASSIFIED	264369
2870	84404574 (5739, 5740)		UNCLASSIFIED	264905, 264908, 264784, 21806789, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gi 5306263 gb AAD41995.1 AC006233 - (AC006233) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312187 (5743, 5744)	Novel Protein sim. GBank gi 112205 pr B39066 - proline-rich protein 15 - rat	kinase	263981
2873	88094252 (5745, 5746)		UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35698423, 35698288, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264558, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264906, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264486, 264766, 18108391

2874	94313548 (5747, 5748)	Novel Protein sim. GBank gij3212854 (AC004005) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	52644507, 52645156, 52646365, 56182575, 22278994, 22278995, 56994075, 35696286, 60432049, 264259, 52645080, 29331822, 56182181, 29331824, 80424269, 29331825, 86714117, 29331826, 29331827, 35696052, 29331828, 33656870, 66712502, 52644045, 285007, 285009, 60433358, 264758, 55812038, 18108348, 52646317, 33109954, 33657084, 265017, 264604, 265018, 265019, 264882, 264369, 264288, 264888, 52644229, 21906766, 21906767, 21906768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52645129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22279000, 22279002, 264563, 264565
2875	88083726 (5749, 5750)	Novel Protein sim. GBank gij2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat	22278996, 22278997, 22278999, 29331826, 29331828, 28146489, 66712502, 265008, 265017, 18108351, 264683, 264689, 21905767, 18108376, 18108377, 55811576, 60170394, 22279000, 264487
2876	88080854 (5751, 5752)	Novel Protein sim. GBank gij2979530 (AC004449) - R33683_2 [Homo sapiens]	Contains protein domain (PF00167) - Igf Fibroblast growth factor	52646365, 65274572, 56182575, 22278997, 22278998, 22278999, 60432049, 52645080, 60424269, 60432289, 29331827, 35696032, 29331828, 66712502, 52644045, 56182435, 60433358, 33657402, 33657084, 265019, 55811150, 264448, 264369, 21906766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264829, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56526486, 60432113, 22279000, 22279002, 264563
2877	94747028 (5753, 5754)	Novel Protein sim. GBank gij4704208[emb]CAB41646.1] - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]	UNCLASSIFIED	264488, 264259, 29331822, 29331826, 264805, 264509, 264907, 264909, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264488, 264567
2878	88085309 (5755, 5756)	Novel Protein sim. GBank gij3876775[emb]CAB03067] - (Z81077) predicted using GeneFinder: Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	Contains protein domain (PF01207) - Uncharacterized protein family UPF0034	264488, 264259, 29331822, 29331826, 264805, 264509, 264907, 264909, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264488, 264567

2879	87669122 (5757, 5758)	Novel Protein sim. GBank gl 4885145 gb AAD32752.1  - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - Uracil-DNA glycosylase	UNCLASSIFIED	18108359, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265008, 264910, 264637, 60170394, 264559, 265017, 264564, 264565, 264587, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gl 4680703 gb AAD27741.1 AF13296 - (AF132966) CGI-32 protein [Homo sapiens]			264488, 52646365, 52646842, 22278994, 35698288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265009, 264910, 264594, 21906754, 52646317, 52644298, 87168559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264769, 21906768, 21906769, 35695917, 265021, 264690, 264692, 33657023, 52645129, 33657109, 33657182, 27486262, 33657349, 264629, 18108374, 35695955, 264634, 264635, 264636, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22279000, 264563, 264483, 264567, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gl 733571 (U23452) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED		22278998, 29331822, 52644045, 21906765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gl 118112 (U41559) - No definition line found [Caenorhabditis elegans]			264488, 22278998, 22278999, 29331822, 29331826, 264908, 60170831, 60433358, 55812038, 264681, 264682, 264686, 264687, 264688, 21906768, 21906769, 264693, 263987, 18108374, 55811576, 56182323, 22279002, 264566
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gl 488008 gb AAD31087.1 AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264112, 264682
2884	87784643 (5767, 5768)	Novel Protein sim. GBank gl 2224697 db BAA20832  - (AB002376) KIAA0378 [Homo sapiens]		UNCLASSIFIED	265018, 264634
2885	83006308 (5769, 5770)	Novel Protein sim. GBank gl 1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264686, 264693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gl 1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	- complement/recept	60432048, 264259, 29331828, 264908, 264511, 264595, 60433438, 264598, 265017, 264605, 263969, 263972, 264555, 83373044, 87168518, 264566
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gl 3882323 db BAA34521.1  - (AB018344) KIAA0801 protein [Homo sapiens]		UNCLASSIFIED	18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gl 4508015 ref NP_003447.1 pZNF2 - zinc finger protein 205	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript/factor	264488, 264259, 29331828, 264508, 264906, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486



2889	87606562 (5777, 5778)				UNCLASSIFIED	56994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5778, 5780)	Novel Protein sim. GBank glj854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	264591, 264766
2891	88094428 (5781, 5782)	Novel Protein sim. GBank glj387750[emb]CAB01508] - (Z78084) predicted using GeneFinder, similar to collagen; cDNA EST EMBL:D65865 comes from this gene; cDNA EST EMBL:D69451 comes from this gene; cDNA EST EMBL:D66026 comes from this gene; cDNA EST EMBL:D69658 comes from this gene...			UNCLASSIFIED	264591, 264595, 264389, 264685, 264683, 264628, 264583, 264586
2892	95418745 (5783, 5784)	Novel Protein sim. GBank glj4929759[gb]AAD34140.1[AF15190 - (AF151803) CGI-145 protein (Homo sapiens)]			UNCLASSIFIED	65274572, 35696286, 29331828, 264110, 285009, 60433438, 285018, 285019, 18108351, 264288, 21906765, 21906766, 21906769, 55611857, 264680, 65274620, 263967, 35695855
2893	87798014 (5785, 5786)				UNCLASSIFIED	264259, 265010, 264682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank glj5668015[gb]AAD46135.1] - (AF080171) zinc finger protein ZNF232 [Homo sapiens]		Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcript factor	264259, 265008, 60433438, 52644296, 265011, 264369, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank glj3924708[emb]CAA84646] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMBL...		Contains protein domain (PF01437) - Plexin repeat		29331824, 265007, 264762, 264636, 264563
2896	87752122 (5781, 5792)	Novel Protein sim. GBank glj4885548[ref]NP_005456.1[pPKBG - protein kinase B gamma]		Contains protein domain (PF000069) - Eukaryotic protein kinase domain	kinase	18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29148499, 264906, 264908, 265007, 265009, 265018, 265019, 264369, 264685, 264689, 21908766, 265021, 264693, 33637182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank glj4502877[ref]NP_001296.1[pCLDN - Clostridium perfringens enterotoxin receptor 1]			UNCLASSIFIED	60424178, 56182575, 22278998, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433358, 60433438, 85274444, 55611386, 265018, 18108351, 264448, 264288, 264687, 21906765, 21908766, 21906767, 21906769, 55611857, 35695917, 264534, 33657023, 33657109, 35695783, 264628, 264629, 60431528, 18108374, 55610764, 55611576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264566
2898	87750340 (5795, 5796)				UNCLASSIFIED	22278995, 264604, 18108385, 264566

2899	80357670 (5797, 5798)					UNCLASSIFIED	284764, 21906764, 284692
2900	94233538 (5789, 5800)	Novel Protein sim. GBank gi 4581470 emb CAB40137.1  - (Y18483) SLC7A8 protein [Homo sapiens]				glycoprotein	65274572, 56182575, 35696286, 60432048, 284259, 29331824, 66714117, 29331828, 35696052, 29331828, 66712502, 56182435, 285006, 265007, 265008, 265009, 60433356, 264758, 265018, 264764, 264765, 264288, 264768, 21906764, 21906768, 21906769, 265020, 264692, 264693, 32833986, 264631, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank gi 4759272 ref NP_004614.1 pTTC4 - tetrairicopapilde repeat domain 4				phosphatase	22278995, 22278997, 22278999, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 284910, 265009, 21906754, 33657084, 87168474, 265010, 265018, 21906764, 21906765, 21906766, 21906767, 21906769, 33657023, 264593, 33657109, 33657349, 35696423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank gi 2414615 emb CAB16354  - (Z99259) hypothetical protein [Schizosaccharomyces pombe]					264683, 264691
2903	87606733 (5805, 5806)	Novel Protein sim. GBank gi 1079318 p S52241 - XLCL2 protein - African clawed frog					264887, 22278994, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 264448, 264683, 264769, 264689, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86458072 (5807, 5808)	Novel Protein sim. GBank gi 5639823 gb AAD45885.1 AF14367 - (AF143676) multispinning nuclear envelope membrane protein nurim [Homo sapiens]				UNCLASSIFIED	52646365, 22278999, 264259, 35696052, 265011, 265017, 264683, 264769, 35695917, 285020, 263967, 18108374, 35695855, 264637, 264952, 18108385, 18108387
2905	84449926 (5809, 5810)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!				oncogene	265009, 264681, 264682
2906	95341051 (5811, 5812)	Novel Protein sim. GBank gi 4689256 gb AAD27831.1 AF12185 - (AF121858) sorting nexin 8 [Homo sapiens]			Contains protein domain (PF00787) - PX domain	UNCLASSIFIED	22278996, 35696286, 22278998, 264259, 60432289, 29331828, 29331830, 66712502, 265009, 60170831, 33109954, 264448, 264683, 264288, 264689, 21906766, 21906767, 21906768, 55811957, 35695917, 265022, 52644150, 264691, 33657023, 264692, 264693, 35695855, 60432113, 264586

2807	91211383 (5813, 5814)	Novel Protein sim. GBank gij1707079 (U80451) - contains strong similarity to a DNAJ-like domain (PS:PS00636) [Caenorhabditis elegans]	Contains protein domain DnaJ domain	eph	52844507, 56182575, 56181666, 22278895, 56994075, 35898286, 60432049, 56182181, 35696052, 60431735, 284595, 55812038, 21908754, 55811386, 265019, 284682, 284389, 56181562, 21908766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2808	80414246 (5815, 5816)	Novel Protein sim. GBank gij2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]		helicase	285009, 33109954, 18108351, 284786, 265021, 264691, 284692, 18108374, 264556, 284638, 264557, 284558
2809	87420225 (5817, 5818)			eph	284259, 87168474, 265018, 18108365, 264628
2810	86601075 (5819, 5820)	Novel Protein sim. GBank gij4539335jemb[CAB37483.1] - (AL035539) putative protein [Arabidopsis thaliana]			22278995, 284509, 284512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2811	94216615 (5821, 5822)	Novel Protein sim. GBank gij4469187jemb[CAB38415.1] - (AL031588) d11163J1.3 (novel protein similar to mouse B99) [Homo sapiens]		glucoamylase	52646365, 18108397, 22278995, 22278897, 22278998, 22278999, 28331824, 28331825, 52844045, 265008, 285018, 284448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2812	87731803 (5823, 5824)	Novel Protein sim. GBank gij4929637jgbAAD34079.1[AF15184 - (AF151842) CGI-84 protein [Homo sapiens]	Contains protein domain Involutrin repeat		52645156, 264092, 60432049, 264259, 52845080, 29331824, 28331825, 68712502, 33109954, 284760, 264683, 264288, 264686, 265021, 264693, 18108368, 263976, 264404
2813	87713823 (5825, 5826)	Novel Protein sim. GBank gij854065jemb[CAA50337] - (X83413) U88 [Human herpesvirus 8]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	52844507, 52645156, 52646842, 58182575, 35696286, 22278997, 264259, 52845080, 29331827, 35696052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21908754, 52644286, 87168474, 285017, 265018, 265019, 18108351, 284682, 264686, 264688, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52844150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2814	87797300 (5827, 5828)				264557

2915	88081972 (5829, 5830)	Novel Protein sim. GBank gi 5174485 ref NP_006030.1 pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain (PF00059) - eph Lecin C-type domain	284559, 264488, 264687, 264768, 21906766, 52648842, 21906767, 21908768, 56182575, 29148629, 35695917, 22278996, 22278997, 22278998, 265021, 22278999, 52644150, 264691, 264259, 60432049, 264692, 52645129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331828, 27486262, 27486264, 27486265, 33657349, 29146498, 29146499, 264906, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433356, 56182323, 18108382, 55812038, 18108385, 33109954, 21906754, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 265019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264369, 264288, 264765
2916	95337780 (5831, 5832)	Novel Protein sim. GBank gi 5104851 dbj BAA80165.1  - (AP000061) 305aa long hypothetical dTDP-4- dehydrohamose reductase [Aeropyrum pernix]	dehydrogenase	52645156, 65274572, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 264509, 264906, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433356, 52646317, 21906754, 33109954, 33657084, 52644286, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811857, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486264, 35695763, 18108376, 55811576, 35696423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gi 3169065 emb CAA19260.1  - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	85690529 (5835, 5836)	Novel Protein sim. GBank gi 539218 pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]		66714117, 66712502, 263981

2920	87769523 (5839, 5840)				35696286, 22278997, 284259, 52645080, 28331824, 29331826, 29331827, 264828, 264909, 56182435, 264511, 264758, 33109954, 21908754, 52844296, 265010, 265011, 264601, 265017, 265019, 264881, 264887, 21908787, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486284, 27486285, 35696423, 35695855, 264832, 264636, 264637, 264638, 56182323, 60170394, 18108385, 87168518, 60432113
2921	91639882 (5841, 5842)	Novel Protein sim. GBank g 4580013 gb AAD24202.1 U83194_ - (U83194) TRAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		35696286, 22278997, 264091, 264092, 264094, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 28146498, 264104, 264105, 264107, 264508, 264110, 264112, 264512, 60433356, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108376, 264555, 263981, 56528486, 87168518, 22279000, 22279002, 284908, 264909, 264511, 265006, 265008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 28146627, 35695917, 264692, 264629, 263978, 55811576, 35695855, 264555, 264558, 56182323, 60170394, 22279000, 264488
2922	87749762 (5843, 5844)	Novel Protein sim. GBank g 4589514 db BAA76779.1  - (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - Glycosyl hydrolases family 38	kinase	264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 284511, 265008, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52844150, 264691, 284692, 33657109, 263974, 18108376, 264631, 284636, 18108385, 18108387, 22279000, 264563, 264568
2923	95337799 (5845, 5846)	Novel Protein sim. GBank g 483526 emb CAB42898.2  - (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	265017, 264628, 20281152, 264556
2924	87791967 (5847, 5848)	Novel Protein sim. GBank g 2133095 pir S72254 - ribosomal protein L36, mitochondrial - yeast [Saccharomyces cerevisiae]	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomal prot	
2925	85080120 (5849, 5850)	Novel Protein sim. GBank g 2388986 emb CAB11718  - (Z88980) actin associated protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 35696286, 264259, 60432289, 29331827, 264508, 52644045, 264910, 264591, 60432229, 55812038, 21908754, 264681, 264448, 264683, 264288, 264685, 52644228, 264689, 21906765, 21906766, 21906768, 21906769, 265021, 265022, 60170615, 264692, 33657023, 264693, 33657109, 35696423, 65274791, 56182323

2928	95343003 (5851, 5852)				29331828, 265011, 264768, 264689
2927	60408018 (5853, 5854)	Novel Protein sim. GBank gij283032[pir][S22456] - hydroxyproline-rich glycoprotein - perennial teasinte			264764, 264288, 264630, 264637
2928	20452179 (5855, 5856)			UNCLASSIFIED	264559
2929	91622020 (5857, 5858)	Novel Protein sim. GBank gij3413320[emb][CAA06915] - (AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	264569, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264084, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33656970, 264109, 29331830, 52644045, 265009, 33109954, 52644296, 87168559, 264760, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906768, 21906769, 35695917, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35698423, 35695855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181886, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52644045, 56182435, 265009, 60170831, 264592, 60432229, 60433356, 87168474, 265010, 265011, 265017, 265018, 265019, 264762, 264448, 264683, 264288, 264766, 21906765, 21906769, 35695917, 60170615, 33657023, 33657109, 264628, 18108370, 18108372, 35698423, 35695855, 264556, 56182323, 60432113, 264567
2931	94312693 (5861, 5862)	Novel Protein sim. GBank gij3788433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52645156, 22278997, 22278998, 29331822, 52645080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21906765, 21906766, 21906767, 21906768, 265020, 52644150, 33657023, 33657109, 33657182, 27486265, 35698423, 35695855, 264555, 87168518, 60432113, 264566
2932	79632623 (5863, 5864)				264906, 264907
2933	91720776 (5865, 5866)	Novel Protein sim. GBank gij3378056 (AF017777) - helicase [Drosophila melanogaster]	helicase		264488, 18108382, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52644045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52644229, 21906765, 21906766, 21906768, 21906769, 265022, 52644150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567

2934	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 264691, 27488282, 264628, 87168518, 22279000
2935	86410578 (5868, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21906754, 265018, 265019, 264448, 264789, 21906764, 21906765, 265021, 264692, 33657023, 33657109, 33657349, 55810784, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gij4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811578, 18108387, 60432113, 264563
2937	94853096 (5873, 5874)	Novel Protein sim. GBank gij517409 [NP_006101.1] pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278999, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264908, 264908, 264909, 56182435, 265006, 264512, 264910, 60170831, 60433358, 265011, 265018, 18108351, 264448, 264288, 264766, 52844229, 21908765, 29148784, 65274791, 264556, 56182323, 60170394, 264558, 60432113, 264565, 264486, 264567
2938	95419773 (5875, 5876)	Novel Protein sim. GBank gij3319990 [emb] CAA76720] - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 56182575, 22278996, 35696286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264805, 66712502, 52844045, 56182435, 264511, 265008, 265009, 60432228, 33657402, 60433438, 55812038, 21906754, 85658542, 265010, 265011, 87168559, 285017, 285018, 265019, 264681, 264288, 264689, 21908765, 21908767, 21906768, 55811957, 35695917, 265020, 60170815, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263976, 35698423, 35695855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56528486, 60432113, 22279002
2939	87766622 (5877, 5878)	Novel Protein sim. GBank gij3979900 [emb] CAA89909] - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292b.....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	264907, 265018, 264681, 264685, 264686

2940	195011103 (5879, 5880)			UNCLASSIFIED	22278996, 29331822, 29331824, 66714117, 29331826, 29331828, 284905, 284908, 66712502, 29331830, 265011, 265017, 284764, 264369, 21906766, 21906767, 33857023, 33857109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264566
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gi 3413872 db BAA32300  - (AB007924) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	264557
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gi 1172845 sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25		glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gi 4929653 gb AAD34087.1 AF15185 - (AF151850) CGI-92 protein [Homo sapiens]		collagen	60432049, 264259, 60432289, 29331827, 29146498, 265008, 284593, 60433356, 60433438, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264567
2944	95081063 (5887, 5888)	Novel Protein sim. GBank gi 4678282 emb CAB41190.1  - (AL049660) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated	58994075, 22278998, 60432049, 264259, 29331822, 29331824, 60424269, 60432289, 29331826, 29331828, 284905, 264907, 52644045, 264909, 264511, 265006, 265009, 284594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 56526486, 87168518, 60432113, 22279002, 264482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	604224179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35696052, 264908, 265006, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264369, 264288, 284687, 58181582, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264693, 60431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264566, 264567



2846	84317315 (5891, 5892)	Novel Protein sim. GBank gil5441852 gb AAD43195.1 AF072864 - (AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	264488, 264258, 264508, 264509, 264808, 264907, 264809, 264510, 264511, 265007, 264512, 264910, 264591, 264593, 18108351, 264764, 264288, 264684, 264769, 265021, 264692, 33657103, 264628, 264628, 18108374, 264631, 264634, 264638, 264637, 18108380, 264638, 264639, 83373044, 264555, 264586, 264486, 264587
2847	87382952 (5893, 5894)	Novel Protein sim. GBank gil3540281 gb AAC34383.1  - (AF056116) All-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278895, 22278896, 22278897, 22278899, 29146498, 264508, 29331830, 265007, 265008, 265009, 60432229, 21906754, 265010, 265017, 265019, 264766, 264685, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113, 52646842, 22278895, 264259, 29331824, 29331825, 29331827, 29331830, 264809, 265007, 265009, 265019, 264763, 264684, 264288, 264685, 264688, 21906767, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22279002, 264563, 264567
2848	87626527 (5895, 5896)	Novel Protein sim. GBank gil5566614 gb AAB5654.2  - (AF001533) milogen-induced [Mus musculus]			22278896, 22278897, 60432289, 29331828, 29331827, 29331828, 35696052, 29146499, 264104, 264107, 264905, 66712502, 264908, 60433356, 60433436, 87168559, 264764, 52644229, 56181562, 21906767, 21906768, 21906769, 265022, 60170615, 33857023, 35696423, 263981, 264558, 60432113, 22279002
2849	88175545 (5897, 5898)	Novel Protein sim. GBank gil2132923 pir S67133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264488, 35696286, 264258, 35696052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35696423, 65274791, 35695955, 264556, 56526486, 264486
2850	95088870 (5899, 5900)	Novel Protein sim. GBank gil466102 sp P34629 Y0J6_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00883) - Cytosol aminopeptidase family	peptidase	264693
2851	87392357 (5901, 5902)	Novel Protein sim. GBank gil4688902 emb CAB41450.1  - (AJ238248) centaurin beta2 [Homo sapiens]			

2952	95328952 (5903, 5904)	Novel Protein sim. GBank gl 559693 emb CAB51405.1  - (AL096881) hypothetical protein [Homo sapiens]		Contains protein domain (PF00850) - CRALTRIO domain.		264687, 52845156, 21908766, 21908769, 22278996, 265020, 264890, 60432049, 264299, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27486262, 264508, 264905, 20281149, 264908, 264907, 29331830, 264908, 264909, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433358, 264639, 264758, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2953	88093575 (5905, 5906)	Novel Protein sim. GBank gl 119522 sp P10658 SERC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPiP)		Contains protein domain (PF00266) - UNCLASSIFIED Amino transferases class-V		18108396, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264586, 264758, 52846317, 21908754, 33657084, 52844298, 87168559, 264600, 264760, 264681, 18108351, 264764, 264389, 264288, 264687, 21906765, 21906766, 21906767, 21908768, 21908769, 35695917, 33657023, 18108384, 52845129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2954	88086288 (5907, 5908)	Novel Protein sim. GBank gl 4885261 ref NP_005251.1 pGDF9 - growth differentiation factor 9		Contains protein domain (PF00019) - Igf Transforming growth factor beta like domain		
2955	87698426 (5909, 5910)	Novel Protein sim. GBank gl 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331826, 35696052, 264908, 52644045, 264512, 60432229, 265018, 265019, 55811150, 264769, 21906767, 21906768, 21908769, 265021, 60170615, 55810764, 264567
2956	85789745 (5911, 5912)	Novel Protein sim. GBank gl 4689254 gb AAD27830.1 AF12185 - (AF12185) sorting nexin 7 [Homo sapiens]		Contains protein domain (PF00787) - PX domain		22278996, 264259, 29331827, 264908, 21908768
2957	90933301 (5913, 5914)	Novel Protein sim. GBank gl 4503023 ref NP_000089.1 pCPT2 - carnitine palmitoyltransferase II precursor			cadherin	22278999, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264683, 264288, 264685, 18108357, 29148629, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 56526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gl 4240257 dbj BAA74907.1  - (AB020691) KIAA0884 protein [Homo sapiens]				264595, 264596, 264681, 264389, 264629, 264631, 264567

2859	95109420 (5917, 5918)	Novel Protein sim. GBank gjl988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - oncogene TBC domain	263994, 22278997, 264259, 60432049, 29331828, 29331828, 35698052, 29331830, 66712502, 56182435, 265008, 264512, 265008, 265009, 60433356, 60433438, 264596, 265017, 265018, 264683, 264288, 264766, 264768, 21906768, 21906787, 21906769, 265020, 60170615, 264692, 27486265, 18108374, 65274791, 35695855, 83373044, 56526488, 60432113
2860	87420091 (5918, 5920)		UNCLASSIFIED	35696286, 56182435, 87168474, 265010, 60170615, 35698423, 56182323, 18108383, 87168518, 264483
2861	95413418 (5921, 5922)	Novel Protein sim. GBank gjl596646[emb](CAB05177.2) - (Z82266) predicted using GeneFinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52644045, 265008, 33657402, 21906754, 87168474, 265011, 87168559, 265017, 21906769, 265020, 60170615, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264567
2862	87912700 (5923, 5924)		UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52646317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264688, 264768, 264789, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 264567, 264486
2863	95313464 (5925, 5926)	Novel Protein sim. GBank gjl4240223[dbj](BAA74890.1) - (AB020674) KIAA0867 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264687, 29148627, 29148784, 265020, 33857023, 264693, 65274620, 33657182, 27486281, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2864	94324617 (5927, 5928)		UNCLASSIFIED	264259, 29331828, 33657402, 265017, 265018, 264692, 18108388, 35698423, 83373044, 18108388

2965	80384762 (5929, 5930)	Novel Protein sim. GBank gi 4865447 ref NP_005452.1 pKRML - Kreiser (mouse) mal- related leucine zipper homolog		transcriptfactor	264259, 29331826, 264508, 264509, 264905, 264907, 264908, 264909, 264511, 265008, 264910, 264591, 264593, 264594, 33657402, 265011, 264760, 264762, 264764, 264288, 264885, 264768, 264692, 33657109, 264628, 264628, 35895855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264583, 264567, 18108391 60432289, 264682, 264448
2966	91725248 (5931, 5932)	Novel Protein sim. GBank gi 5262751 emb CAB5690.1  - (AJ243177) Xenopus RPA Interacting protein alpha [Xenopus laevis]			
2967	94658303 (5933, 5934)	Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]		UNCLASSIFIED	264488, 264508, 264509, 264908, 264909, 264511, 264910, 264594, 264758, 85658542, 264762, 264764, 265021, 264556, 18108381, 264564, 264486
2968	95302776 (5935, 5936)	Novel Protein sim. GBank gi 4929715 gb AAD34118.1 AF15188 - (AF15188) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)		264687, 52645156, 21906765, 52646365, 21906787, 18108398, 35696423, 22278996, 35696286, 22278997, 265020, 22278998, 265021, 265022, 264093, 264638, 264690, 52644150, 264259, 33657023, 52645080, 264693, 29331822, 56182181, 29331824, 68714117, 29331825, 33109954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35896052, 27486282, 87168518, 87168474, 265010, 87168559, 265018, 22278000, 265019, 22279002, 264563, 18108351, 264906, 264907, 264448, 66712502, 264568, 264369, 264288
2969	95310957 (5937, 5938)	Novel Protein sim. GBank gi 3024743 sp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph	52646842, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331828, 264509, 264909, 52844045, 56182435, 265009, 60433438, 55812038, 21906754, 265011, 87168559, 265018, 265019, 264448, 264288, 264369, 52644229, 21906768, 21906788, 21906789, 29148784, 265020, 265021, 52644150, 264691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2970	86088071 (5939, 5940)	Novel Protein sim. GBank gi 3165407 (AC004755) - fos37502_1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2971	94196930 (5941, 5942)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		Im7	264488, 56182575, 35896286, 56994075, 29331824, 29331826, 29148489, 264508, 264905, 264907, 264112, 264910, 21908754, 87188559, 285018, 285019, 18108351, 264889, 21908765, 21906767, 21908768, 265020, 265021, 60170615, 18108364, 264628, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264564, 264567
2972	86625943 (5943, 5944)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		kinase	265017, 35895917, 265021, 33657109, 22278002, 264563
2973	91215301 (5945, 5946)	Novel Protein sim. GBank gi 2746789 (AF040642) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 264692, 33657349, 55811576, 264563
2974	91673002 (5947, 5948)	Novel Protein sim. GBank gi 788117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	18108392, 52644507, 56182575, 56181686, 22278985, 22278996, 35896286, 22278987, 22278988, 22278989, 264259, 52645080, 29331824, 29331825, 66714117, 60424289, 29331826, 29331827, 29331828, 35696052, 66712502, 264908, 52644045, 265007, 264910, 265009, 60433438, 33109954, 21908754, 55811386, 52644296, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264368, 264288, 52644229, 18108358, 21908785, 21908787, 21908788, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486262, 27486264, 35695763, 18108370, 18108376, 55810764, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87168518, 60432113, 22278000, 264482, 264487
2975	95325213 (5949, 5950)	Novel Protein sim. GBank gi 3880812 emb CAA19508  - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - HECT-domain (ubiquitin- transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85658542, 265011, 265018, 264448, 264288, 264769, 21906767, 265020, 264691, 264559, 83373044
2976	87771202 (5951, 5952)	Novel Protein sim. GBank gi 567913 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	22278988, 264908, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2977	91725254 (5953, 5954)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1  - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2978	87332059 (5955, 5956)	Novel Protein sim. GBank gl 746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - UNCLASSIFIED ROK family	22278995, 22278996, 22278997, 22278999, 264259, 60432289, 29331827, 29146499, 56182435, 265006, 265007, 265009, 60433358, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22278000, 22279002
2979	91725258 (5957, 5958)	Novel Protein sim. GBank gl 5262751[emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	complement	264488, 65274572, 56994075, 22278999, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482
2980	86296600 (5959, 5960)			
2981	87376330 (5961, 5962)			
2982	95303675 (5963, 5964)	Novel Protein sim. GBank gl 4929767[gb]AAD34144.1 AF15190 - (AF151907) CGI-149 protein [Homo sapiens]	UNCLASSIFIED	265009, 21906767, 263981, 22279000, 264628, 264564
2983	91725258 (5965, 5966)	Novel Protein sim. GBank gl 5262751[emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264598, 33657084, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 18108365, 33657182, 33657349, 35696423, 83373044, 22279000, 22279002
2984	94136467 (5967, 5968)	Novel Protein sim. GBank gl 2393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:gl130619) [Homo sapiens]	ATPase_associated	60424179, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52644045, 265006, 60431735, 87168474, 265018, 265019, 18108351, 264448, 21906765, 21906768, 35695917, 33657023, 52645129, 18108370, 35696423, 83373044, 56526486, 60432113, 264404, 22279002
2985	87099072 (5969, 5970)	Novel Protein sim. GBank gl 103160[pir]S22126 - (finger protein unkempt - fruit fly (Drosophila melanogaster))	UNCLASSIFIED	264910, 55812038, 56181582, 55811957, 264628, 55810764, 264632, 264635, 60432113
2986	86284881 (5971, 5972)			
2987	86455934 (5973, 5974)		UNCLASSIFIED	55811957, 264566, 264369

2988	95357753 (5975, 5976)	Novel Protein sim. GBank gi 4678028 gb AAD27002.1  - (AF077207) HSPC021 (Homo sapiens)	UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 22278997, 22278998, 284092, 284094, 264259, 60432048, 29331824, 29331826, 60432289, 35698052, 29331828, 284107, 264905, 264907, 264908, 68712502, 284828, 264909, 56182435, 265006, 265007, 265008, 60170831, 60432228, 284593, 60433358, 284757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 284682, 264448, 264389, 284288, 264685, 52644228, 21806765, 21906767, 21906789, 35895917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810784, 65274791, 35695855, 284635, 284636, 284637, 263981, 264638, 58182323, 83373044, 60432113, 22279000, 284563, 264584, 264565, 264588, 284567, 22278996, 22278997, 284905, 264511, 80170831, 264583, 265019, 21906765, 21906767, 21906788, 18108374, 265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gi 113671 sp P23984 ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII	kinase	264563
2990	87330444 (5978, 5980)	Novel Protein sim. GBank gi 2829836 sp P97348 RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - Ras family	264259, 265019, 264688, 18108385, 264488, 29331822, 265017, 264761, 21906769, 65274781, 263981, 264365, 22278994, 22278995, 56994075, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 33657023, 284693, 35695855, 83373044, 18108385, 22279000, 284585, 264586, 264905, 264907, 265019, 18108351, 264683
2991	94325361 (5981, 5982)		UNCLASSIFIED	
2992	85425164 (5983, 5984)		UNCLASSIFIED	
2993	94325363 (5985, 5986)		UNCLASSIFIED	
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gi 2498549 sp Q50658 YU02_MYCTU - HYPOTHETICAL 28.7 KD PROTEIN CY339.02	transport	
2995	87591070 (5988, 5990)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		
2996	91013798 (5991, 5992)	Novel Protein sim. GBank gi 2829912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - helicase DEAD/DEAH box helicase	55274572, 35698286, 284259, 29331824, 35698052, 29146499, 284508, 284907, 265007, 265008, 60433438, 18108348, 265017, 284681, 284683, 264288, 284766, 284769, 264689, 35695917, 60170615, 33657023, 284692, 284634, 284555, 18108381, 18108382, 18108388, 264484

2997	87627440 (5993, 5994)	Novel Protein sim. GBank gij4589652[dj]BAA76848.1] - (AB023221) KIAA1004 protein [Homo sapiens]		homeobox	264488, 56182575, 264259, 66714117, 29331826, 35696052, 264508, 264509, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518, 52846365, 22278997, 264508, 264908, 18108351, 21906765, 21906767, 18108370, 18108374, 35696423, 264636, 264639
2998	88095381 (5995, 5996)	Novel Protein sim. GBank gij3947589[emb]CAA22252] - (AL034364) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278996, 29147620, 29331825, 29146498, 29146499, 264905, 66712502, 265006, 265009, 21906754, 85858542, 18108351, 29146627, 29146629, 60170615, 33657109, 27486262, 18108370, 18108374, 264556, 264557, 264558, 60170394, 18108385, 264563
2999	94847055 (5997, 5998)	Novel Protein sim. GBank gij115408[sp]P18835[CC]19_CAEEL - CUTICLE COLLAGEN 19		UNCLASSIFIED	264488, 22278997, 22278999, 264259, 29331822, 29331824, 35696052, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 265008, 265009, 264910, 33657402, 264757, 264595, 264596, 264758, 21906754, 265011, 264600, 265017, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21906765, 21906768, 35695917, 265020, 264691, 264692, 33657023, 264693, 33657109, 33657182, 27486261, 264628, 264628, 18108374, 18108376, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20798451, 22279002, 264563, 264486, 264567
3000	95099370 (5999, 6000)	Novel Protein sim. GBank gij1163174 (U32575) - similar to yeast Sec6p. Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]		UNCLASSIFIED	18108394, 52846842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52644286, 265017, 265019, 264288, 265020, 265021, 52644150, 264692, 35695763, 55810764, 35696423, 56182323, 18108387, 264563, 264564
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gij2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g844442), AA158721 (NID:g1733515), R58640 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]		calthepsin	264488, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264510, 265009, 21906754, 264682, 264688, 33657023, 264565
3002	87718167 (6003, 8004)	Novel Protein sim. GBank gij3599478 (AF085185) - Myosin-IA [Acanthamoeba castellanii]		UNCLASSIFIED	



3003	86848079 (6005, 6006)	Novel Protein sim. GBank gij1754969 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - collagen Collagen triple helix repeat (20 copies)	264512, 264593, 264584, 264567, 264486
3004	88066876 (6007, 6008)	Novel Protein sim. GBank gij2224629[dj]BAA208021 - (AB002342) KIAA0344 [Homo sapiens]		29331830, 21906769, 264601, 33657108, 293972, 18108385
3005	87794843 (6008, 6010)	Novel Protein sim. GBank gij4880659[g]b AAD27719.1 AF13294 - (AF132944) CGI-10 protein [Homo sapiens]	Contains protein domain (PF01360) - oxygenase Monooxygenase	29331822, 29331824, 29331827, 60433438, 265011, 265019, 21908766, 21908787, 21908788, 265020, 33657023, 33657349, 60170394, 22279002, 264587
3006	87422224 (6011, 6012)	Novel Protein sim. GBank gij3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - MHC Ank repeat	264259, 29331822, 264512, 21908754, 265018, 264687, 21908765, 264691, 264555, 264556, 264558, 18108385
3007	90936005 (6013, 6014)	Novel Protein sim. GBank gij2565052 (U80736) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - zinc finger, C2H2 type	52644507, 52645156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170615, 18108374, 20281152, 264635, 52644332
3008	80416249 (6015, 6016)			264505, 264593, 264766, 264636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank gij3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - synthase AMP-binding enzyme	52646842, 56182575, 22278995, 22278986, 264259, 29331825, 29331826, 29331827, 29331828, 35698052, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264757, 264758, 55812038, 264759, 33109954, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264760, 18108351, 264288, 264368, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 264891, 18108368, 27486282, 20281149, 18108370, 55811576, 264637, 264556, 264557, 18108381, 264558, 56182323, 264558, 18108385, 18108386, 22279002, 264488
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gij4927370[g]b AAD33084.1 AF06797 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01823) - Protein of unknown function	UNCLASSIFIED 264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108384, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 264909, 55811576, 35695955, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264584, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gij5052319[g]b AAD38501.1 AF11883 - (AF118838) citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	35695052, 56182435, 264758, 21906754, 265018, 264760, 264762, 18108351, 264682, 264448, 21906766, 65274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)		UNCLASSIFIED	263972

3013	91238789 (6025, 6026)	Novel Protein sim. GBank gi 3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	264488, 263994, 35696286, 22278997, 264259, 29331824, 60424269, 66714117, 35696052, 264905, 264906, 264907, 264908, 264909, 56182435, 264511, 264512, 264910, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21906754, 265010, 265018, 264604, 264760, 264682, 264683, 264764, 264369, 264288, 264765, 264766, 264686, 264768, 264687, 21906767, 35695917, 265020, 33657023, 264692, 264693, 33657109, 264628, 264629, 55811578, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264563, 264585, 264566, 264587
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gi 3878374 emb CAA93081  (Z68879) Similarity to Yeast Chi12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33316 comes from...		ATPase_associated	264760
3015	86995468 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331828, 264906, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264564
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gi 1168819 sp P41733 CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	5264507, 52846842, 56994075, 52845080, 29331822, 29331824, 35696052, 33656970, 52644045, 264596, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 35695855, 87168518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gi 4589658 dbj BAA76851.1  (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278996, 35696286, 22278999, 264259, 29331822, 60432289, 264908, 29331830, 264909, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52646317, 21906754, 55811386, 265010, 265011, 87168559, 265017, 265018, 265019, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 65274620, 52645129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52644332, 83373044, 18108385, 18108388, 56526486, 87168518, 264404, 60432113, 22279000, 264567

3018	11073891 (6035, 6036)				264558	
3019	94148231 (6037, 6038)	Novel Protein sim. GBank gj3219332 (AC004020) - Unknown gene product (Homo sapiens)			264569, 52844507, 18108394, 65274572, 5618575, 22278994, 22278995, 56894075, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264908, 58182435, 285007, 265009, 60432229, 264593, 60433356, 55812038, 21906754, 87168474, 265011, 87168559, 285017, 285018, 285019, 264681, 18108351, 284448, 264682, 264683, 18108354, 264685, 264687, 264688, 21906766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52845129, 33657349, 264629, 65274791, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 264563	oncogene
3020	94318251 (6039, 6040)	Novel Protein sim. GBank gj3414809 (AF061629) - rjs [Mus musculus]	Contains protein domain (PF00415) - ATPase associated Regulator of chromosome condensation (RCC1)		264488, 263994, 35696286, 264259, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264783, 264784, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 264488	ATPase associated
3021	80478512 (6041, 6042)	Novel Protein sim. GBank gj3880889 (emb) (CAB09005) - (Z95559) cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL:C13455 comes from this gene; cDNA EST yk329g8.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			22279000, 22279002, 264563	
3022	87718500 (6043, 6044)				264769, 264629, 264482	
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gj416592 (sp) P32333JAG1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED	264259, 29331826, 29331828, 264288, 264566	
3024	86675305 (6047, 6048)			UNCLASSIFIED	264488, 22278995, 35696286, 22278997, 29331826, 35696052, 264907, 29331830, 52844045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21906767, 55811957, 35695917, 265021, 18108376, 263978, 264635, 264558, 22279000	
3025	65706629 (6049, 6050)	Novel Protein sim. GBank gj295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	60432049, 264760, 21906769, 55811957, 35695917, 264690, 264555, 264559, 264593, 55811576	

3026	87643662 (6051, 6052)	Novel Protein sim. GBank gi 3024052 sp P97924 KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87168559, 265019, 21906765, 29148627, 263957, 20281149, 20281069, 263975, 263977, 20281071, 56526486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gi 4929647 gb AAD34084.1 AF15184 - (AF151847) CGI-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264769, 264688, 21906765, 21906766, 21908767, 21908768, 21908769, 29148629, 35695917, 265020, 265021, 265022, 52644150, 264692, 33657023, 264693, 52645129, 33657109, 27486281, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56526486, 22279000, 22279002
3028	94231897 (6055, 6056)	Novel Protein sim. GBank gi 3080521 emb CAA18650  - (AL022598) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 284762, 264683, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33657109, 27486285, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264564
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 284534, 264690, 264693, 263969, 18108370, 264558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim. GBank gi 3757726 emb CAA18782  - (AL022727) dJ80119.1 (olfactory receptor-like protein [Hs6M1-1]) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	im7	
3031	91677853 (6061, 6062)	Novel Protein sim. GBank gi 4530587 gb AAD22105.1  - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331828, 29331827, 29331828, 35696052, 264908, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 56526486, 22279000, 22279002

3032	94130124 (6063, 6064)	Novel Protein sim. GBank gij1019951 (U37429) - similar to M. musculus MERS and other AHPCT/SA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - synthase Glycosyl transferases group 1	22278996, 35696286, 264259, 29331824, 29331828, 264907, 29331830, 264758, 33109954, 87168474, 87168559, 265019, 264288, 21808789, 265021, 264693, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gij5031573refJNP_005712.1lpACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - struct Actin	35696286, 264259, 29331826, 35696052, 264508, 264905, 264806, 264907, 264908, 264909, 265008, 264581, 21808754, 265010, 265019, 264681, 264388, 264788, 21808784, 21808768, 35695917, 33657023, 264628, 35695855, 264632, 264635, 264638, 264482, 264563
3034	80415373 (6067, 6068)		UNCLASSIFIED	264906, 264907, 264510, 264592, 265010, 264782, 264788, 264637, 264638, 264488, 264636
3035	91220692 (6069, 6070)	Novel Protein sim. GBank gij3738207lembjCAA212621 - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]	UNCLASSIFIED	
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gij728837ispP39194JALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III	kinase	264907, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gij4406590jgbjAAD200401 - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]		265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gij5360093jgbjAAD2865.1jAF15509 - (AF15509) NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UNCLASSIFIED	22278996, 22278997, 264259, 264905, 265007, 265009, 60433356, 21808754, 265018, 265019, 18108351, 264687, 21808785, 265020, 265021, 65274620, 27486262, 264636, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gij475712lembjCAB42094.1j - (AJ238717) ZRP protein [Rattus norvegicus]	UNCLASSIFIED	35696286, 29331828, 264109, 264110, 264511, 265007, 21808754, 265011, 264681, 264683, 264687, 21808768, 264681, 18108370, 263972, 264629, 18108374, 263977, 35696423, 264564, 18108391, 264692, 264558, 18108382, 18108385, 264587
3040	90933517 (6079, 6080)	Novel Protein sim. GBank gij4884278lembjCAB43247.1j - (AL050037) hypothetical protein [Homo sapiens]		
3041	88312357 (6081, 6082)	Novel Protein sim. GBank gij3876073lembjCAB04122.1j - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...	UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 35659970, 33108954, 21808754, 87168559, 264600, 264683, 21808765, 21808768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gij790236 (U21156) - sarcolemmal associated protein-2 [Oryctolagus cuniculus]	glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X63413) U88 [Human herpesvirus 6]		UNCLASSIFIED	35698286, 60424269, 35696052, 264508, 264805, 66712502, 56182435, 55811388, 52644296, 55811150, 35695917, 60170615, 33657109, 18108374, 264834, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gi 4104922 (AF042276) - o251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) ubiE/COQ5 methyltransferase family	glycoprotein	22278998, 22278998, 22278999, 29331824, 56182435, 264511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108388, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gi 4589680 dbj BAA76859.1  - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00096) Zinc finger, C2H2 type	dna_rna_bind	264488, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264909, 264511, 265006, 264591, 264593, 33109954, 264604, 264764, 264683, 264288, 264766, 264768, 21906765, 21906768, 55811957, 35695917, 27486262, 18108370, 264628, 18108374, 35695855, 264830, 264632, 264635, 264563, 264564, 264566
3046	88089247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 52646317, 55811957, 60432113, 22279000, 22279002, 264482, 264564
3047	95089924 (6093, 6094)			UNCLASSIFIED	264488, 22278996, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264766, 21906768, 21906769, 35695917, 52644150, 33657349, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank gi 4588034 gb AAD25962.1 AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	284102, 29148784
3049	88228955 (6097, 6098)	Novel Protein sim. GBank gi 5454158 ref NP_006286.1 pVARS - vavl-IRNA synthetase 1	Contains protein domain (PF01406) IRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 264907, 264758, 87168559, 265018, 264448, 21906768, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643679 (6099, 6100)	Novel Protein sim. GBank gi 4589642 dbj BAA76843.1  - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265019, 264288, 21906768, 265020, 264693, 18108385, 56526486, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)				22278997, 264595, 265019, 264288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gi 117528 sp P14755 CRYL_RABIT - LAMBDA-CRYSTALLIN		dehydrogenase	264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gi 3947613 emb CAA19465.1 - (AL023828) cDNA EST EMBL:M89008 comes from this gene: cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21908754, 265010, 87188559, 264603, 265018, 265019, 264763, 264764, 264288, 21908765, 21908766, 21908768, 21908769, 35695917, 18108374, 35696423, 264638, 56182323, 22279000, 264563
3054	86943510 (6107, 6108)	Novel Protein sim. GBank gi 1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35698286, 35696052, 28331830, 264908, 264909, 264512, 264810, 265017, 264604, 264766, 265020, 33657109, 284628, 35695955, 264638, 284584, 264566, 264488
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gi 4880655 gb AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	60424179, 65274572, 56182575, 35696286, 22278996, 22278998, 60432049, 264259, 60424269, 60432289, 35696052, 56182435, 265006, 265009, 60170831, 60432229, 60431735, 60433356, 284594, 60433438, 21908754, 55811386, 265011, 87188559, 265019, 18108351, 264683, 284288, 264369, 264689, 21908768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810764, 55811576, 35696423, 65274791, 264638, 60431850, 18108381, 56182323, 60170384, 18108385, 60432113, 264564, 264565, 264586
3056	91681636 (6111, 6112)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7 SQ WARNING ENTRY IIII		glycoprotein	264488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331828, 29331827, 35696052, 264508, 264509, 264805, 264806, 264807, 264808, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264769, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 264681, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695955, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264583, 264584, 264585, 264566, 264486, 264567

3057	95412746 (6113, 6114)	Novel Protein sim. GBank gi 3878119 emb CAA8860  - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...			264508, 264905, 264807, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264767, 18108374, 264635, 264555, 264637, 264639, 264563, 264564, 264565, 264488
3058	78646226 (6115, 6116)	Novel Protein sim. GBank gi 458034 gb AAD25962.1 AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264693
3059	87629425 (6117, 6118)	Novel Protein sim. GBank gi 458034 gb AAD25962.1 AF092878) zinc RING finger protein SAG [Homo sapiens]	Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264490, 264259, 29331824, 29331825, 29331827, 35696052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906769, 29148629, 29148784, 265022, 52644150, 18108370, 264636, 18108385, 264563, 264567
3060	79346691 (6119, 6120)			UNCLASSIFIED	264567
3061	87740964 (6121, 6122)			UNCLASSIFIED	264112, 52644296, 21906768, 33657023, 263974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gi 4454690 gb AAD20963  - (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 (Kaposi's sarcoma-associated herpesvirus)		UNCLASSIFIED	18108359, 264558
3064	91241526 (6127, 6128)	Novel Protein sim. GBank gi 4240315 db BAA74936.1  - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52646355, 52646842, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52644286, 265018, 264682, 264288, 264686, 264768, 264687, 52644229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811576, 264636, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gi 5656743 gb AAD45960.1 AC00506 - (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and genscan [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424269, 66714117, 264100, 264907, 265007, 264591, 60432229, 264593, 265011, 265019, 18108351, 264766, 264767, 21906765, 21906768, 264693, 20281069, 22279000, 22279002, 264482, 264566, 264567



3066	91224437 (6131, 6132)	Novel Protein sim. GBank gi 4884268 emb CAB43245.1 - (AL050028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278998, 264905, 66712502, 265006, 264512, 264910, 264756, 60174639, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264567
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gi 4689258 gb AAD27632.1 AF121859 sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	struct	264488, 264489, 35696286, 22278998, 56994075, 264259, 29331822, 29331825, 35696052, 29331828, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265010, 265011, 87168559, 264601, 264602, 264603, 264604, 264605, 265018, 264760, 264762, 264448, 264763, 264764, 264288, 264369, 264766, 264768, 264687, 264768, 264689, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 264534, 52644150, 264691, 33657023, 264693, 264628, 60431528, 283977, 35695855, 284630, 264631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264567, 264486
3068	85360651 (6135, 6136)				264112
3069	95412753 (6137, 6138)	Novel Protein sim. GBank gi 3878119 emb CAA88860  - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...	Contains protein domain (PF01826) - GTPase of unknown function	struct	22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 29331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109954, 87168474, 87168559, 265017, 264448, 264764, 264683, 264768, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56182323, 18108385, 87168518, 22279000, 264482

3070	94319173 (6139, 6140)	Novel Protein sim. GBank gi 3877788 emb CAB05527  - (283110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...		synthase	264488, 22278994, 22278995, 22278996, 56894075, 22278997, 22278999, 264259, 29331822, 29147620, 29331824, 66714117, 29331826, 29146488, 29146499, 66712502, 29331830, 52644045, 58182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33109954, 21906754, 87168474, 265019, 18108351, 264448, 264683, 264288, 52644229, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35695855, 264634, 264635, 18108381, 60170394, 558182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gi 4502425 ref NP_001709.1 pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Igl Thioedoxin	lgf	264488, 55274572, 18108398, 22278996, 35695828, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35695052, 29331828, 29146488, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 264592, 60433356, 33657402, 60433438, 33109954, 52644296, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 55274791, 35695855, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264584, 264565, 264566, 264567
3072	95115892 (6143, 6144)	Novel Protein sim. GBank gi 1263289 (U47856) - fibronin-4 (Araneus diadematus)		transcriptfactor	56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 55274791, 264555, 56182323, 60432113, 284564

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gi 134840 sp P22528 CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gi 3419847 AC004982 - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21908767, 264893, 18108388, 18108370, 18108374, 264567
3075	88095752 (6149, 6150)	Novel Protein sim. GBank gi 4557349 ref NP_000456.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264899, 264893, 56526486
3076	87819219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264691, 264693
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gi 3023956 sp Q00808 HET1_PODAN - VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 35696032, 284511, 60170831, 87168474, 264369, 35695917, 33657182, 27486264, 33657349, 35695763, 35695855, 264639
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gi 3900850 AC004994 - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22279002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gi 3875410 emb CA02876  - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52844229, 21908768, 265020, 265021, 264893, 18108376, 264631, 52644332, 22279002
3080	95298274 (6159, 6160)	Novel Protein sim. GBank gi 525722 gb AA041265.1  - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278996, 22278998, 264490, 264259, 29331824, 68714117, 29331825, 29331826, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 56182435, 265006, 264591, 264596, 21908754, 60174639, 265010, 264682, 264448, 264763, 264683, 264784, 264288, 264685, 264769, 264688, 264689, 21908765, 21908767, 21908769, 55811857, 35695917, 265020, 60170615, 52844150, 264692, 33657023, 264693, 65274620, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264565, 264484
3081	88094864 (6161, 6162)	Novel Protein sim. GBank gi 72883 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	18108398, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264595, 264758, 265011, 285018, 264760, 264761, 264763, 264764, 18108354, 264885, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264566
3082	80310121 (6163, 6164)				264764, 55811857, 264555, 264564

3083	88095756 (6165, 6166)	Novel Protein sim. GBank gi 888241 (U29488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906754, 264288, 264767, 21906788, 21906769, 29148784, 264691, 264632, 22279000
3084	87448588 (6167, 6168)	Novel Protein sim. GBank gi 476774 pir J37475 - probable structural component p38 - borna disease virus			22278995, 60432289, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264593, 264595, 264758, 264369, 264288, 264766, 35695917, 265020, 18108374, 35696423, 264631, 284556, 264585, 264586, 264567, 264486
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gi 2565057 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	265011, 264681
3086	87769942 (6171, 6172)	Novel Protein sim. GBank gi 3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263987, 263974, 55810764, 263981, 18108365, 264487
3087	87462988 (6173, 6174)				52646365, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21906754, 52646317, 265017, 264682, 264369, 264684, 21906767, 21906768, 265020, 264691, 33657023, 33657109, 52645129, 33657182, 27488262, 35695855, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gi 3355304 (AF001549) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gi 4689146 gb AAD27782.1 AF07704 - (AF077049) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	dehydrogenase	18108397, 65274572, 56182575, 56181686, 56994075, 35696286, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21906754, 55811386, 265017, 265018, 265019, 264760, 55811150, 264288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170815, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 264486

3090	95342371 (6179, 6180)	Novel Protein sim. GBank gi 1354050 (U47024) - MEM3 (Mus musculus)	UNCLASSIFIED	50424179, 52645156, 65274572, 56182575, 56181688, 22278995, 35698286, 56994075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696032, 33858970, 264908, 264908, 52644045, 264828, 265006, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264758, 21906754, 33109854, 52646317, 55811386, 52644298, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264369, 18108357, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170815, 264690, 52644150, 264691, 33657023, 18108365, 65274620, 33657109, 18108368, 33657182, 27486261, 27486285, 35695763, 18108374, 18108376, 55810784, 35698423, 55811578, 65274791, 35695855, 264557, 56182323, 93373044, 18108387, 18108388, 87168518, 22278000, 22278002, 264583, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gi 3873932 emb CAB01859  - (Z79598) Similarity to Bovine asparyl beta hydroxylase (TR:G162694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68139 comes f...	UNCLASSIFIED	35698286, 29331822, 35696032, 264508, 264509, 264905, 264908, 264908, 264909, 264510, 264758, 265010, 265011, 264683, 264885, 264768, 264768, 264768, 264769, 264893, 264828, 35698423, 35695855, 264632, 264635, 264639, 264482, 264563, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gii1710756[sp]P15880[RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)]	Contains protein domain (PF00333) - ribosomal prot Ribosomal protein S5	264488, 60424179, 18108396, 22278995, 56994075, 22278996, 35896288, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 284909, 284113, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264591, 264592, 60431735, 264593, 264594, 60433438, 264595, 264758, 21906754, 265010, 265011, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 265019, 264760, 264762, 264681, 18108351, 264763, 264682, 264448, 264764, 264683, 264288, 264369, 264765, 264766, 264686, 264767, 264687, 264768, 264769, 264688, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 29148784, 35695917, 265020, 265021, 264534, 60170815, 264690, 264691, 264692, 65274620, 33657109, 27486262, 264628, 264629, 18108374, 263978, 18108377, 35696423, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264557, 264558, 264639, 60170394, 18108385, 264259, 29331824, 35696052, 264905, 265006, 60432229, 60431735, 264684, 264369, 264288, 264766, 21906767, 35696423, 83373044, 18108385
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gii5002587[emb]CAB44347.1]- (Y17454) LSFR1 protein [Homo sapiens]	UNCLASSIFIED	18108398, 264259, 60432289, 29331827, 264511, 264763, 264288, 264767, 265022, 264691, 264693, 65274791, 56182323, 264584, 264585
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gii400734[sp]P31044[PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN)] (P23K)	Contains protein domain (PF01161) - collagen protein	

3095	94848162 (6189, 6180)	Novel Protein sim. GBank gi 4677759 gb AAD31421.1 AF12444 - (AF124440) MAGE (tumor antigen D1 [Homo sapiens])	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 33656970, 29146499, 264508, 264905, 264509, 29331830, 264809, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264764, 264368, 264288, 264886, 264768, 264769, 264689, 21908785, 21908768, 21906787, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33857023, 264693, 263972, 18108376, 55811576, 35696423, 264952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gi 3882221 dbj BAA34470.1  - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - struct Calponin homology (CH) domain		22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33857402, 265011, 265017, 265018, 264369, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486282, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566
3097	88264895 (6193, 6194)	Novel Protein sim. GBank gi 4468288 emb CAB37981  - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	284488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21806765, 21908767, 18108378, 35696423, 52644332, 264638, 60432113, 22279002
3098	80258024 (6195, 6196)				264634, 264637, 264565
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gi 303603 dbj BAA02145.1  - (D12621) cytochrome P-450LTV [Homo sapiens]		Cyto450	264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22279002, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank gi 1083764 pir B48013 - proline- rich proteoglycan 2 precursor, parotid - rat		UNCLASSIFIED	29331825, 60432288, 35696052, 264910, 60432229, 264592, 264288, 264693, 263967, 264635
3101	79602134 (6201, 6202)			UNCLASSIFIED	264908, 264693, 264628, 264630, 264632

3102	91220892 (6203, 6204)	Novel Protein sim. GBank gi 5305706 gb AAD41781.1 AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	SH3 domain	3569286, 22278996, 22278999, 29331827, 35695052, 264909, 264512, 265008, 60170831, 60433356, 33109954, 18108351, 264684, 264689, 21906767, 60170515, 264692, 33657023, 264638, 22279000, 264482, 264564
3103	90938004 (6205, 6206)	Novel Protein sim. GBank gi 64564 sp P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17	UNCLASSIFIED	UNCLASSIFIED	35695917, 264565
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gi 5032207 ref NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6	UNCLASSIFIED	UNCLASSIFIED	264259, 264684, 264532, 33657182, 264558
3105	94148603 (6208, 6210)				22278997, 264259, 29331824, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22279002, 264563, 264565, 264566, 264486, 264567
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gi 1938574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264906, 264907, 264908, 32644045, 56182435, 264112, 265008, 265009, 55812038, 265017, 285018, 264683, 264686, 264687, 264768, 52644229, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gi 3341441 emb CAA768511 - (Y17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265009, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906766, 21906767, 21906769, 265021, 264691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811578, 18108385, 56526486, 264482, 264487
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gi 5032207 ref NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6	UNCLASSIFIED	UNCLASSIFIED	56182435, 264288, 264690, 264564



3109	94318461 (6217, 6218)	Novel Protein sim. GBank gl 5002587 emb CAB44347.1  - (Y17454) LSFRI protein [Homo sapiens]	Contains protein domain (PF000096) - struct Zinc finger, C2H2 type	264480, 264908, 265007, 264910, 264593, 264883, 264884, 264687, 21908767, 21908768, 264693, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95090716 (6218, 6220)	Novel Protein sim. GBank gl 1076211 pir IS50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii	UNCLASSIFIED	264488, 65274572, 22278995, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264908, 264510, 265008, 265007, 265008, 265009, 60432228, 33857402, 60433356, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264288, 264369, 21906766, 21906787, 21906768, 265020, 60170615, 264693, 65274620, 18108370, 264638, 18108384, 22278000, 264563, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gl 3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF000096) - transcript factor Zinc finger, C2H2 type	264488, 18108388, 66712502, 265017, 265018, 265019, 264448, 21908767, 265020, 33857023, 18108385, 18108388, 35696423, 52844332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gl 3900848 (AC005023) - match to EST AA381117 (NID,g2013436) [Homo sapiens]	Contains protein domain (PF00046) - homeobox	
3113	88207098 (6225, 6226)	Novel Protein sim. GBank gl 2459910 (AF005856) - anon2A5 [Drosophila yakuba]	Homeobox domain	18108397, 22278999, 264259, 29331824, 35898052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21906767, 21906768, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22279000, 22278002, 264909, 56182435, 264910, 21906754
3114	79843167 (6227, 6228)	Novel Protein sim. GBank gl 4986270 gb AAB52261.2  - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1 [C...]	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	
3115	94117886 (6228, 6230)	Novel Protein sim. GBank gl 5032225 ref NP_005676.1 pWBSC - Williams-Beuren syndrome chromosome region 11	transcript factor	60424179, 56182575, 264259, 29331824, 60424269, 29331826, 66712502, 264510, 265007, 60431735, 60433356, 55812038, 55811386, 265019, 264288, 264689, 21906789, 264691, 33857023, 264693, 60431528, 263974, 80431850, 56182323, 264558, 22279000, 22278002
3116	79842855 (6231, 6232)		UNCLASSIFIED	264905, 264758, 21906764, 264690
3117	87771288 (6233, 6234)		UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264691, 18108368, 18108372, 263981, 264558, 264564

3118	94665848 (6235, 6236)	Novel Protein sim. GBank gi 3880563 emb CAB01444.1  - (Z78018) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - EGF-like domain	52645156, 52646842, 65274572, 56182575, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 264905, 264908, 29331830, 52644045, 56182435, 264510, 264511, 265007, 265008, 265009, 264757, 52646317, 21806754, 33657084, 52644298, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 284448, 264682, 264684, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264690, 52644150, 264691, 33657023, 264693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35696423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264486, 265006, 264288
3119	85728796 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase	UNCLASSIFIED
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gi 5019819 gb AAD37863.1 AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]		264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gi 4501877 ref NP_001088.1 pACR1 - acrosin		52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)			264638
3123	88063003 (6245, 6246)	Novel Protein sim. GBank gi 2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID: g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87786898 (6247, 6248)			264905
3125	81216607 (6249, 6250)	Novel Protein sim. GBank gi 4980826 gb AAD35412.1 AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	56181686, 264259, 66714117, 60432289, 29331826, 29331827, 264907, 264908, 264828, 265009, 60433356, 33657402, 60433438, 264758, 18108351, 264288, 28148627, 29148628, 33657023, 33657109, 18108382, 56526486

3126	95337205 (6251, 6252)			UNCLASSIFIED	22278989, 264490, 264259, 60432049, 29331822, 60432289, 29146498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264389, 264685, 29146629, 33657023, 264693, 33857109, 18108374, 55811576, 18108385, 60432113, 22279002, 35656266, 22278996, 22278999, 29331828, 264908, 60433438, 87168559, 264604, 21906765, 21906769, 33657023, 33857349, 264629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gi 2828280 emb CAA16694.1  - (AL021687) putative protein [Arabidopsis thaliana]			
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gi 3865828 (AF090133) - lin-7-A [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	misc_channel	22278996, 264259, 52644045, 265008, 21906754, 265017, 265018, 21906768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gi 3135273 (AC003056) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 264259, 29331825, 29331828, 52644045, 56182435, 60433356, 264600, 264682, 264763, 264764, 264369, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 284584, 264566, 264636
3130	14993960 (6259, 6260)	Novel Protein sim. GBank gi 3329465 (AF064553) - NSD1 protein [Mus musculus]			
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gi 1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331824, 264807, 56182435, 264594, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 264448, 264766, 21906769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486281, 33657349, 65274791, 60170394, 56182323, 83373044, 87168518, 264584

3132	95415459 (6263, 6264)	Novel Protein sim. GBank g j4680647 gb AAD27713.1 AF13293 - (AF132938) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52644507, 52646842, 52646365, 65274572, 56182575, 22278994, 22278995, 35698286, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 52644045, 56182435, 264910, 60170831, 60432229, 60433356, 33657402, 55812038, 52646317, 21908754, 52644286, 85658542, 87168559, 265017, 265018, 265019, 264448, 264288, 264369, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 264892, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56526486, 87168518, 60432113, 22279002
3133	87379414 (6265, 6266)	Novel Protein sim. GBank g j4507613 e NP_003738.1 pTNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265006, 265007, 87168559, 264760, 21906767, 18108374, 22279000, 22279002, 264563 264595, 264369, 264685, 264628, 264568
3134	94649816 (6267, 6268)	Novel Protein sim. GBank g j1729827 sp P54633 TALA_DICDI - FILOPODIN (TALIN HOMOLOG)			
3135	86389356 (6269, 6270)	Novel Protein sim. GBank g j3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]		struct	22278998, 264095, 29331826, 33657402, 18108348, 263974
3136	94845839 (6271, 6272)	Novel Protein sim. GBank g j627101 p j S44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264769, 264689, 265020, 27486262, 263972, 65274791, 264557, 264558
3137	88257847 (6273, 6274)	Novel Protein sim. GBank g j3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331828, 29331827, 29331828, 264510, 265008, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264769, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264486

3138	94130186 (6275, 6276)	Novel Protein sim. GBank gij4406759jgbjAAD20070j - (AC006836) hypothetical protein (Arabidopsis thaliana)			264569, 264488, 264907, 264511, 264593, 33109954, 87188559, 264881, 264884, 264685, 264688, 264687, 264768, 264688, 264688, 264691, 264692, 264693, 33857109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 60432113, 22278900, 22278902
3139	87325503 (6277, 6278)	Novel Protein sim. GBank gij228938jprfj1814452C - Hyp-rich glycoprotein [Zea diploperennis]	UNCLASSIFIED		22278997, 22278998, 22278999, 264905, 265018, 265019, 21908765, 265020, 264636, 264557
3140	91222682 (6279, 6280)	Novel Protein sim. GBank gij932jembCAA37773j - (X53744) 88kDa subunit of signal recognition particle [Canis familiaris]	siRNA		22278995, 56894075, 35696286, 264908, 264809, 60433356, 21908754, 52644296, 87188474, 87188559, 264683, 264288, 264685, 264686, 265022, 264693, 27486282, 35695855, 264630, 264555, 264556
3141	87323584 (6281, 6282)	Novel Protein sim. GBank gij3213227 (AF035209) - putative v-SNARE Vti1a [Mus musculus]	UNCLASSIFIED		56182575, 35696286, 28331828, 264909, 265009, 265018, 18108351, 284389, 21908766, 29148627, 265020, 264628, 264628, 264631, 18108385
3142	85419028 (6283, 6284)	Novel Protein sim. GBank gij2498197jspiQ95245jC561_PIG - CYTOCHROME B561 (CYTOCHROME B-561)	cytochrome		52645158, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 28331822, 29331824, 29331827, 29146409, 56182435, 265007, 80170831, 60432229, 33657402, 264595, 60433438, 264758, 21908754, 264288, 264766, 264687, 52644229, 21908765, 21908767, 21908768, 60170815, 52644150, 63274620, 33657109, 35695763, 18108370, 18108376, 85274781, 35695855, 264631, 264557, 87168518, 60432113, 22278900
3143	95351475 (6285, 6286)	Novel Protein sim. GBank gij5420387jembCAB46679.1j - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		264488, 56182575, 22278996, 22278998, 22278999, 29331822, 29331824, 60432289, 35696052, 28331828, 264508, 264905, 264908, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 285008, 264910, 60432229, 33657402, 60433356, 60433438, 55812038, 265011, 265019, 264760, 264763, 264448, 264764, 264884, 264288, 264685, 264686, 264768, 264889, 21908765, 21908766, 21908767, 35695917, 264690, 33657023, 264693, 263987, 33657109, 264628, 264629, 18108374, 263976, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 60432113, 22278900, 22278902, 264563, 264566, 264488

3144	85336329 (6287, 6288)	Novel Protein sim. GBank gij4884468[emb](CAB43322.1) - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108396, 22278996, 35696286, 22278997, 22278998, 29331826, 29331827, 35696052, 29331828, 264108, 265006, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21906765, 21906766, 21906767, 285020, 265021, 52844150, 27486281, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 284567
3145	86611657 (6289, 6290)	Novel Protein sim. GBank gij3878709[emb](CAB03330) - (Z81118) Similarity to Human endosomal protein P162 (TRQ15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from l...	UNCLASSIFIED		18108397, 29331824, 29146499, 20281100, 265006, 55812038, 265010, 21906766, 29148627, 21906769, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87168518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gij2135746[pir](S69890) - mitogen Inducible gene mig-2 - human	Contains protein domain (PF00169) - PH domain	struct	264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 284448, 264369, 21906766, 265021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 264564
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gij3874279[emb](CAB07315.1) - (Z92825) predicted using GeneFINDER; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	UNCLASSIFIED	56181886, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433356, 60433438, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 65274791, 284631, 56182323, 264404, 22279002
3148	95362169 (6295, 6296)	Novel Protein sim. GBank gij5225322[gb](AAD40851.1)(AF083108) sirtuin type 3 [Homo sapiens]	UNCLASSIFIED		35696288, 35696052, 264511, 85658542, 87168474, 264784, 35696423, 264555, 264556, 264557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gij4200446 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01363) - FYVE zinc finger	eph	29331822, 35696052, 264109, 29148629, 18108381
3150	87655472 (6298, 6300)	Novel Protein sim. GBank gij3378454[emb](CAA76893) - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - Glutathione S-transferases.	transferase	264259, 29331822, 29331824, 29331825, 29331827, 52846317, 284686, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gij172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	oncogene	29331822, 265008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21906754, 87168559, 264605, 21906768, 52844150, 27486264, 35696423, 22279000

3153	85317298 (6305, 6306)	Novel Protein sim. GBank gi4895041 gb AAD32705.1 AF14395 - (AF143957) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - struct WD domain, G-beta repeat		264488, 52846365, 35696286, 22278996, 22278997, 22278998, 60432049, 284259, 29331826, 60432289, 33656970, 284508, 264908, 33657402, 264595, 60433438, 87168474, 87168559, 284601, 265019, 264448, 284682, 284764, 284288, 264369, 264788, 21906765, 21906766, 21906787, 21906768, 21906769, 29148784, 265021, 265022, 60170615, 52844150, 264690, 284691, 33657023, 65274620, 33657109, 18108370, 35695855, 264638, 60170394, 87168518, 60432113, 22279000, 22279002, 22278998, 264259, 29331824, 66712502, 265008, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi4680861 gb AAD27720.1 AF13294 - (AF132945) CGI-11 protein [Homo sapiens]	ATPase-associated		264488, 52846365, 264563, 264488, 56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109854, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 284288, 264689, 21906768, 21906769, 21906769, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3155	87762394 (6309, 6310)	Novel Protein sim. GBank gi728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	UNCLASSIFIED		264488, 52846365, 264563, 264488, 56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109854, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 284288, 264689, 21906768, 21906769, 21906769, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3156	87737449 (6311, 6312)	Novel Protein sim. GBank gi5630078 gb AAD45821.1 AC00601 - (AC006017) N-acetylglucosaminyltransferase, similar to Q10473 (PID:g1709559) [Homo sapiens]	transferase		264488, 52846365, 264563, 264488, 56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109854, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 284288, 264689, 21906768, 21906769, 21906769, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3157	88259577 (6313, 6314)				264488, 52846365, 264563, 264488, 56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109854, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 284288, 264689, 21906768, 21906769, 21906769, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi5306084 gb AAD41895.1 AF15677 - (AF156778) ASB-3 protein [Homo sapiens]	kinase		264488, 52846365, 264563, 264488, 56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109854, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 284288, 264689, 21906768, 21906769, 21906769, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3159	84124114 (6317, 6318)	Novel Protein sim. GBank gi5531272 emb CAB50897.1  - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]	UNCLASSIFIED		264488, 52846365, 264563, 264488, 56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109854, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 284288, 264689, 21906768, 21906769, 21906769, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3160	80221088 (6319, 6320)	Novel Protein sim. GBank gi3930525 (AF084447) - sex-determination protein homolog Fem1a [Mus musculus]	struct		264488, 52846365, 264563, 264488, 56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109854, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 284288, 264689, 21906768, 21906769, 21906769, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002

3161	8807411 (6321, 6322)				264488, 2227895, 2227897, 2227898, 264259, 29331822, 60432269, 29331828, 52644045, 265017, 265018, 264448, 264288, 21906764, 21906767, 265020, 18108374, 264638, 264566
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (UiSMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis ,Atrial septal defect (ASD),Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (P) pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH 56.3 (Utricle)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema, Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (UIMVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer



60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenITP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RE-LIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	nQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5: 1:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen 1		

# Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences

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 <213> Homo sapiens

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 Pro Pro Pro Ile Ser Ala Ala Arg Leu Ser Arg Met Ser Leu Val Glu  
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 Arg Cys Ser Ala Ser Ala Ser Cys Ser Ala Val Leu Arg Asp Trp Ala  
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Thr Val His Lys Val Met Val Ala Glu Gly Ala Asp Ile Ala Glu Glu  
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 Tyr Arg Asp Glu Asp Ala Thr Leu Val Glu Val Asn Pro Met Ile Lys  
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 Thr Gly Asp Gly Arg Ile Leu Ala Ile Asp Gly Lys Met Thr Val Asp  
 165 170 175  
 Asn Asn Ala Ser Phe Arg Gln Pro Asp Arg Ala Gly Leu Val Asp Arg  
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 Ala Thr Thr Asp Pro Leu Glu Leu Arg Ala Gly Glu Leu Gly Leu Asn  
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 Tyr Val Lys Leu Asp Gly Asn Val Gly Val Ile Gly Asn Gly Ala Gly  
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 Pro Gly Ser Pro Ala Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala  
 245 250 255  
 Ser Ala Glu Ile Met Ala Asn Gly Leu Asp Leu Ile Met Ser Asp Glu  
 260 265 270  
 Gln Val Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys  
 275 280 285  
 Asp Gln Val Ala Leu Gly Ile Lys Gly Ala Leu Glu Lys Leu Gly Asp  
 290 295 300  
 Lys Ala Val Lys Pro Leu Val Val Arg Leu Asp Gly Asn Ala Val Ala  
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 Glu Gly Arg Lys Ile Leu Glu Glu Phe  
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&lt;211&gt; 622

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg  
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Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg  
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<213> Homo sapiens

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Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
      35           40           45
Leu Cys Ala Leu Leu Leu Phe Trp Leu Cys Val Tyr His Gly Ile Arg
      50           55           60
Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
      65           70           75           80
Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
      85           90           95
Thr Val Asn Glu Leu His Asp Pro Met Tyr Gln Tyr Arg Val Asp Thr
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<212> DNA

<213> Homo sapiens

<400> 11

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<212> PRT

<213> Homo sapiens

<400> 12

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<212> DNA
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&lt;210&gt; 14

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

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			20					25					30		
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
		35				40					45				
Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50					55				60					
Gly	Ala	Leu	Thr	Pro	Leu	Cys	Arg	Ser	Leu	Val	His	Leu	Ala	Gln	Lys
65					70					75				80	
Arg	Gln	Glu	Ala	Gly	Ala	Asp	Ala	Phe	Leu	Ile	Gln	Tyr	Asp	Ala	His

85							90							95			
Ala	Ser	Leu	Pro	Ser	Pro	Tyr	Ala	Val	Thr	Gly	Arg	Leu	Leu	Val	Val		
100							105							110			
Ser	Ser	Ser	Pro	Tyr	Leu	Gly	Asp	Gly	Arg	Gly	Ala	Ala	Ala	Leu	Arg		
115							120							125			
Leu	Leu	Ser	Val	Leu	His	Pro	Asn	Ile	His	Pro	Leu	Leu	Gly	Gln	His		
130							135							140			
Trp	Glu	Thr	Thr	Val	Pro	Leu	Leu	Gly	Tyr	Leu	Asp	Glu	His	Thr			
145							150							155			
Glu	Glu	Thr	Leu	Pro	Gln	Glu	Glu	Trp	Glu	Glu	Lys	Leu	Leu	Met	Val		
165							170							175			
Arg	Ala	Gly	Val	Arg	Pro	Ile	Leu	Gly	Leu	Lys	Val	Leu	Ser	Gly	Leu		
180							185							190			
Gly	Gly	Ala	Gly	Val	Ala	Glu	Ala	Gly	Pro	Pro	Ala	Ser	Thr	Ser	Pro		
195							200							205			
Arg	Gly	Leu	Ala	Gly	Glu	Pro	Arg	Ile	Arg	Gln	His	Gln	Gly				
210							215							220			

```
<210> 15
<211> 363
<212> DNA
<213> Homo sapiens
```

```

<400> 15
naccgcttgc tggctcgcca cggcaagggc catgtcggct gcgatatctg caagccggcg
60
gtgggttcga tccttgctc gtgctggaac cagccgatca tggacccggc gttggtgccg
120
ttgcaggaca ccaatgacac cttcatggcc aacatgcaga agaacggtac ctattcgatc
180
atcccgcgta tcgccggcgg cgagatcacc ccggacaaac tgatcgccct cggcgcggtg
240
gcgaagaaat acgatctgta caccaagatc accggcggcc agcggatcga cctgttcggc
300
gccagttgc acgaattgcc gcagatctgg ggcgagctgg tggatgccgg attcgagacc
360
ggt
363

```

```
<210> 16
<211> 121
<212> PRT
<213> Homo sapiens
```

```

<400> 16
Xaa Ala Leu Leu Ala Arg His Gly Lys Gly His Val Gly Cys Asp Ile
 1           5           10           15
Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
      20           25           30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
      35           40           45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
      50           55           60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val

```

```

65              70              75              80
Ala Lys Lys Tyr Asp Leu Tyr Thr Lys Ile Thr Gly Gly Gln Arg Ile
              85              90              95
Asp Leu Phe Gly Ala Gln Leu His Glu Leu Pro Gln Ile Trp Gly Glu
              100              105              110
Leu Val Asp Ala Gly Phe Glu Thr Gly
              115              120

```

<210> 17  
 <211> 682  
 <212> DNA  
 <213> Homo sapiens

```

<400> 17
gaattccatt ttgtggagta agaggtgact ggggtatagg gtacaacca tagccatcca
60
tggtcatctt tgttttgaat ataattggct agaagatata catatatcta tgtaacttcc
120
tctagcatcc tccagtatgg aggctgcatt aagactgcat gaaggagagg gagagaaggg
180
agaaacagag cagctggaca agaggacagg tatagggaat aagggagaag ccagtaaggc
240
aggaaagacc ctccgtgaca aaggggcagg gaacagaact caaacattta atggcaggta
300
acccaggtta gaatggtaaa ttgaaagggtg aatataaagg gagaatggtg aaatgaattt
360
tctgaaatta attgctgtgt ttatagtttt tagccatgca tcggaatcac ctcaggactc
420
cactcccaat caattatata tctggggggag gaccaaggcg ttggtatttt tcagaagctc
480
cactgggtgat tctgacagca cagctaggat taagaaactg atcaatggga acagcatgcc
540
tgttgcagag gagcttcctt gggaaatgtc acacacagaa catcaatctt ccttccccac
600
tcctgagatc cctcattctt tggcaccagg aacagttgca attagtaaac cctggttccc
660
tgctgtctca caaatcgcaa ga
682

```

<210> 18  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

```

<400> 18
Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala
1              5              10              15
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
20              25              30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
35              40              45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
50              55              60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

```



130

<210> 21  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
 gtgcgcacaa aagagcacgt tcgcaagggg aggaagagcg tgccaccggt tctgccgagc  
 60  
 tagacgcggt gcctatgggt gcggaggacc atggagtga gcgagtaaga ctagatgatg  
 120  
 caacaaatgt gcctgagggt gaaatggcac gagccagtgc caatgagggc atgacacctg  
 180  
 ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg  
 240  
 atacaatgac tgcttgcaat gatgggttca caattgagca attggagctt acacgatctc  
 300  
 tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctggctcaag  
 360  
 aattaaagca agttgtccaa ggcatccatn  
 390

<210> 22  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Val Ala Glu Asp His Gly Val Lys Arg Val Arg Leu Asp Asp Ala  
 1 5 10 15  
 Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly  
 20 25 30  
 Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu  
 35 40 45  
 Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly  
 50 55 60  
 Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg  
 65 70 75 80  
 Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu  
 85 90 95  
 Leu Lys Gln Val Val Gln Gly Ile His  
 100 105

<210> 23  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<400> 23  
 ntctcggagg ccgacagcct ggcgggctgg aagccctcgg tgtaccacgt gctgctcatt  
 60  
 ctgggcctgt tcgccgtgct gctgtcctgc tgcgcctcgg ccatgtacac cagcgtggag  
 120

ggctgggact acgtggactc gctctacttc tgcttcgtca ccttcagcac catcggcttc  
 180  
 ggggacctgg tgagcagcca gcacgccgcc taccggaacc aggggctcta cgcctggggc  
 240  
 aacttcctct tcatactgct cggcgtgtgc tgcatttact cgctcttcaa cgtcactcc  
 300  
 atcctcatca agcaggtgct caactggatg ctgcgcaagc tgagctgccg ctgctgcgcg  
 360  
 cgctgctgcc cggctcctgg cgcgc  
 385

<210> 24

<211> 128

<212> PRT

<213> Homo sapiens

<400> 24

Xaa	Ser	Glu	Ala	Asp	Ser	Leu	Ala	Gly	Trp	Lys	Pro	Ser	Val	Tyr	His
1				5					10					15	
Val	Leu	Leu	Ile	Leu	Gly	Leu	Phe	Ala	Val	Leu	Leu	Ser	Cys	Cys	Ala
			20					25					30		
Ser	Ala	Met	Tyr	Thr	Ser	Val	Glu	Gly	Trp	Asp	Tyr	Val	Asp	Ser	Leu
		35					40				45				
Tyr	Phe	Cys	Phe	Val	Thr	Phe	Ser	Thr	Ile	Gly	Phe	Gly	Asp	Leu	Val
	50					55					60				
Ser	Ser	Gln	His	Ala	Ala	Tyr	Arg	Asn	Gln	Gly	Leu	Tyr	Arg	Leu	Gly
65				70					75					80	
Asn	Phe	Leu	Phe	Ile	Leu	Leu	Gly	Val	Cys	Cys	Ile	Tyr	Ser	Leu	Phe
			85					90						95	
Asn	Val	Ile	Ser	Ile	Leu	Ile	Lys	Gln	Val	Leu	Asn	Trp	Met	Leu	Arg
			100					105					110		
Lys	Leu	Ser	Cys	Arg	Cys	Cys	Ala	Arg	Cys	Cys	Pro	Ala	Pro	Gly	Ala
			115				120						125		

<210> 25

<211> 337

<212> DNA

<213> Homo sapiens

<400> 25

ccatgggaga gaccgtgcat tttcttctag gtctgcgtgg gaagtcaactg cagagtttctg  
 60  
 aggaggggag ttcccagctc tgtatttttg aagggtcagt cttgttgctt ggaccagtga  
 120  
 ggagccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac  
 180  
 tggaggaaag ctggtcgaat gcaactgtgta tttggaggca gaaccagcag agggtcctct  
 240  
 gggttgagtg tagggcaaaa gagaaagaag gcaccaagcc tggggctctgg gttttctctc  
 300  
 ttacacttgc tgggtggacg gtggtgccac tgaatga  
 337

<210> 26



<211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 26  
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu  
 1 5 10 15  
 Gln Ser Phe Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser  
 20 25 30  
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu  
 35 40 45  
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp  
 50 55 60  
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp  
 65 70 75 80  
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp  
 85 90 95  
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn  
 100 105 110

<210> 27  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 ccgacgtcga atatccatgc agccgcgcgc aggatggaga gagcgatgga gcaactcaac  
 60  
 cgcttgacgc gctcgctgcg ccgcgcgcgc accgtggagt tgcccgagga taatgaaact  
 120  
 gctgtttata cattaatgcc aatgggttatg gctgatcaac acaggtctgt ttctgaacta  
 180  
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt  
 240  
 cacattgcag caaattgtgg atcgggtggaa tgcttggttt tgctgttaaa gaaaggagca  
 300  
 aatcctaact atcaagatat ttcaggctgt aca  
 333

<210> 28  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Pro Thr Ser Asn Ile His Ala Ala Ala Pro Arg Met Glu Arg Ala Met  
 1 5 10 15  
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val  
 20 25 30  
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met  
 35 40 45  
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Leu Ser Asn Ser  
 50 55 60  
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

```

65              70              75              80
His Ile Ala Ala Asn Cys Gly Ser Val Glu Cys Leu Val Leu Leu Leu
              85              90              95
Lys Lys Gly Ala Asn Pro Asn Tyr Gln Asp Ile Ser Gly Cys Thr
              100              105              110

```

<210> 29  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

```

<400> 29
ncgccgtccg tgctggctat tatgacggcg ggtagcgacc agggcgagga ggtcaactcg
60
gagagctatt tgagcgccgt gacgccgctg agtcccaaag agattcgtca gctgccccgc
120
tacaatatca cgatcaagcg cgctcgtgaac atgacgggca agggccgcac gccgagctgg
180
tactcgctcg tcgtggctgg caatggtcgg ggcctcgtgg gctatggcga aggcaaagat
240
actaacatca gccgcgcgaa caaaaaggcg ttccacgccg cggtgaaaaa catggacttg
300
gtatcgggtcc accggtcgaa gagtggcgcc aacacgctcg agccccccgt cgagggccgc
360
tggggcgcta cgcgt
375

```

<210> 30  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

```

<400> 30
Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
1              5              10              15
Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
20              25              30
Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
35              40              45
Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
50              55              60
Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
65              70              75              80
Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
85              90              95
Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
100              105              110
Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
115              120              125

```

<210> 31  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc  
 60  
 gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctgggccctt gagagtgcag  
 120  
 agattcctgg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggtc  
 180  
 cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttggcc  
 240  
 ctgcagagtg cacaaacctt gccgcgttc ctccactgca gcttacgtct ttgcagcagc  
 300  
 cactcccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca  
 360  
 tggcctgcat tgttt  
 375

<210> 32  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 32  
 Met Gln Ala Met Ser Leu Lys Leu His Thr Leu Trp Ser His Arg Trp  
 1 5 10 15  
 Gln Trp Gln Pro Ile Gly Ser Gly Cys Cys Lys Asp Val Ser Cys Ser  
 20 25 30  
 Gly Gly Ser Ala Ala Arg Phe Val His Ser Ala Gly Pro Thr Gly Ala  
 35 40 45  
 Arg Asn Arg Gln Glu Pro Pro Phe Pro Phe Glu Leu Ala Gly Arg Glu  
 50 55 60  
 Pro Cys Thr Pro Arg Arg Ser Cys Ser Arg Pro Ala Ala Ala Leu Asp  
 65 70 75 80  
 Pro Gly Ile Ser Ala Leu Ser Gly Ala Gln Glu Ala Ser Leu Thr Arg  
 85 90 95  
 Arg Leu Val Ser Ala Cys Ser Arg Ser Ser Pro Leu Leu Ala Pro Thr  
 100 105 110  
 Ser Ile Ser Glu Gln Ser  
 115

<210> 33  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
 ccatgcagcc caaccgttgg cgataaagtc cgtttaggcg ataccaattt atgggcaacc  
 60  
 attgaacaag atttattaac caaaggatgat gagggtgaaat ttggtggcgg taaaagtgtg  
 120  
 cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt  
 180  
 gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaagc cgatattggt  
 240

attcgcgatg gtcgtattgt cggatcggga caagcaggta accctgacac catggatgac  
 300  
 gtcacgccaa acatgattat cggtgctagc acagaagtac ataacgggtgc a  
 351

<210> 34  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn  
 1 5 10 15  
 Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys  
 20 25 30  
 Lys Phe Gly Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly  
 35 40 45  
 Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn  
 50 55 60  
 Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly  
 65 70 75 80  
 Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp  
 85 90 95  
 Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu  
 100 105 110  
 Val His Asn Gly Ala  
 115

<210> 35  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
 nngctagctg caccaccacc tgttcattgca ggcagagcgg ccaccctca tggaagaaga  
 60  
 ggaatccact gtattgggca caggcttcct gctggacett ggcaagcagg tgcttggtg  
 120  
 gtaccaggaa gtccagcgtg tacctcagtg cgtcctcccg ataagtcctc tccaccacct  
 180  
 ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa ggggtggatac agggcgggca  
 240  
 gagtgctctg cacacagtcc tccactggct caggctccat ggctcggcgc cgggcccgcgt  
 300  
 ccgacgcttg gtcggggcgg cggggccggg cgcgccaccg cctcccttca cgcgt  
 355

<210> 36  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```

1           5           10           15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
20           25           30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
35           40           45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Gly Thr Pro Gly
50           55           60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
65           70           75           80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
85           90           95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
100          105          110
Thr Ala Ser Leu His Ala
115

```

<210> 37  
 <211> 492  
 <212> DNA  
 <213> Homo sapiens

```

<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggaccgcgc
60
gcaaccatga caaggcgat gttgtgatct ggggtggatc cttctccgac atgctcgagg
120
gatcggatct ctccggcgga gtcacggtgc ttgccgaggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc gggttgacgt ggatcactac cggtcagctc gacgggtctc
240
ggcgtcggct gcgcgctggt ctgcacgtgc tggcaccctc gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcgtaga tgacgcactc cgctctctg
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca cctcgtctag caggccacac cctcgtcgtc cagccccatt
480
gtcatccgcg gg
492

```

<210> 38  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

```

<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
1           5           10           15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
20           25           30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
35           40           45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```

```

      50              55              60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu
65              70              75              80
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met
      85              90              95
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser
      100             105             110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala
      115             120             125

```

&lt;210&gt; 39

&lt;211&gt; 412

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

```

aacgaaggtn ccgtacgcgc tctgaaagcc ctgcgttaaag agcgttccga tcgccgggaa
60
gtgatngca ccgcaaaat gcaggtggtc gaagccgcga gttcaggcaa gattgtcttt
120
gaaatggaag acgtttatta cagcattgcc ggaaaacaac tggtagcaa cttctctgcg
180
caagtcatgc gtggtgataa aattgcgctg attggcccga acggttgtgg taaaacgacg
240
ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
300
aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga gcgtacggtg
360
atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
412

```

&lt;210&gt; 40

&lt;211&gt; 137

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 40

```

Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1              5              10              15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
      20              25              30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
      35              40              45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
      50              55              60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65              70              75              80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
      85              90              95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
      100             105             110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
      115             120             125
Gln Glu Val Met Val Asn Gly Arg Val

```

130

135

<210> 41  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<400> 41  
 gaattcaagt ggacacaggc tccacgcccg cgtctcaccg ataagagcta caagcacaac  
 60  
 tactatgacg agcgggtttc gtcgaagag cgtcttgagc gcactgtggc taaggatttc  
 120  
 gtcacgacgg aggtcgagcc catgtgggat gcggctgatg tcatgcggat gggtaaggat  
 180  
 ctcttcatcc agcacggtct gacgacaaat cggaagtcaa tggagtgggt taagcgttac  
 240  
 taccccgatt tccgcgttca cgcggtgaat ttccctgggg atccgtaccc gatccatc  
 300  
 gacgcgacct ttgtgccgct tcgtccgggg ctcatcatca acaacccgaa tcgtccactg  
 360  
 ccgcaggagc agaggaagat cttcgaggcc aatgactggc agatcggtga tgctgctcag  
 420  
 ccggcgcacg acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc  
 480  
 ttggtacttg atccgaagac ggtcatctgc gaggcttcgg aagttcatca gatggagcag  
 540  
 atggacaagc tgggtatgaa cgtcatcccg gtcgccttcc gtgacgcgta cccattcggt  
 600  
 ggagggtctc actgcgccac agctgatgta tatcgagaag gtacctgtga ggactacttc  
 660  
 ccgaatcagg tcgacgaccc gaccttgggt tgagaaaacc ccgtgggtcat gtcatgactg  
 720  
 acggatctcg gtggctcggg acggaactta cgttgctcgt taccgggccc ccgggtctga  
 780  
 tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc  
 840  
 aacgtcaaac aggaagtcc aggcgtcggg acgatgaacc agaaagtggg attcgtgtcc  
 900  
 atgcttcttt ctgcaacggg tatgggggtg gtgggtactt tcgggcgtct cagcactcct  
 960  
 gtggatccca cgacgggcag taagtacatc atcgggtgatt ttttggccac tggtaggatg  
 1020  
 atagtcgggg tcctgggatt tctgcttatt atcgtcatatc ttggaaaatg gtctgagctc  
 1080

<210> 42  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 42  
 Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser  
 1 5 10 15  
 Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu

```

      20      25      30
Glu Arg Thr Val Ala Lys Asp Phe Val Thr Thr Glu Val Glu Pro Met
      35      40      45
Trp Asp Ala Ala Asp Val Met Arg Met Gly Lys Asp Leu Phe Ile Gln
      50      55      60
His Gly Leu Thr Thr Asn Arg Lys Ser Met Glu Trp Phe Lys Arg Tyr
      65      70      75      80
Tyr Pro Asp Phe Arg Val His Ala Val Asn Phe Pro Gly Asp Pro Tyr
      85      90      95
Pro Ile His Ile Asp Ala Thr Phe Val Pro Leu Arg Pro Gly Leu Ile
      100      105      110
Ile Asn Asn Pro Asn Arg Pro Leu Pro Gln Glu Gln Arg Lys Ile Phe
      115      120      125
Glu Ala Asn Asp Trp Gln Ile Val Asp Ala Ala Gln Pro Ala His Asp
      130      135      140
Thr Pro Pro Glu Leu Cys Tyr Ser Ser Val Trp Leu Ser Met Asn Cys
      145      150      155      160
Leu Val Leu Asp Pro Lys Thr Val Ile Cys Glu Ala Ser Glu Val His
      165      170      175
Gln Met Glu Gln Met Asp Lys Leu Gly Met Asn Val Ile Pro Val Ala
      180      185      190
Phe Arg Asp Ala Tyr Pro Phe Gly Gly Gly Leu His Cys Ala Thr Ala
      195      200      205
Asp Val Tyr Arg Glu Gly Thr Cys Glu Asp Tyr Phe Pro Asn Gln Val
      210      215      220
Asp Asp Pro Thr Leu Val
      225      230

```

&lt;210&gt; 43

&lt;211&gt; 358

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

```

gggcccccca catagtggac acagggtttct gggatgtcag catggagtgc caagaggtgg
60
gtgaccacct ggtggggaat aaggcgcttc tgggacatag aggctgcctt ccagctgcgc
120
ctggcagagc tgttgacaca acagcatggt ctgcagtgcc gggccactgc caccacacc
180
gatgtccttt aaggatggat ttgggttttc ggattcgcgt ggcctatcag cgggagtcct
240
agatcctgaa ggaagtgcag agcccagagg ggatgatctc gctgagggac acagctgcct
300
ccctccgctt tgagagagac acaaggcagt tgccactgct caccagtgcc ctgcacgn
358

```

&lt;210&gt; 44

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

Met Glu Cys Gln Glu Val Gly Asp His Leu Val Gly Asn Lys Ala Leu



1				5					10					15				
Leu	Gly	His	Arg	Gly	Cys	Leu	Pro	Ala	Ala	Pro	Gly	Arg	Ala	Val	Asp			
			20					25					30					
Thr	Thr	Ala	Trp	Ser	Ala	Val	Pro	Gly	His	Cys	His	Ala	His	Arg	Cys			
		35					40					45						
Pro	Leu	Arg	Met	Asp	Leu	Gly	Phe	Arg	Ile	Arg	Val	Ala	Tyr	Gln	Arg			
	50					55					60							
Glu	Ser	Gln	Ile	Leu	Lys	Glu	Val	Gln	Ser	Pro	Glu	Gly	Met	Ile	Ser			
65					70					75					80			
Leu	Arg	Asp	Thr	Ala	Ala	Ser	Leu	Arg	Leu	Glu	Arg	Asp	Thr	Arg	Gln			
			85					90					95					
Leu	Pro	Leu	Leu	Thr	Ser	Ala	Leu	His										
			100					105										

&lt;210&gt; 45

&lt;211&gt; 905

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcgttga ggcgggtttc  
 60  
 gcggctcctg gaatcccaga gcagtatggt ggcgacggtg cggatgcgat tgcgtccgca  
 120  
 ataatcatgg aagaggtcgc tcgagtctgt gcgtcgtcgt ccaccgtcat atcgtccaat  
 180  
 gagcttggtg ccgtccctct cctcaaatac ggtagcagg agcagaggaa acgttatctt  
 240  
 tctgaagttg cttcgggtaa ggcacttttc ggatatgcgc tctccgaggc tgatgctgga  
 300  
 tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat  
 360  
 ggcgttaagg cttgggtcac ggaggctggc gaggccaagt acctggtgat atttgcggtt  
 420  
 actgaccag acgatccgcg ccacagaatc agcgcgttga tggatccatgc agatgacccg  
 480  
 ggcattagct acggggtcc ggagcacaaa atggggatac gcgggtcagt taccagggaa  
 540  
 gtggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgtcg agggcacggt  
 600  
 ctgagtgttg ctctaggtac gcttgataac tctcgtgtct cgattgctgc tcaagcagtg  
 660  
 ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt  
 720  
 ggccagccac tgtccaattt tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt  
 780  
 ttggaggcgg cgcgagcgct gacatactct gcagctgac gtagtgggcg ccagactgac  
 840  
 gatgtgagtt acttcggcgc ggcgggccaaa tgtttcgctt ccgacacagc gatggcagtg  
 900  
 tgcac  
 905

&lt;210&gt; 46

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

```

Val Asp Asp Lys Gly Val Phe Ala Gln Gln Gln Tyr Asp Ala Leu Val
 1           5           10           15
Glu Ala Gly Phe Ala Ala Pro Gly Ile Pro Glu Gln Tyr Gly Gly Asp
      20           25           30
Gly Ala Asp Ala Ile Ala Ser Ala Ile Ile Met Glu Glu Val Ala Arg
      35           40           45
Val Cys Ala Ser Ser Ser Thr Val Ile Ser Ser Asn Glu Leu Gly Thr
      50           55           60
Val Pro Leu Leu Lys Tyr Gly Ser Glu Glu Gln Arg Lys Arg Tyr Leu
      65           70           75           80
Ser Glu Val Ala Ser Gly Lys Ala Leu Phe Gly Tyr Ala Leu Ser Glu
      85           90           95
Ala Asp Ala Gly Ser Asp Pro Ala Ala Leu Lys Cys Arg Ala Asp Glu
      100          105          110
Asp Gly Asp Ser Phe Val Leu Asn Gly Val Lys Ala Trp Val Thr Glu
      115          120          125
Ala Gly Glu Ala Lys Tyr Leu Val Ile Phe Ala Val Thr Asp Pro Asp
      130          135          140
Asp Pro Arg His Arg Ile Ser Ala Leu Met Val His Ala Asp Asp Pro
      145          150          155          160
Gly Ile Ser Tyr Gly Ala Pro Glu His Lys Met Gly Ile Arg Gly Ser
      165          170          175
Val Thr Arg Glu Val Val Phe Lys Asn Thr Arg Ile Pro Lys Glu Arg
      180          185          190
Val Ile Gly Arg Arg Gly His Gly Leu Ser Val Ala Leu Gly Thr Leu
      195          200          205
Asp Asn Ser Arg Val Ser Ile Ala Ala Gln Ala Val Gly Ile Ala Gln
      210          215          220
Gly Ala Leu Asp Ile Ala Thr Asp Tyr Val Gln Lys Arg Lys Gln Phe
      225          230          235          240
Gly Gln Pro Leu Ser Asn Phe Glu Gly Ile Gln Phe Met Leu Ala Asp
      245          250          255
Met Ala Met Arg Leu Glu Ala Ala Arg Ala Leu Thr Tyr Ser Ala Ala
      260          265          270
Asp Arg Ser Gly Arg Gln Thr Asp Asp Val Ser Tyr Phe Gly Ala Ala
      275          280          285
Ala Lys Cys Phe Ala Ser Asp Thr Ala Met Ala Val Cys
      290          295          300

```

&lt;210&gt; 47

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

```

aagcttgtag agctagtcg aagcggactg tcggtacgcc aagctgctaa aagatgtggg
60
atgcattcta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt
120

```

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg  
 180  
 gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgctg actgcgttta  
 240  
 gatttcgaaa aaggactcac caaatcccag ggtcgacgag aagagttcat acccgctcggc  
 300  
 gaagacgcca gcacgtataa cagacttatg aaagcgctgc gccaacgcca tgatgtcatc  
 360  
 aaatccggaa agcttgccc  
 379

<210> 48  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
 Met His Leu Thr Ala Ala Tyr Ala Val Ala Thr Glu Ala Gly Cys His  
 1 5 10 15  
 Ile Arg Leu Ser Gln Tyr Ala Arg Lys Val Arg Gln Thr Gln Leu Arg  
 20 25 30  
 Val Glu Tyr Leu Arg Leu Arg Leu Ala Ser Leu Pro Gly Gly Asp Ala  
 35 40 45  
 Gly Ala Ala Val Gly Ile Asp Arg Arg Leu Arg Leu Asp Phe Glu Lys  
 50 55 60  
 Gly Leu Thr Lys Ser Gln Gly Arg Arg Glu Glu Phe Ile Pro Val Gly  
 65 70 75 80  
 Glu Asp Ala Ser Thr Tyr Asn Arg Leu Met Lys Ala Leu Arg Gln Arg  
 85 90 95  
 His Asp Val Ile Lys Ser Gly Lys Leu Ala  
 100 105

<210> 49  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 tgatcatgat gctggcatgg actattctgg tcctgttcc tctctcacct gctgaaggac  
 60  
 atccctctaa tttttgtgtc tccttctgta tcatcaaatt ttcctctctt actgagtctc  
 120  
 ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc cccttgctctg  
 180  
 cacattaccc tctgccagct ggctcatttt tctgctcccc ttacagggga aactcttcaa  
 240  
 aaagtatatc ccacctcctt ccattctcatg ttctcttgaa cctgcagtac tgggtgctcc  
 300  
 ctcccttttg  
 309

<210> 50  
 <211> 101  
 <212> PRT

<213> Homo sapiens

<400> 50

```

Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
 1           5           10           15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
          20           25           30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
        35           40           45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
      50           55           60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
 65           70           75           80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
          85           90           95
Val Leu Pro Pro Phe
          100

```

<210> 51

<211> 512

<212> DNA

<213> Homo sapiens

<400> 51

```

agatctttga agaattgcca cactgtcttc ctccctgctt ataatttctt tattccctag
60
gatgtgatcc ttgttcttgg ggctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgcgtggc attcccactt gcattctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt cttgtacttc atgtgccctt
300
caaaatcttc tgttgetgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgtcccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggetgg gctggatggg acatcaggtg ggcctctgt ttcatttatg tgacctcca
480
tcaggtcttc tggttggatc ctgctttcta ga
512

```

<210> 52

<211> 125

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Glu Lys Lys Arg Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
 1           5           10           15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
      20           25           30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```

```

      35              40              45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Leu Arg Glu Lys
      50              55              60
Arg Pro Ala Gly Ile Glu Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
      65              70              75              80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
      85              90              95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
      100             105             110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
      115             120             125

```

<210> 53  
 <211> 474  
 <212> DNA  
 <213> Homo sapiens

```

<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccg gatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gaggcccgct aatggccaaa
120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaagcccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcatcgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgcgggtt acgtaaccgt
300
gaccaagtcg acgggcgtcc ccgcggctac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttcctgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcceg ttcgaccacg cgtcataggc gggc
474

```

<210> 54  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

```

<400> 54
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
1      5      10      15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
20     25     30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
35     40     45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
50     55     60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
65     70     75     80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
85     90     95
Ala Lys Ser Ser Trp

```

100

<210> 55  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<400> 55  
 ccatggccca ggacagccgg catatcggct acgactacgg tacaccggtg gcgccacagt  
 60  
 tcggcgccgc caagcccgcg gcgtgctgcc aggcgcaagc gacaaacacc ggcccgtggg  
 120  
 tgggtgttcga ccatgtgcgt tgcacccacg acacctttct gatcgacgtc tttctcaacc  
 180  
 agcccgatgc caccgcgcag caggtcaatg ccgacaaccc gcactacgtc gggcgtttca  
 240  
 gccgcacccg catgggcctg gtggatgaca agggccgttg cattaccagc ggcgatccgc  
 300  
 gcgcgttgaa tgccgcgcgc agcaccaagg cgctgaacct gggaccgagt gacgcggcgc  
 360  
 agttatcggg gaggcgta  
 378

<210> 56  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val  
 1 5 10 15  
 Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln  
 20 25 30  
 Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr  
 35 40 45  
 His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr  
 50 55 60  
 Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser  
 65 70 75 80  
 Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln  
 85 90 95  
 Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn  
 100 105 110  
 Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg  
 115 120 125

<210> 57  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
 agaccacccc gacacagatc aggagtcgtc atgtccagaa agaagaaggt eggcatcctc  
 60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggctgcc  
 120  
 atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcggga  
 180  
 aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggt cggcgggacc  
 240  
 atcctgggaa ctagccgtga caaggtaaat cacatgatta tcgacggcga ggaacgggat  
 300  
 atggtcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg  
 360  
 ggtggcgggtg gcaccgcaa gaacgcgt  
 388

<210> 58  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Arg Pro Thr Arg His Arg Ser Gly Val Val Met Ser Arg Lys Lys Lys  
 1 5 10 15  
 Val Gly Ile Leu Thr Ala Gly Gly Asp Cys Pro Gly Leu Asn Ala Ala  
 20 25 30  
 Ile Arg Gly Phe Gly Lys Ala Ala Ile Arg Gln His Asp Met Glu Leu  
 35 40 45  
 Ile Gly Ile Gln Asp Gly Phe Leu Gly Leu Ala Gly Asn Arg Thr Ile  
 50 55 60  
 Ser Leu Gly Pro Arg Ala Leu Ser Gly Ile Leu Thr Val Gly Gly Thr  
 65 70 75 80  
 Ile Leu Gly Thr Ser Arg Asp Lys Val Asn His Met Ile Ile Asp Gly  
 85 90 95  
 Glu Glu Arg Asp Met Val Pro Thr Thr Val Glu Asn Tyr Glu Lys Leu  
 100 105 110  
 Gly Leu Asp Ala Leu Val Thr Leu Gly Gly Gly Gly Thr Ala Lys Asn  
 115 120 125  
 Ala

<210> 59  
 <211> 417  
 <212> DNA  
 <213> Homo sapiens

<400> 59  
 ggtaccatcg gagctcgaca agaaatgggt gggatgaagtc gtggcttctg ctccaccag  
 60  
 tgccctcatg ggtagcccca cctgaatatc ttcatgcctg tgcatttctc ctgatgttca  
 120  
 cgtgtgccct gtgtttttac gcactctgtga tcgtgcaccc acgcgtctca gagaggagcc  
 180  
 cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaacct  
 240  
 cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttgggtg gaagggaacc  
 300

tggcaaccga ggcaagccta gtggttcttg acacactgga gatcatcgtg cagacgggtga  
 360  
 tgctttcaga agccccgggag agcgtcttg<sup>g</sup> gggcagtgtc gaaggttgtg ctgtaca  
 417

<210> 60  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 60  
 Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro  
 1 5 10 15  
 Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp  
 20 25 30  
 Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys  
 35 40 45  
 Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala  
 50 55 60  
 Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln  
 65 70 75 80  
 Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu  
 85 90 95  
 Lys Val Val Leu Tyr  
 100

<210> 61  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
 agatcttcac agccttagac ttttttcatg ggtgccttac agttttggag gtccctatcc  
 60  
 gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag  
 120  
 tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga  
 180  
 ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc  
 240  
 tcccctagac cgggcccctg gccaggcctg accacagagc tccattgcc tttctgcac  
 300  
 gcgt  
 304

<210> 62  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
 Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala  
 1 5 10 15



Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr  
 20 25 30  
 Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe  
 35 40 45  
 Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala  
 50 55 60  
 Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly  
 65 70 75 80  
 Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala  
 85 90

&lt;210&gt; 63

&lt;211&gt; 577

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

cgcgctcaagg ggggtctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgcg  
 60  
 ctgacgggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc  
 120  
 accgtggtcg ggctggccca aaccctcggc cctccgtgc gagcactggg cgtcgacacc  
 180  
 gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc  
 240  
 ccggcagcct ggcagatcca ccccgacgac ggtgcccga ccacaccggg tgatggcccc  
 300  
 gtggagttgc acatcccggg cagggatttc cagcttgacg tcgccggcgg caccatgtg  
 360  
 ggtatcatgg cgcctcaatc ggtctgtgac gccttgccg aggcgataga ccacggctcc  
 420  
 gagaccgtct tgaatggggg tcccggcagt cgctcaacc ctgcccacg gcgtcgtctg  
 480  
 gtgctggtgg ctccccgctc cccgaactg ttcgacgata ctgcccgctg gaacatcgtg  
 540  
 cttgacagcc agacgactgt cgccaggctg aatgcat  
 577

&lt;210&gt; 64

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val  
 1 5 10 15  
 Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly  
 20 25 30  
 Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr  
 35 40 45  
 Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu  
 50 55 60  
 Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser  
 65 70 75 80

```

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
      85                      90                      95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
      100                      105                      110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
      115                      120                      125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
      130                      135                      140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
145                      150                      155                      160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
      165                      170                      175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
      180                      185                      190

```

&lt;210&gt; 65

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 65

```

gtcgaccgcg ccttgggata gctcgaaggg gccagcctgg accaggtagc ggaagaagtc
60
aagaaggccg ctttcaagat caccgcgcgc gggcaactag tgggcacccat ggccctccgag
120
cgcccttgcg tacccttcgg catcatcgac ctttcgcttg cccctactgc cgaattggga
180
gattcggggg ccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggctctgct taacgacgcc gtaaagaaag gcggcatgat ggctgcccc
300
cgcgtcgcg gtttgcctgg ctccttcac cgggctcc
339

```

&lt;210&gt; 66

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

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Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
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Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
      20      25      30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
      35      40      45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
      50      55      60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
65      70      75      80
Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys Lys Gly Gly Met
      85      90      95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
      100      105      110

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Ser

&lt;210&gt; 67

&lt;211&gt; 446

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

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 446

&lt;210&gt; 68

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

Met Trp His Thr Tyr Leu Arg Val Ala Asp Ala Ala Gln Ala Arg Val  
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 Arg Gly Val Arg Gly Ala Ser Trp His Asn Phe Ala Thr Gly Asp Lys  
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 Gly Ser Phe Asp Ala Asn Glu Leu Ala Val Thr Pro Asp Thr Asp Thr  
 35 40 45  
 Val Ile Gln Gly Val Gly Pro Ala Leu Ala Leu Leu Asp Ser Ala Trp  
 50 55 60  
 Gly Arg Gln Ile His Val Glu Thr Thr Gly Cys Pro Ser Ala Val Val  
 65 70 75 80  
 Trp Asn Pro Arg Ser Ser Ser Thr His Ala Asp Asn Pro Thr Ala Gln  
 85 90 95  
 Ala Trp Arg Asp Phe Val Cys Val Glu Thr Gly Ala Cys Lys Asp Asn  
 100 105 110  
 Ala Val Ile Val Ala Pro His Ser Asp Leu Thr Met Ser Thr Arg Ile  
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 Ser Val Glu Thr Leu  
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&lt;210&gt; 69

&lt;211&gt; 552

&lt;212&gt; DNA

<213> Homo sapiens

<400> 69

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agtcctccaa gattgccagc ttcattccca aaggggggaa gctcaacagt gccaagaagg  
180  
agcncatgg ccccttcctt cagtgaata ccaaaaccag gaatgaaaag catgcccggg  
240  
aaatccccaa gtgcccagc gccttccaag gaaggggagc ggagccggag tgggaagctg  
300  
agctcaggac tccccagca gaagccccag ctggacggca gacactccag ttccttttc  
360  
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420  
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ctttcctgta ca  
552

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

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Gln	Leu	Cys	Pro	Arg	Cys	Gln	Lys	Ser	Pro	Pro	Arg	Leu	Pro	Ala	Ser
		35					40					45			
Ser	Pro	Lys	Gly	Gly	Ser	Ser	Thr	Val	Pro	Arg	Arg	Ser	Xaa	Met	Ala
	50					55					60				
Pro	Ser	Leu	Ser	Gly	Ile	Pro	Lys	Pro	Gly	Met	Lys	Ser	Met	Pro	Gly
	65				70					75				80	
Lys	Ser	Pro	Ser	Ala	Pro	Ala	Pro	Ser	Lys	Glu	Gly	Glu	Arg	Ser	Arg
			85						90					95	
Ser	Gly	Lys	Leu	Ser	Ser	Gly	Leu	Pro	Gln	Gln	Lys	Pro	Gln	Leu	Asp
			100					105					110		
Gly	Arg	His	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Ala	Ser	Ser	Ser	Glu	Lys
		115					120						125		
Gly	Pro	Gly	Gly	Thr	Thr	Leu	Asn	His	Ser	Ile	Ser	Ser	Gln	Thr	Val
	130					135						140			
Ser	Gly	Ser	Val	Gly	Thr	Thr	Gln	Thr	Thr	Gly	Ser	Asn	Xaa	Pro	Ser
	145				150					155				160	
Val	Phe	Ser	Tyr	Leu	Ser	Pro	Ser	Ser	Asn	Thr	Thr	Ile	Pro	Thr	Leu
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Pro	Arg	Leu	His	Leu	Ser	Cys	Thr								
			180												

<210> 71  
 <211> 316  
 <212> DNA  
 <213> Homo sapiens

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 attcaagact tggagt.  
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<210> 72  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
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 Glu Ala Leu Arg Pro Leu Asn Ile Leu Arg Thr Phe Ala Val Phe Arg  
 35 40 45  
 Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val  
 50 55 60  
 Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly  
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 Ile Met Val Gly Gly Tyr Leu Thr Thr Gly Gly Arg Ser Pro Gln Asp  
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 Asp Leu Gln Met Ile Gln Asp Leu Glu  
 100 105

<210> 73  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

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 120  
 ccacgagtga ccgtcgtcac cccgccgtgg aacttcgccc tgtctattac cgccggatcc  
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 384

<210> 74  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 74  
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 Ile Asp Phe Ala Trp Tyr Val Asp Arg Ala Glu Glu Leu Glu Gly  
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 35 40 45  
 Pro Trp Asn Phe Ala Leu Ser Ile Thr Ala Gly Ser Thr Leu Ala Ala  
 50 55 60  
 Leu Ala Ala Gly Ser Ser Val Leu Leu Lys Pro Ala Pro Gln Ala Arg  
 65 70 75 80  
 His Cys Ala Ala Val Ile Ser Glu Cys Leu Trp Glu Ala Gly Ile Pro  
 85 90 95  
 Arg Asp Val Leu Gln Leu Val Asp Val Glu Glu Asn Glu Ala Gly Lys  
 100 105 110  
 His Leu Val Ser His Pro Glu Val Asp Arg Val Ile Leu Thr Gly Gly  
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<210> 75  
 <211> 405  
 <212> DNA  
 <213> Homo sapiens

<400> 75  
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 180  
 cacctgctga ccggaaaaat ctcgacgccc ggcaacagcc cgttctcgct gaccgggcag  
 240  
 ccacgggcct gcggcacggc gcgcgaggtc ggtaccttct cgcacgcct gcccgccgac  
 300  
 atggtgggtca ccagcaaggc gcaccgcgac atcgccgaga agatctggca gctgccggaa  
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 405

<210> 76

<211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 76  
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 20 25 30  
 Lys Thr Arg Val Val Ser Phe Trp Thr Met Gly Phe Asn Gln His Thr  
 35 40 45  
 Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr  
 50 55 60  
 Gly Lys Ile Ser Thr Pro Gly Asn Ser Pro Phe Ser Leu Thr Gly Gln  
 65 70 75 80  
 Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg  
 85 90 95  
 Leu Pro Ala Asp Met Val Val Thr Ser Lys Ala His Arg Asp Ile Ala  
 100 105 110  
 Glu Lys Ile Trp Gln Leu Pro Glu Gly Pro Val Pro Asp Lys Pro Gly  
 115 120 125  
 Tyr His Ala Val Leu Gln Ser  
 130 135

<210> 77  
 <211> 5816  
 <212> DNA  
 <213> Homo sapiens

<400> 77  
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<210> 78  
 <211> 799  
 <212> PRT  
 <213> Homo sapiens

<400> 78  
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 Thr Ala Ser Ile Ile Gly Asp Val Met Gly Pro Thr Leu Asn His Leu  
 35 40 45  
 Asn Asn Leu Leu Arg Leu Pro Phe Gly Cys Gly Glu Gln Asn Met Ile  
 50 55 60  
 His Phe Ala Pro Asn Val Phe Val Leu Lys Tyr Leu Gln Lys Thr Gln  
 65 70 75 80  
 Gln Leu Ser Pro Glu Val Glu Arg Glu Thr Thr Asp Tyr Leu Val Gln  
 85 90 95  
 Gly Tyr Gln Arg Gln Leu Thr Tyr Lys Arg Gln Asp Gly Ser Tyr Ser  
 100 105 110  
 Ala Phe Gly Glu Arg Asp Ala Ser Gly Ser Met Trp Leu Thr Ala Phe  
 115 120 125  
 Val Leu Lys Ser Phe Ala Gln Ala Arg Ser Phe Ile Phe Val Asp Pro  
 130 135 140  
 Arg Glu Leu Ala Ala Ala Lys Ser Trp Ile Ile Gln Gln Gln Gln Ala  
 145 150 155 160  
 Asp Gly Ser Phe Leu Ala Val Gly Arg Val Leu Asn Lys Asp Ile Gln  
 165 170 175  
 Gly Gly Ile His Gly Ile Val Pro Leu Thr Ala Tyr Val Val Val Ala  
 180 185 190  
 Leu Leu Glu Thr Gly Thr Ala Ser Glu Glu Glu Arg Gly Ser Thr Asp  
 195 200 205  
 Lys Ala Arg His Phe Leu Glu Ser Ala Ala Pro Leu Ala Met Asp Pro  
 210 215 220  
 Tyr Ser Cys Ala Leu Thr Thr Tyr Ala Leu Thr Leu Leu Arg Ser Pro  
 225 230 235 240  
 Ala Ala Pro Glu Ala Leu Arg Lys Leu Arg Ser Leu Ala Ile Met Arg  
 245 250 255  
 Asp Gly Val Thr His Trp Ser Leu Ser Asn Ser Trp Asp Val Asp Lys  
 260 265 270  
 Gly Thr Phe Leu Ser Phe Ser Asp Arg Val Ser Gln Ser Val Val Ser  
 275 280 285  
 Ala Glu Val Glu Met Thr Ala Tyr Ala Leu Leu Thr Tyr Thr Leu Leu  
 290 295 300  
 Gly Asp Val Ala Ala Ala Leu Pro Val Val Lys Trp Leu Ser Gln Gln

```

305          310          315          320
Arg Asn Ala Leu Gly Gly Phe Ser Ser Thr Gln Asp Thr Cys Val Ala
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Leu Gln Ala Leu Ala Glu Tyr Ala Ile Leu Ser Tyr Ala Gly Gly Ile
          340          345          350
Asn Leu Thr Val Ser Leu Ala Ser Thr Asn Leu Asp Tyr Gln Glu Thr
          355          360          365
Phe Glu Leu His Arg Thr Asn Gln Lys Val Leu Gln Thr Ala Ala Ile
          370          375          380
Pro Ser Leu Pro Thr Gly Leu Phe Val Ser Ala Lys Gly Asp Gly Cys
385          390          395          400
Cys Leu Met Gln Ile Asp Val Thr Tyr Asn Val Pro Asp Pro Val Ala
          405          410          415
Lys Pro Ala Phe Gln Leu Leu Val Ser Leu Gln Glu Pro Glu Ala Gln
          420          425          430
Gly Arg Pro Pro Pro Met Pro Ala Ser Ala Ala Glu Gly Ser Arg Gly
          435          440          445
Asp Trp Pro Pro Ala Asp Asp Asp Asp Pro Ala Ala Asp Gln His His
          450          455          460
Gln Glu Tyr Lys Val Met Leu Glu Val Cys Thr Arg Trp Leu His Ala
465          470          475          480
Gly Ser Ser Asn Met Ala Val Leu Glu Val Pro Leu Leu Ser Gly Phe
          485          490          495
Arg Ala Asp Ile Glu Ser Leu Glu Gln Leu Leu Leu Asp Lys His Met
          500          505          510
Gly Met Lys Arg Tyr Glu Val Ala Gly Arg Arg Val Leu Phe Tyr Phe
          515          520          525
Asp Glu Ile Pro Ser Arg Cys Leu Thr Cys Val Arg Phe Arg Ala Leu
          530          535          540
Arg Glu Cys Val Val Gly Arg Thr Ser Ala Leu Pro Val Ser Val Tyr
545          550          555          560
Asp Tyr Tyr Glu Pro Ala Phe Glu Ala Thr Arg Phe Tyr Asn Val Ser
          565          570          575
Thr His Ser Pro Leu Ala Arg Glu Leu Cys Ala Gly Pro Ala Cys Asn
          580          585          590
Glu Val Glu Arg Ala Pro Ala Arg Gly Pro Gly Trp Phe Pro Gly Glu
          595          600          605
Ser Gly Pro Ala Val Ala Pro Glu Glu Gly Ala Ala Ile Ala Arg Cys
          610          615          620
Gly Cys Asp His Asp Cys Gly Ala Gln Gly Asn Pro Val Cys Gly Ser
625          630          635          640
Asp Gly Val Val Tyr Ala Ser Ala Cys Arg Leu Arg Glu Ala Ala Cys
          645          650          655
Arg Gln Ala Ala Pro Leu Glu Pro Ala Pro Pro Ser Cys Cys Ala Leu
          660          665          670
Glu Gln Arg Leu Pro Ala Ser Ser Ser Thr Tyr Gly Asp Asp Leu
          675          680          685
Ala Ser Val Ala Pro Gly Pro Leu Gln Gln Asp Val Lys Leu Asn Gly
          690          695          700
Ala Gly Leu Glu Val Glu Asp Ser Asp Pro Glu Pro Glu Gly Glu Ala
705          710          715          720
Glu Asp Arg Val Thr Ala Gly Pro Arg Pro Pro Val Ser Ser Gly Asn
          725          730          735
Leu Glu Ser Ser Thr Gln Ser Ala Ser Pro Phe His Arg Trp Gly Gln

```

```

              740              745              750
Thr Pro Ala Pro Gln Arg His Ser Gly Arg Val Val Gly Ala His Arg
              755              760              765
Pro Gly Leu Leu Ser Pro Val Phe Val Tyr Ser Pro Ala Phe Gln Ser
              770              775              780
Gly Gly Glu Glu Gly Leu Trp Met Ser Asn Thr Cys Thr Leu Arg
785              790              795

```

<210> 79  
 <211> 346  
 <212> DNA  
 <213> Homo sapiens

```

<400> 79
acgcgttgcc gtcggggaag tggtagatgt aaggctcttc catttctgcg gcggttctt
60
cgctgatagg cgcgaggttc atgccgcaa agcccgggaa acccacgctg taggcatccg
120
ccgatgcaac ggcataata ctcaaggcca tgaagtcgtt ggtgcggctc tggaagtact
180
tcaccgcgcc ttccgacaag cccacgtcct tgagcaggaa gtcgcggtag ctggtggccg
240
ccgatactc ggctttttct tcggcggact tgcccggcag gtaatccttg ggcgcgacgt
300
gcatggcgat caatgcccg gctgccgctt ccgncnnnc cnnncn
346

```

<210> 80  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

```

<400> 80
Met His Val Ala Pro Lys Asp Tyr Leu Pro Gly Lys Ser Ala Glu Glu
1      5      10      15
Lys Ala Glu Tyr Leu Ala Ala Thr Ser Tyr Arg Asp Phe Leu Leu Lys
20     25     30
Asp Val Gly Leu Ser Glu Gly Ala Val Lys Tyr Phe Gln Ser Arg Thr
35     40     45
Asn Asp Phe Met Ala Leu Ser Ile Asp Ala Val Ala Ser Ala Asp Ala
50     55     60
Tyr Ser Val Gly Phe Pro Gly Phe Gly Gly Met Asn Leu Ala Pro Ile
65     70     75     80
Ser Glu Glu Ala Ala Ala Glu Met Glu Glu Pro Tyr Ile Tyr His Phe
85     90     95
Pro Asp Gly Asn Ala
100

```

<210> 81  
 <211> 429  
 <212> DNA  
 <213> Homo sapiens

<400> 81

nngcttttct cncctcgca cctgatctgc tgctgacgtg cgggaggggc attaaaagat  
 60  
 tgactttaat ttgataccag aaatgtcagt gtggctttgc ttgaacagcc gcgtgcgggg  
 120  
 cctctatgag tggaatccag tctcatggcc ccccccattg ctcctgttac cctggaggag  
 180  
 gctactccat gaggtctggt cgggtggcac tgcctcgggg ctgcatgtac atgtgtgtgc  
 240  
 atgnntgtgt gcatgtgctg gtgcacgtgt nngtgtgtgc cgtgtgcat gtgcccgtgt  
 300  
 gcgtgtctgt gctgtgtgtg tgcgtgcatg tgtgcgtgtc tgtgcgtgnc tgtgtgtgtg  
 360  
 cgtgcatgtg tgtgcacgtg tgtgcatgtg cacgtgtgcg caccgtgtg catgtccgtg  
 420  
 tgcacgcgt  
 429

<210> 82

<211> 79

<212> PRT

<213> Homo sapiens

<400> 82

Gly	Trp	Leu	Arg	Trp	His	Cys	Leu	Gly	Ala	Ala	Cys	Thr	Cys	Val	Cys
1				5				10					15		
Met	Xaa	Val	Cys	Met	Cys	Val	Cys	Thr	Cys	Xaa	Cys	Val	Pro	Val	Cys
		20					25					30			
Met	Cys	Pro	Cys	Ala	Cys	Leu	Cys	Cys	Val	Cys	Ala	Cys	Met	Cys	Ala
		35				40				45					
Cys	Leu	Cys	Val	Xaa	Val	Cys	Val	Arg	Ala	Cys	Val	Cys	Thr	Cys	Val
	50					55				60					
His	Val	His	Val	Cys	Ala	Pro	Val	Cys	Met	Ser	Val	Cys	Thr	Arg	
65					70					75					

<210> 83

<211> 411

<212> DNA

<213> Homo sapiens

<400> 83

gtgcacttct tcggacgagg gtccttcggc gcccgcgata acgagagggt gcggagattt  
 60  
 cgtgcgctct ttaaaaagcg caaaggcttt tataagttcg atgtgctttt tttcaggccc  
 120  
 ggaaagacgc gatccgtaga taaaataggg ccgctttatc gcaaattggc ttatgggttac  
 180  
 cgtttccgca tcgatttgca gctgcggaaa aaaaggcctg tggtcgatgc cgttgtggat  
 240  
 gatttcgatt ttcgctttgt cgatgccaag ccctatcaaa tcgtttcgca aaaactcgct  
 300  
 cgcggcgacg atcttttgca cctttgtaag cccccgcttt atctgcatgc gcatcatgcg  
 360  
 gtcgctcttt tctttgagca tgacggaaac gatggaattg acgacggcga c  
 411

<210> 84  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
 Met Leu Lys Glu Lys Ser Asp Arg Met Met Arg Met Gln Ile Lys Arg  
 1 5 10 15  
 Gly Leu Thr Lys Val Gln Lys Ile Val Ala Ala Ser Glu Phe Leu Arg  
 20 25 30  
 Asn Asp Leu Ile Gly Leu Gly Ile Asp Lys Ala Lys Ile Glu Ile Ile  
 35 40 45  
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp  
 50 55 60  
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe  
 65 70 75 80  
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu  
 85 90 95  
 Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro  
 100 105 110  
 Leu Val Ile Ala Gly Ala Glu Gly Pro Ser Ser Glu Glu Val His  
 115 120 125

<210> 85  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
 nnacgcgtgc cgcgcaaggg aaccatgttc gtgtcgggtgc gcgaaaccga caaggcgcgc  
 60  
 atcctcgacg cgggtgaaact gctgagttcg ctcggttca aggtgatcgc cacctcgggc  
 120  
 acccagcgtt tcttggtgga gaacggagta ccggcggaag agatcaacaa ggtgctggaa  
 180  
 ggccgcccgc acattgttga cgcaattacc aacggcgagg tgcaactcgt tttcaatacc  
 240  
 accgaggggc cacaggcgct ggctgacagc cgctcgttgc gacgcgctgc cctcttgc  
 300  
 aaagtgccat attacaccac tctttcaggt gca  
 333

<210> 86  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
 Xaa Arg Val Pro Arg Lys Gly Thr Met Phe Val Ser Val Arg Glu Thr  
 1 5 10 15  
 Asp Lys Ala Arg Ile Leu Asp Ala Val Lys Leu Leu Ser Ser Leu Gly  
 20 25 30  
 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn

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```

      35          40          45
Gly Val Pro Ala Glu Lys Ile Asn Lys Val Leu Glu Gly Arg Pro His
  50          55          60
Ile Val Asp Ala Ile Thr Asn Gly Glu Val Gln Leu Val Phe Asn Thr
  65          70          75          80
Thr Glu Gly Pro Gln Ala Leu Ala Asp Ser Arg Ser Leu Arg Arg Ala
      85          90          95
Ala Leu Leu His Lys Val Pro Tyr Tyr Thr Thr Leu Ser Gly Ala
      100          105          110

```

&lt;210&gt; 87

&lt;211&gt; 355

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 87

```

acgcgtgagg aaatgggggc cgcaggcctg gatcgcaagg tatggcagtg cccggtcgtc
  60
ctcctgagcg atgttcattc ggtaggggta cagggtgacg ggcgtactta tggttctccc
  120
attgtgcttc gcccggtgac gaggtaggac gccatgactg cggactgggc acgtatccca
  180
tatgacgtac tggaaaagat ctgactcgc attacgaatg cgtgtccgca aatcaaccgg
  240
gtggtactcg atatcacatc taaaccgccg gccaccatcg agtgggaatg agccccgtct
  300
caccgtgaac atgacatggc ccgcaccttt cttggggcgg gccatgccgt gtttag
  355

```

&lt;210&gt; 88

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 88

```

Thr Arg Glu Glu Met Gly Ala Ala Gly Leu Asp Arg Lys Val Trp Gln
  1          5          10          15
Cys Pro Val Val Leu Leu Ser Asp Val His Ser Val Gly Val Gln Gly
      20          25          30
Asp Gly Arg Thr Tyr Gly Ser Pro Ile Val Leu Arg Pro Val Thr Ser
      35          40          45
Glu Asp Ala Met Thr Ala Asp Trp Ala Arg Ile Pro Tyr Asp Val Leu
      50          55          60
Glu Lys Ile Ser Thr Arg Ile Thr Asn Ala Cys Pro Gln Ile Asn Arg
      65          70          75          80
Val Val Leu Asp Ile Thr Ser Lys Pro Pro Ala Thr Ile Glu Trp Glu
      85          90          95

```

&lt;210&gt; 89

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 89



## ATTORNEY DOCKET NO.: 15966-543

nacgcgtcaa caccaggcta cggtgggtat gatcatgata agggctggga cccgcaggag  
 60  
 agggcaagag ttatataata gacgggtgta tgggtttaag gtatacatgg tgatgagaca  
 120  
 ggtgattgga taaggccaga gggttgggcg gggttctgcc cctgctgaag cctgggtggg  
 180  
 cccaggtctg tgatctggga ccggaacaac acatctgctc tgggcctgct ggatgtggcg  
 240  
 caagccctgg aacagaacca cagcctcaag tccatgccgc tgccactgaa tgacgtaacc  
 300  
 caggctcatc gcagccggcc agaactcaca actcgagcgg tccatcagat c  
 351

&lt;210&gt; 90

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

Ser	Leu	Val	Gly	Pro	Arg	Ser	Val	Ile	Trp	Asp	Arg	Asn	Asn	Thr	Ser
1				5				10						15	
Ala	Leu	Gly	Leu	Leu	Asp	Val	Ala	Gln	Ala	Leu	Glu	Gln	Asn	His	Ser
			20				25						30		
Leu	Lys	Ser	Met	Pro	Leu	Pro	Leu	Asn	Asp	Val	Thr	Gln	Ala	His	Arg
		35					40					45			
Ser	Arg	Pro	Glu	Leu	Thr	Thr	Arg	Ala	Val	His	Gln	Ile			
	50					55					60				

&lt;210&gt; 91

&lt;211&gt; 327

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

nggtgggtcc tctcgcagga caggtaatcc tgagacctac gcagctccct ggagctctgc  
 60  
 acgtcgaagc ccagcagggc ctctctcagg tccctggggc agccagcaca cacaagtc  
 120  
 cggaaggggc tgtagactcc ctgccagcgg ctttcccggg gaaggcacc acgcccagct  
 180  
 gcctcttgca ggtactgctc ggggtctggtg ggagggcagc cgtgtccagc acaccctgtg  
 240  
 tgtgcagtcc tctccctgcc cactgccga acgagccctc cacggtgaag ccattgggga  
 300  
 acgtgacctt gcccttcccc atgaggt  
 327

&lt;210&gt; 92

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 92

Met	Gly	Lys	Gly	Lys	Val	Thr	Phe	Pro	Asn	Gly	Phe	Thr	Val	Glu	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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```

1           5           10           15
Ser Phe Gly Ser Gly Ala Gly Arg Gly Leu His Thr Gln Gly Val Leu
      20           25           30
Asp Thr Ala Ala Leu Pro Pro Asp Pro Ser Ser Thr Cys Lys Arg Gln
      35           40           45
Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr
      50           55           60
Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg
65           70           75           80
Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly
      85           90           95
Leu Arg Ile Thr Cys Pro Ala Arg Gly Pro Thr
      100           105

```

<210> 93  
 <211> 394  
 <212> DNA  
 <213> Homo sapiens

```

<400> 93
nccgcgtacg acaagcagta cctcgagggg cggttacgggtg cggacccata cctgagcaac
60
atgctcgaat gggacggcgg acatgagcaa taggccgcca aagcacagcg agaggaaggc
120
ggcgcgctct gggcctcgc ggatgaagga ggggtggtcg cgcaagagac gccccgcgcc
180
ttttgtaccg ataaatcccg ggcgccacct gatcgtgacc gagggtagca aaacggaacc
240
gctctatttc gaggtatca ggttgctgt caacaaccgt tatcacggcc agtgggtgac
300
aatggaagtt gtcgttaccg gcaagcatac caggggactt ctcgatcgtg cagtcactct
360
ggcggaagaa agtgccacag gattcactca cgta
394

```

<210> 94  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

```

<400> 94
Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
1           5           10           15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
      20           25           30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
      35           40           45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
      50           55           60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
65           70           75           80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
      85           90           95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg

```

100

105

<210> 95  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 95  
 ggtacctctt ccaagtacct tctaaatgaa acactcaaga gagtgtact caggaaactt  
 60  
 tgcttggatc ctaaaatgga ctgggtcttg gtgtgtaacc ccggtgaagt tatagcctcc  
 120  
 ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat  
 180  
 cagtggcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggccctc  
 240  
 tggggctctg cttggccata ggcactgcac attgtgccac ctgctcatca cctcctctag  
 300  
 tctcacactg agcatcggag tacctgttgt gcagacagga aaactgagga gctctgagag  
 360  
 gctgagcatg gagctcacc catgccatag ggtgtgggaa gagggcacag gaggcctcat  
 420  
 ccatggggga aagggttgag gatggacatg ggtggggaga gggcatagac atcccttctc  
 480  
 aatctctgtt cccaccacat ttcataggag atgagttagg agatgacagc t  
 531

<210> 96  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser  
 1 5 10 15  
 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr  
 20 25 30  
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp  
 35 40 45  
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe  
 50 55 60  
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu  
 65 70 75 80  
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val  
 85 90 95  
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg  
 100 105 110  
 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu  
 115 120

<210> 97  
 <211> 405  
 <212> DNA  
 <213> Homo sapiens

<400> 97  
 ggctcggggcca gtcgaacttc attcccgctt cgagggtctt gctgcggatg ggccgtacgc  
 60  
 tcgcggtgcc ttgcgcgcgg gctggttagt ggagaagccg cgcgagtacg cgccgtagag  
 120  
 cgacatcgtg tctgagacgt cgaagctcag gccagcttt ggcgctccagg cgcgctcggg  
 180  
 cggtcgcgcc tcttgccgga attgattcag cgcaatcccg gccatcacat gccagcgctt  
 240  
 gtccagggtc atgaaatcct gggcataggc gcgcgaggag cgcagcggcg aattggacag  
 300  
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt  
 360  
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat  
 405

<210> 98  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 98  
 Met Ala Ser Gly Asp Leu Phe Pro Gly Asn Val Phe Ser Pro Arg Val  
 1 5 10 15  
 Pro Phe Pro Ser Ser Asp Ile Thr Pro Asn Ile Glu Arg Leu Ser Asn  
 20 25 30  
 Ser Pro Leu Arg Ser Ser Arg Ala Tyr Ala Gln Asp Phe Met Thr Leu  
 35 40 45  
 Asp Lys Arg Trp His Val Met Ala Gly Ile Ala Leu Asn Gln Leu Pro  
 50 55 60  
 Gln Glu Gly Gly Pro Thr Glu Arg Ala Trp Thr Pro Lys Leu Gly Leu  
 65 70 75 80  
 Ser Phe Asp Val Ser Asp Thr Met Ser Leu Tyr Gly Ala Tyr Ser Arg  
 85 90 95  
 Gly Phe Ser Thr Tyr Gln Pro Ala Arg Lys Ala Pro Arg Ala Tyr Gly  
 100 105 110  
 Pro Ser Ala Ala Arg Pro Ser Lys Arg Glu  
 115 120

<210> 99  
 <211> 545  
 <212> DNA  
 <213> Homo sapiens

<400> 99  
 acgcgtccgc tcccgatgtc gttgacgagc tgcgctcagc gatgacggta ctcacccatc  
 60  
 tgccccgacg acccagcaaa cgccccggc tgttctcat tgaccacgcc gaccggatcg  
 120  
 tcgatcccat cactcgggat ttgctggaat ccctgggtcg cgaagccggc gaggctgcgg  
 180  
 tgatcttggg tgcccagcgt cgcggctcgca tcgattggct ctccccacag atcatccaca  
 240

acctggccga acaccatttt gagtcgtcct ctggaggtac tcgatgatga ctgaacgttc  
 300  
 ccattccacg atcagggttaa ggtggccggc ggtggtggtt ctcgtcctcg ttccgctgct  
 360  
 ggtggctgcc ggattggtcc gggacgacct ggcataccac cgaccggttg ggccgggtga  
 420  
 aagcggccgt cgtcaacgag gacaaggccg tcaagggtcg tggacaactg gttccgatgg  
 480  
 gccgccaaact caccgccgcc ttgatggact ctggctcgca caccactgat ggccacaccg  
 540  
 tcgac  
 545

<210> 100

<211> 101

<212> PRT

<213> Homo sapiens

<400> 100

Met	Gly	Thr	Phe	Ser	His	His	Arg	Val	Pro	Pro	Glu	Asp	Asp	Ser	Lys
1				5					10					15	
Trp	Cys	Ser	Ala	Arg	Leu	Trp	Met	Ile	Cys	Gly	Glu	Ser	Gln	Ser	Met
			20					25					30		
Arg	Pro	Arg	Arg	Trp	Ala	Pro	Lys	Ile	Thr	Ala	Ala	Ser	Pro	Ala	Ser
			35				40					45			
Arg	Thr	Arg	Asp	Ser	Ser	Lys	Ser	Arg	Val	Met	Gly	Ser	Thr	Ile	Arg
			50			55					60				
Ser	Ala	Trp	Ser	Met	Arg	Asn	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Arg	Arg
65					70				75					80	
Gly	Arg	Trp	Val	Ser	Thr	Val	Ile	Ala	Glu	Arg	Ser	Ser	Ser	Thr	Thr
			85					90						95	
Ser	Gly	Ala	Asp	Ala											
				100											

<210> 101

<211> 619

<212> DNA

<213> Homo sapiens

<400> 101

ngcgcgccac agaagtgaag aagtacggtc tcaagcccgt gggagcggtc ttccctgtccg  
 60  
 tcatgcacga tccggacttc gatccgatcc ccatggtgaa caaggagctt gacgccttcg  
 120  
 aagctgccgg gggtgactat ctcacccctc ccacggattc cggacgcaag ggatacacga  
 180  
 ccgcccgtcc tcacgaggcc ggcggaaaac gctattacca acctggacca gatccgcgaa  
 240  
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatggtccag  
 300  
 aacctgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact  
 360  
 ggtcatctgg cctgtggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc  
 420

gtcgacattg tccacgcaa agatgtccat aaggagatgg ccgacaagct ttgacctggc  
 480  
 gagatcacct ggtccgaagg cattcgcgcc gggatgttcg cacccatcgg cgacggatgat  
 540  
 atcgactttg cagccatcgt gaggtcctt gatgaagccg ggttcgatgg ttattacgtc  
 600  
 ctagagcagg acatcatga  
 619

<210> 102

<211> 173

<212> PRT

<213> Homo sapiens

<400> 102

Thr	Arg	Ser	Leu	Thr	Pro	Ser	Lys	Leu	Pro	Gly	Val	Thr	Ile	Ser	Ser
1			5					10					15		
Ser	Pro	Arg	Ile	Pro	Asp	Ala	Arg	Asp	Thr	Arg	Pro	Pro	Val	Leu	Thr
		20					25					30			
Arg	Pro	Ala	Glu	Asn	Ala	Ile	Thr	Asn	Leu	Asp	Gln	Ile	Arg	Glu	Val
		35				40					45				
Cys	Ala	Ser	Arg	Asn	Val	Thr	Ala	Cys	Leu	His	Pro	His	Trp	Gly	Thr
	50				55				60						
Met	Val	Gln	Asn	Arg	Asp	Glu	Val	Ile	Arg	Val	Leu	Glu	Asn	Ser	Ser
65				70				75					80		
Ile	Gly	Leu	Cys	Leu	Asp	Thr	Gly	His	Leu	Ala	Cys	Gly	Gly	Thr	Asp
		85					90					95			
Val	Val	Glu	Leu	Val	Arg	Lys	Tyr	Ala	Asn	Arg	Val	Asp	Ile	Val	His
		100					105					110			
Ala	Lys	Asp	Val	His	Lys	Glu	Met	Ala	Asp	Lys	Leu	Leu	Pro	Gly	Glu
	115					120					125				
Ile	Thr	Trp	Ser	Glu	Gly	Ile	Arg	Ala	Gly	Met	Phe	Ala	Pro	Ile	Gly
	130				135					140					
Asp	Gly	Asp	Ile	Asp	Phe	Ala	Ala	Ile	Val	Arg	Leu	Leu	Asp	Glu	Ala
145				150						155				160	
Gly	Phe	Asp	Gly	Tyr	Tyr	Val	Leu	Glu	Gln	Asp	Ile	Met			
			165					170							

<210> 103

<211> 321

<212> DNA

<213> Homo sapiens

<400> 103

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 120  
 actgggggga gacccttgcc gctgggggga gaccgagcc attgggggga gacccttgcc  
 180  
 atggggaaag acccctgcca ttgggggaga ntacctgcca ttgggggaga tccctgccgt  
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 300

agtgggtggg gcgaagaccc c  
321

<210> 104  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 104  
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20 25 30  
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu  
35 40 45  
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp  
50 55 60  
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg  
65 70 75 80  
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85 90 95  
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro  
100 105

<210> 105  
<211> 344  
<212> DNA  
<213> Homo sapiens

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ccgggtcaac gaggggttgg cgcaagggtcc actccgtggc gcccggggtg atgtgcaaca  
120  
gggcgggggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgtcc cagtacccat  
180  
ccagcgcatt gccccaagcgg tcggcatccc agccgtggtc gccgtcgagc gccccaggg  
240  
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344

<210> 106  
<211> 62  
<212> PRT  
<213> Homo sapiens

<400> 106  
Cys Ala Thr Gly Arg Ala Arg Ala Arg Pro Gly Leu Ile Pro Ala Ser  
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Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His  
20 25 30  
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His





&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

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gatattgggg taagttacca atttacttta cagcccttaa gtaaataatc tgctttcctc
180
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660
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748

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&lt;210&gt; 110

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

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Met Gln Leu Phe Tyr Phe Arg Gln Glu Cys Ser Lys Leu Arg Glu Glu
1           5           10           15
Leu Arg Leu Gln His Glu Glu Asp Lys Lys Ser Ala Met Ser Gln Leu
20           25           30
Leu Gln Leu Lys Asp Arg Glu Lys Asn Ala Ala Arg Asp Ser Trp Gln
35           40           45
Lys Lys Val Glu Asp Leu Leu Asn Gln Ile Ser Leu Leu Lys Gln Asn
50           55           60
Leu Glu Ile Gln Leu Ser Gln Ser Gln Thr Ser Leu Gln Gln Leu Gln
65           70           75           80
Ala Gln Phe Thr Gln Glu Arg Gln Arg Leu Thr Gln Glu Leu Glu Glu
85           90           95
Leu Glu Glu Gln His Gln Gln Arg His Lys Ser Leu Lys Glu Ala His
100          105          110
Val Leu Ala Phe Gln Thr Met Glu Glu Glu Lys Glu Lys Glu Gln Arg
115          120          125
Ala Leu Glu Asn His Leu Gln Gln Lys His Ser Ala Glu Leu Gln Ser

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130                      135                      140  
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 <212> DNA  
 <213> Homo sapiens

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<210> 112  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

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 20                      25                      30  
 Ile Thr Gly Phe Asp Gly Ile Leu Ser Ala Tyr Xaa Arg His Gln His  
 35                      40                      45  
 Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile  
 50                      55                      60  
 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu  
 65                      70                      75                      80  
 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro  
 85                      90                      95  
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val  
 100                      105                      110  
 Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu  
 115                      120                      125  
 Thr Thr Gln His Val Arg Glu Ala Thr Ala Ala Val Glu Ser Gly  
 130                      135                      140

<210> 113  
 <211> 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 113

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382

&lt;210&gt; 114

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 114

Met	Leu	Gly	Ser	Gly	Arg	Thr	Pro	Cys	Pro	Arg	Leu	Arg	Ala	Val	Ala
1				5					10					15	
Trp	Ala	Thr	Met	Arg	Ala	Ala	Ser	Ile	Leu	Arg	Pro	Gly	Val	Pro	Gly
			20					25					30		
Ala	Gln	Lys	Glu	Thr	Arg	Arg	Trp	Leu	Pro	Pro	Arg	Asp	Arg	Pro	Ser
		35					40					45			
Ala	Cys	Cys	Cys	Ala	Ser	Ser	Ala	Ile	Ser	Ala	Val	Ser	Tyr	Ser	Ser
	50					55					60				
Thr	Ala	Lys	Pro	Phe	Ser	Cys	Pro	Ser	Trp	Pro	His	Ala	Ser	Trp	Gln
65					70					75				80	
Lys	Val	Gly	Leu	Trp	Thr	Ala	Asp	Ser	Ala	Arg	His	Arg	Ala	Ser	Thr
			85						90					95	
Ser	Leu	Lys	Pro	Gly	Gly	Arg	Arg	Ser	Thr	Gln	Arg	Gln	Gln	Glu	Trp
			100					105						110	
Arg	Arg	Ala	Gly	Leu	Ser	Ser	Pro	Ala	Ser	Val	Gln	Cys			
		115					120					125			

&lt;210&gt; 115

&lt;211&gt; 4798

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 115

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&lt;210&gt; 116

&lt;211&gt; 1062

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 116

Met Met Gly Thr Ser Gln Gly His Val Ala Arg Lys Ser Arg Asn Trp

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 20 25 30  
 Cys His Leu Ser Pro Ser Ser Leu Ser Pro Phe Ser Val Ala Glu Arg  
 35 40 45  
 Lys Pro Pro Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile  
 50 55 60  
 Ala Gln Asn Glu Ser Pro Val Leu Gln Ser Gly His Trp Ser Glu Tyr  
 65 70 75 80  
 Phe Arg Asn Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg  
 85 90 95  
 Pro Thr Ser Glu Val Leu Leu Lys His Arg Phe Val Leu Arg Glu Arg  
 100 105 110  
 Pro Pro Thr Val Ile Met Asp Leu Ile Gln Arg Thr Lys Asp Ala Val  
 115 120 125  
 Arg Glu Leu Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Ile Leu Phe  
 130 135 140  
 Gln Glu Ala Pro Asn Gly Pro Gly Ala Glu Ala Pro Glu Glu Glu Glu  
 145 150 155 160  
 Glu Ala Glu Pro Tyr Met His Arg Ala Gly Thr Leu Thr Ser Leu Glu  
 165 170 175  
 Ser Ser His Ser Val Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser  
 180 185 190  
 Ser Ser Val Asn Ser Leu Ala Asp Ala Ser Asp Asn Glu Glu Glu Glu  
 195 200 205  
 Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Pro Glu Ala Arg  
 210 215 220  
 Glu Met Ala Met Met Gln Glu Gly Glu His Thr Val Thr Ser His Ser  
 225 230 235 240  
 Ser Ile Ile His Arg Leu Pro Gly Ser Asp Asn Leu Tyr Asp Asp Pro  
 245 250 255  
 Tyr Gln Pro Glu Ile Thr Pro Ser Pro Leu Gln Pro Pro Ala Ala Pro  
 260 265 270  
 Ala Pro Thr Ser Thr Thr Ser Ser Ala Arg Arg Arg Ala Tyr Cys Arg  
 275 280 285  
 Asn Arg Asp His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Ser Arg  
 290 295 300  
 Gln Ile Gln Glu His Glu Gln Asp Ser Ala Leu Arg Glu Gln Leu Ser  
 305 310 315 320  
 Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Leu Ala Leu  
 325 330 335  
 Glu Ser Arg Leu Arg Gly Glu Arg Glu Glu His Ser Ala Arg Leu Gln  
 340 345 350  
 Arg Glu Leu Glu Ala Gln Arg Ala Gly Phe Gly Ala Glu Ala Glu Lys  
 355 360 365  
 Leu Ala Arg Arg His Gln Ala Ile Gly Glu Lys Glu Ala Arg Ala Ala  
 370 375 380  
 Gln Ala Glu Glu Arg Lys Phe Gln Gln His Ile Leu Gly Gln Gln Lys  
 385 390 395 400  
 Lys Glu Leu Ala Ala Leu Leu Glu Ala Gln Lys Arg Thr Tyr Lys Leu  
 405 410 415  
 Arg Lys Glu Gln Leu Lys Glu Glu Leu Gln Glu Asn Pro Ser Thr Pro  
 420 425 430  
 Lys Arg Glu Lys Ala Glu Trp Leu Leu Arg Gln Lys Glu Gln Leu Gln

435					440					445						
Gln	Cys	Gln	Ala	Glu	Glu	Glu	Glu	Ala	Gly	Leu	Leu	Arg	Arg	Gln	Arg	Gln
450					455					460						
Tyr	Phe	Glu	Leu	Gln	Cys	Arg	Gln	Tyr	Lys	Arg	Lys	Met	Leu	Leu	Ala	480
465	470					475					480					
Arg	His	Ser	Leu	Asp	Gln	Asp	Leu	Leu	Arg	Glu	Asp	Leu	Asn	Lys	Lys	495
485					490					495						
Gln	Thr	Gln	Lys	Asp	Leu	Glu	Cys	Ala	Leu	Leu	Leu	Arg	Gln	His	Glu	510
500					505					510						
Ala	Thr	Arg	Glu	Leu	Glu	Leu	Arg	Gln	Leu	Gln	Ala	Val	Gln	Arg	Thr	525
515					520					525						
Arg	Ala	Glu	Leu	Thr	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Gly	Asn	Gln	540
530					535					540						
Leu	Glu	Tyr	Asn	Lys	Arg	Arg	Glu	Gln	Glu	Leu	Arg	Gln	Lys	His	Ala	560
545	550					555					560					
Ala	Gln	Val	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Val	Arg	Ala	Gly	Gln	575
565					570					575						
Arg	Pro	Pro	Gly	Leu	Pro	Leu	Pro	Ile	Pro	Gly	Ala	Leu	Gly	Pro	Pro	590
580					585					590						
Asn	Thr	Gly	Thr	Pro	Ile	Glu	Gln	Gln	Pro	Cys	Ser	Pro	Gly	Gln	Glu	605
595					600					605						
Ala	Val	Leu	Asp	Gln	Arg	Met	Leu	Gly	Glu	Glu	Glu	Ala	Val	Gly	620	640
610					615					620						
Glu	Arg	Arg	Ile	Leu	Gly	Lys	Glu	Gly	Ala	Thr	Leu	Glu	Pro	Lys	Gln	640
625	630					635					640					
Gln	Arg	Ile	Leu	Gly	Glu	Glu	Ser	Gly	Ala	Pro	Ser	Pro	Ser	Pro	Gln	655
645					650					655						
Lys	His	Gly	Ser	Leu	Val	Asp	Glu	Glu	Val	Trp	Gly	Leu	Pro	Glu	Glu	670
660					665					670						
Ile	Glu	Glu	Leu	Arg	Val	Pro	Ser	Leu	Val	Pro	Gln	Glu	Arg	Ser	Ile	685
675					680					685						
Val	Gly	Gln	Glu	Glu	Ala	Gly	Thr	Trp	Ser	Leu	Trp	Gly	Lys	Glu	Asp	700
690					695					700						
Glu	Ser	Leu	Leu	Asp	Glu	Glu	Phe	Glu	Leu	Gly	Trp	Val	Gln	Gly	Pro	720
705	710					715					720					
Ala	Leu	Thr	Pro	Val	Pro	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	735
725					730					735						
Pro	Ile	Gly	Thr	Pro	Arg	Asp	Pro	Gly	Asp	Gly	Cys	Pro	Ser	Pro	Asp	750
740					745					750						
Ile	Pro	Pro	Glu	Pro	Pro	Pro	Thr	His	Leu	Arg	Pro	Cys	Pro	Ala	Ser	765
755					760					765						
Gln	Leu	Pro	Gly	Leu	Leu	Ser	His	Gly	Leu	Leu	Ala	Gly	Leu	Ser	Phe	780
770					775					780						
Ala	Val	Gly	Ser	Ser	Ser	Gly	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	800
785	790					795					800					
Leu	Pro	Leu	Leu	Ala	Ala	Gln	Gly	Gly	Gly	Gly	Leu	Gln	Ala	Ala	Leu	815
805					810					815						
Leu	Ala	Leu	Glu	Val	Gly	Leu	Val	Gly	Leu	Gly	Ala	Ser	Tyr	Leu	Leu	830
820					825					830						
Leu	Cys	Thr	Ala	Leu	His	Leu	Pro	Ser	Ser	Leu	Phe	Leu	Leu	Leu	Ala	845



```

865              870              875              880
Pro Gly Leu Ala Leu Pro Leu Val Ala Met Ala Ala Gly Gly Arg Trp
              885              890              895
Val Arg Gln Gln Gly Pro Arg Val Arg Arg Gly Ile Ser Arg Leu Trp
              900              905              910
Leu Arg Val Leu Leu Arg Leu Ser Pro Met Ala Phe Arg Ala Leu Gln
              915              920              925
Gly Cys Gly Ala Val Gly Asp Arg Gly Leu Phe Ala Leu Tyr Pro Lys
              930              935              940
Thr Asn Lys Asp Gly Phe Arg Ser Arg Leu Pro Val Pro Gly Pro Arg
945              950              955              960
Arg Arg Asn Pro Arg Thr Thr Gln His Pro Leu Ala Leu Leu Ala Arg
              965              970              975
Val Trp Val Leu Cys Lys Gly Trp Asn Trp Arg Leu Ala Arg Ala Ser
              980              985              990
Gln Gly Leu Ala Ser His Leu Pro Pro Trp Ala Ile His Thr Leu Ala
              995              1000              1005
Ser Trp Gly Leu Leu Arg Gly Glu Arg Pro Thr Arg Ile Pro Arg Leu
              1010              1015              1020
Leu Pro Arg Ser Gln Arg Gln Leu Gly Pro Pro Ala Ser Arg Gln Pro
1025              1030              1035              1040
Leu Pro Gly Thr Leu Ala Gly Arg Arg Ser Arg Thr Arg Gln Ser Arg
              1045              1050              1055
Ala Leu Pro Pro Trp Arg
              1060

```

```

<210> 117
<211> 471
<212> DNA
<213> Homo sapiens

```

```

<400> 117
naccgcttga cgatctgtct ggctggtgta gtgatctgcg ctgtgggtgt cgtcgatgac
60
ctgctcgacc ttctgcctt ggccaaggca gctggccagg tattagcggc cggcatcgtc
120
gtcacgggcg gagtgcgaat gttttggatc ccgctgccga actccatcat tgctttgggg
180
acgcctactt cgatcttggt gacggtgttc ttcatgtgt tgtgcgcaa tgcggtgaat
240
ttcattgatg gacttgacgg cctggcatcc ggtgtggtgg ccatcgggtc cttggctttc
300
ttctcataca cctacctgct ggctcacgaa caggactttg ttgttgcgac gactaccagt
360
ctcattacgg ctgcgacggc gggcgctgtg ctcggttttt tgccccacaa ctggcatccg
420
gcgaggatgt tcatgggtga ttccggagct ctgctacttg gcttattgct a
471

```

```

<210> 118
<211> 157
<212> PRT
<213> Homo sapiens

```

&lt;400&gt; 118

Xaa Ala Leu Thr Ile Cys Leu Ala Gly Val Val Ile Cys Ala Val Gly  
 1 5 10 15  
 Val Val Asp Asp Leu Leu Asp Leu Pro Ala Leu Ala Lys Ala Ala Gly  
 20 25 30  
 Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe  
 35 40 45  
 Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser  
 50 55 60  
 Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn  
 65 70 75 80  
 Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly  
 85 90 95  
 Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp  
 100 105 110  
 Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly  
 115 120 125  
 Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe  
 130 135 140  
 Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu Leu  
 145 150 155

&lt;210&gt; 119

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

ntcaaacatg agcagtcgtg gcggccgagg ccgcggtggc tattatcgcg agctttatgg  
 60  
 tagccgaggt cgaggcagta aatctaataa aactttcgca aaaaattcgg atgtctactc  
 120  
 tcagaaaaag actcgaacag tacgaggcac ctccgaagat ttagcacgat cgctccataa  
 180  
 gcttcatatg cgcccgatcc ctgcgtatca tgacattgag ggtatgtggg ctttcccagc  
 240  
 ctttactttt tatctggatc atgcacaagc agaccatac gctgccccaa ataaggcacg  
 300  
 cn  
 302

&lt;210&gt; 120

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 120

Met Ser Ser Arg Gly Gly Arg Gly Arg Gly Tyr Tyr Arg Glu Leu  
 1 5 10 15  
 Tyr Gly Ser Arg Gly Arg Gly Ser Lys Ser Asn Glu Thr Phe Ala Lys  
 20 25 30  
 Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr  
 35 40 45  
 Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

50                      55                      60  
 Pro Ala Tyr His Asp Ile Glu Gly Met Trp Ala Phe Pro Ala Phe Thr  
 65                      70                      75                      80  
 Phe Tyr Leu Asp His Ala Gln Ala Asp Pro Tyr Ala Ala Pro Asn Lys  
                     85                      90                      95  
 Ala Arg

<210> 121  
 <211> 318  
 <212> DNA  
 <213> Homo sapiens

<400> 121  
 ngcatggggg gccctgggac cgcacttgtg cccctttttt ttttagggaa aaaattgagc  
 60  
 cctaaaggat ttgccgcatt acaggaaagt tttttggtta gtttgggggt gtttctgtgc  
 120  
 tgtgtgagaa ggagtagaag cagctccagt agagtggggc ttttcatttt tatccagagg  
 180  
 aaattttagt gctgtggcta ttacttcctt ttttttcttt tttttttttg ttttagagaca  
 240  
 gagtctgnet ctgtcgccag gctggagtga agtggcacga ttcagctca ctgcaacctc  
 300  
 tgcctcccag gttcaagc  
 318

<210> 122  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 122  
 Xaa Met Gly Gly Pro Gly Thr Ala Leu Val Pro Leu Phe Phe Leu Gly  
 1                      5                      10                      15  
 Lys Lys Leu Ser Pro Lys Gly Phe Ala Ala Leu Gln Glu Ser Phe Leu  
                     20                      25                      30  
 Val Ser Leu Gly Leu Phe Leu Cys Cys Val Arg Arg Ser Arg Ser Ser  
                     35                      40                      45  
 Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly  
                     50                      55                      60  
 Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Phe Cys Leu Glu Thr  
 65                      70                      75                      80  
 Glu Ser Xaa Ser Val Ala Arg Leu Glu  
                     85

<210> 123  
 <211> 338  
 <212> DNA  
 <213> Homo sapiens

<400> 123  
 acgcgtctag ggtagaaatc aactccagta actgtcattc aacctcagca atgctgggga  
 60

cgggcagagg cagggcagct gtgtgccaca ttctgccag ggctggtcag gccccggctc  
 120  
 tcaccactcc tcttcctgc ttgaacctg tggaacaaag ggccctgca ccccaactca  
 180  
 ttctcttttg ccacataagg gcctcaagtc atgtgtccc ctctgcctgg gttgcttttt  
 240  
 ctccctctgc ttgggtcact gttcacacca ctggccactt tcctcagga agggccctca  
 300  
 ctgcccacac acctaaacat gcccctgct cctccata  
 338

<210> 124  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 124  
 Met Leu Gly Thr Gly Arg Gly Arg Ala Ala Val Cys His Ile Pro Ala  
 1 5 10 15  
 Arg Ala Gly Gln Ala Pro Ala Leu Thr Thr Pro Pro Pro Cys Phe Glu  
 20 25 30  
 Pro Val Glu Gln Arg Ala Pro Ala Pro Gln Leu Ile Pro Leu Cys His  
 35 40 45  
 Ile Arg Ala Ser Ser His Ala Val Pro Ser Ala Trp Val Ala Phe Ser  
 50 55 60  
 Pro Ser Ala Trp Val Thr Val His Thr Thr Gly His Phe Pro Gln Gly  
 65 70 75 80  
 Arg Ala Leu Thr Ala His Thr Pro Lys His Ala Pro Cys Ser Ser Ile  
 85 90 95

<210> 125  
 <211> 280  
 <212> DNA  
 <213> Homo sapiens

<400> 125  
 ccatggacct ggccagccac catcacctgc ctctgcctc acccaccctg ggtgcctgcc  
 60  
 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga  
 120  
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca cttttctgca  
 180  
 tttccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg  
 240  
 gcttctgctg tcttggecca ttctggatag gctgatcta  
 280

<210> 126  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 126  
 Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

```

      1             5             10             15
Gly Ala Cys Arg Gln Gly Leu Glu Gly Arg Leu Leu Glu Arg Glu Thr
      20             25             30
Arg Pro Ile Cys Leu Ser Gly Asn Leu Gln Pro Pro Thr Gly Ala Asp
      35             40             45
Cys Gln Leu Ser Gly Glu Lys Ser Leu Phe Cys Ile Pro Thr Thr Leu
      50             55             60
Ser Ile Cys Ala Ile Arg Gln Arg Asp Ser Thr His Leu Ile Glu Gly
      65             70             75             80
Phe Cys Cys Pro Gly Pro Phe Trp Ile Gly Leu Ile
      85             90

```

&lt;210&gt; 127

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

```

cgcgatgatcg ccgtggcgga gggccgcggc gccgactcga tcgccagct gacaaccgag
60
ctgcaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
120
gcgttcacga ggggctgcgc cgagcacctg cccaacgcgc gcgtcacctt cgacaagttc
180
cacgtcatcg ggcacgcaa tgcggccgtg gacaggatgc gccgcatcga gcagcgcagc
240
gacaagtccc tcaaggggat gcgctggctg ctgctgaaga accgcgccag cctcaagccc
300
gaggctgccg ccgatctgga tgccctgac gccaggatgg ccaactgtgcg caccgcgcgc
360
gcctgggtct acaaggagca gctgcgcgag atcctcgcgc gcaagcagat caactgggca
420
cgcgacatgc tcaagcactg gtgc
444

```

&lt;210&gt; 128

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 128

```

Arg Val Ile Ala Val Ala Glu Gly Arg Gly Ala Asp Ser Ile Ala Gln
      1             5             10             15
Leu Thr Thr Glu Leu Gln Ser Arg His Cys Pro Ala Glu Gln Ile Thr
      20             25             30
Ser Val Ser Ile Asp Met Ser Pro Ala Phe Ile Arg Gly Cys Ala Glu
      35             40             45
His Leu Pro Asn Ala Arg Val Thr Phe Asp Lys Phe His Val Ile Gly
      50             55             60
His Ala Asn Ala Ala Val Asp Arg Met Arg Arg Ile Glu Gln Arg Ser
      65             70             75             80
Asp Lys Ser Leu Lys Gly Met Arg Trp Ser Leu Leu Lys Asn Arg Ala
      85             90             95
Ser Leu Lys Pro Glu Ala Ala Ala Asp Leu Asp Ala Leu Ile Ala Arg

```

100 105 110  
 Met Ala Thr Val Arg Thr Ala Arg Ala Trp Val Tyr Lys Glu Gln Leu  
 115 120 125  
 Arg Glu Ile Leu Ala Arg Lys Gln Ile Asn Val Ala Arg Asp Met Leu  
 130 135 140  
 Lys His Trp Cys  
 145

<210> 129  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 129  
 gagggaggac gtaccgtccc cggttatagcc aagctcgaga agccgcaagc taccgagaac  
 60  
 ttggacgaga ttattgacgt ctttgacgcc gtcattggtg cccgtggcga tatggccgct  
 120  
 gaggcgccgc tcgaggaagt tccgctgac caaaagcaga taccgagaa ggctcgttta  
 180  
 caggctaagc ccgtcattgt ggccaccag atgcttgagt cgatgatcca cgctcccgct  
 240  
 ccgacccgcg ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g  
 291

<210> 130  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 130  
 Glu Glu Gly Arg Thr Val Pro Val Ile Ala Lys Leu Glu Lys Pro Gln  
 1 5 10 15  
 Ala Ile Glu Asn Leu Asp Glu Ile Ile Asp Val Phe Asp Ala Val Met  
 20 25 30  
 Val Ala Arg Gly Asp Met Ala Val Glu Cys Pro Leu Glu Glu Val Pro  
 35 40 45  
 Leu Ile Gln Lys Gln Ile Ile Glu Lys Ala Arg Leu Gln Ala Lys Pro  
 50 55 60  
 Val Ile Val Ala Thr Gln Met Leu Glu Ser Met Ile His Ala Pro Arg  
 65 70 75 80  
 Pro Thr Arg Ala Glu Ala Ala Asp Val Ala Asn Ala Ile Leu Asp Gly  
 85 90 95  
 Ala

<210> 131  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
 tccggagcgt ccgtggccct catgggtgtg tcagcgtggt tgctgtctcg ggccgcagag  
 60

attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc  
 120  
 cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag  
 180  
 ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tgggnnacgt  
 240  
 cgccgggggtg acctgctggt acgggttact gccgacgtcg acgcgggtgtt ggacatggtc  
 300  
 gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggtcctt  
 360  
 ctttgtccga gagaagggtg agttttctta gccggattcc aacacagcct gggggc  
 416

<210> 132

<211> 126

<212> PRT

<213> Homo sapiens

<400> 132

Ser	Gly	Ala	Ser	Val	Ala	Leu	Met	Gly	Val	Ser	Ala	Trp	Leu	Leu	Ser
1				5					10					15	
Arg	Ala	Ala	Glu	Ile	Pro	Pro	Val	Leu	Tyr	Leu	Glu	Ala	Ala	Ala	Val
			20					25					30		
Gly	Val	Arg	Phe	Phe	Gly	Ile	Ser	Arg	Gly	Val	Phe	Arg	Tyr	Ala	Glu
		35					40				45				
Arg	Leu	Val	Gly	His	Asp	Leu	Ala	Leu	Arg	Met	Gln	Gly	Ala	Leu	Arg
	50					55				60					
Met	Arg	Val	Tyr	Asp	Arg	Leu	Ser	Arg	Thr	Xaa	Pro	Ala	Gly	Xaa	Arg
65				70					75					80	
Arg	Arg	Gly	Asp	Leu	Val	Arg	Val	Thr	Ala	Asp	Val	Asp	Ala	Val	
			85					90					95		
Leu	Asp	Met	Val	Val	Arg	Val	Ile	Val	Pro	Ala	Cys	Ala	Ser	Ser	Leu
		100					105						110		
Val	Ile	Ile	Gly	Thr	Thr	Val	Leu	Leu	Cys	Pro	Arg	Glu	Gly		
		115					120						125		

<210> 133

<211> 327

<212> DNA

<213> Homo sapiens

<400> 133

gccgttgcta tcgctgctgg tatgcgtgca gacgtcactg tttttgatat caatategct  
 60  
 gcgttgaaga gactcgccga catctaccag ggtcgtgttc acacagtagt atccaccgcg  
 120  
 gccgaaattg cgaaggcgct agaaaccgct gacgttgtga tcggttctgt ccttattccg  
 180  
 ggtagttcta ccccgaaagt tgttactacc gatatgggtg ctcacatgca gcctgggtct  
 240  
 gttcttattg atattgctat agaccaaggc ggctgcttcg aggattcgca cccaccact  
 300  
 tacgatgacc ccactttcac tgtgcac  
 327

<210> 134  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
 Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp  
 1 5 10 15  
 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg  
 20 25 30  
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu  
 35 40 45  
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr  
 50 55 60  
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser  
 65 70 75 80  
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser  
 85 90 95  
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His  
 100 105

<210> 135  
 <211> 560  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
 taagatgtgg tcctgccctg ttcctgaagg ggctgcagct ctgatggaaa atacagggat  
 60  
 ttacactcag ggctacagcc acggggggct gagggccaag gctgcaatct cgggggaagg  
 120  
 ggaagttggc ttttcttggt ggattggaaa catcctcttg gaggcaaaga cttttcctgg  
 180  
 atcttacaga cttcccggga tttttagatt agaattattgg gggcaaagga ggctgtcttg  
 240  
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag  
 300  
 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt  
 360  
 ccccatctc ccatggataa gtacgttcta gaacattctc tttgggtcta atactctgaa  
 420  
 atgacatctt gtcttcatgc tcgagagaga attacttcac tggctccact tggagtgcc  
 480  
 gtgttcagac accaagcctg actgggaggg ttccgttttc ttaacacctt cccaccgccg  
 540  
 acttccaagt cccacgcgt  
 560

<210> 136  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens



&lt;400&gt; 136

```

Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1           5           10           15
Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
      20           25           30
Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
      35           40           45
Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
 50           55           60
Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
65           70           75           80
Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
      85           90           95
Ile Ser Ser Gly
      100

```

&lt;210&gt; 137

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

```

accgggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
60
gaggcaaaca gctggtcgcg cacctgcttg aggtccaccg attgcgcatc gcccttgagc
120
aaggcgcgcc agttggtttt gtcggccact tggtcgcgga acaggtcttc gacaaaaccg
180
gactgctggc gggtcgcaac gcgcatgata ggcagcgcct ggctggcgcc ctggtcgagc
240
cagcgcgctc gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
300
aggtacacca catggtcggt catgcagaat gtttcgcccc agccgggata acggcaagtg
360
ccggcgctcgt aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
420
gtcatgccc
429

```

&lt;210&gt; 138

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

```

Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1           5           10           15
Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
      20           25           30
Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
      35           40           45
Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
 50           55           60
Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```

```

65          70          75          80
Gln Ser Gly Phe Val Glu Asp Leu Phe Arg Ser Gln Val Ala Asp Lys
          85          90          95
Thr Asn Trp Arg Ala Leu Leu Lys Gly Asp Ala Gln Ser Val Asp Leu
          100          105          110
Lys Gln Val Arg Asp Gln Leu Phe Ala Ser Cys Ala Glu Gly Leu Leu
          115          120          125
Ser Leu Gln Glu Arg Phe Gly Leu Gln Ala Ile Gln Pro
          130          135          140

```

<210> 139  
 <211> 341  
 <212> DNA  
 <213> Homo sapiens

```

<400> 139
acgcgtcggt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgccgcagc
60
ttgtgaacag cagaatcaag ccgctggtta atcttcctgg gagcttcata ggcggggatg
120
ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
180
tttgcagcct gtaacgactg aggggttcgga tggaaaaaca catgctccag gatggggaccg
240
acggccactt caccgatctc ttcatagccc tggcgtttgt agaaatccag gtagcgcgaa
300
tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
341

```

<210> 140  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

```

<400> 140
Met Thr Arg Thr His Gln Ala Ser Cys Ser Thr Leu Ala Ile Arg Ala
1          5          10          15
Thr Trp Ile Ser Thr Asn Ala Arg Ala Met Lys Arg Ser Val Lys Trp
          20          25          30
Pro Ser Val Pro Ser Trp Ser Met Cys Phe Ser Ile Arg Thr Leu Ser
          35          40          45
Arg Tyr Arg Leu Gln Arg Phe Glu Thr Glu Leu Phe Arg Gln Phe Arg
          50          55          60
Val Gln Ser Val Ser Pro Ala Arg Val Ala Ser Pro Pro Met Lys Leu
65          70          75          80
Pro Gly Arg Phe Thr Ser Gly Leu Ile Leu Leu Phe Thr Ser Cys Gly
          85          90          95
Ala Leu Ala Gln Ser Glu Leu Asp Val Arg Ile Lys Pro Ser Asn Asp
          100          105          110
Ala

```

<210> 141  
 <211> 324

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

gaattcctct tggatagctt cgggtaaatg ggtacagcaa atatcaggag cgcaaccgca  
60  
acctttactt actggtacat gaacaccatt tacattacag ctatcgtagt caccaccagt  
120  
catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc  
180  
gtcaactgtg aacaccgcta agtaatagcc tgcgggggct tgcattgaact cctttgacca  
240  
tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca  
300  
gcagttatca ccgccatac gcgt  
324

&lt;210&gt; 142

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met	Gly	Gly	Asp	Asn	Cys	Cys	Arg	Ser	Phe	Cys	Phe	Ala	Pro	Ser	Gly
1				5					10					15	
Val	Thr	Asn	Asp	Gly	Arg	Ile	Tyr	Tyr	Ala	Trp	Ser	Lys	Glu	Phe	Met
			20					25					30		
Gln	Ala	Pro	Ala	Gly	Tyr	Tyr	Leu	Ala	Val	Phe	Thr	Val	Asp	Gly	His
		35					40				45				
Thr	Tyr	Arg	Glu	Thr	Val	Val	Tyr	Lys	Pro	Phe	Ser	Tyr	Val	Ser	Val
	50					55					60				
His	Met	Thr	Trp	Gly	Glu	Tyr	Asp	Ser	Cys	Asn	Val	Asn	Gly	Val	His
65					70					75				80	
Val	Pro	Val	Ser	Lys	Gly	Cys	Gly	Cys	Ala	Pro	Asp	Ile	Cys	Cys	Thr
				85					90					95	
His	Leu	Pro	Glu	Ala	Ile	Gln	Glu	Glu	Phe						
			100					105							

&lt;210&gt; 143

&lt;211&gt; 1325

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 143

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gcaccccagg agaagaactt cctgtacaaa tgcattaggca ccaccctggg tgctgcttca  
120  
agtaaggagg tggtaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag  
180  
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240  
gacacgctgg ccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc  
300

attctcaaca tttttaagga tcgaagtgag aacgaagtgg agaagggtgaa gagtgtctctg  
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 420  
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 480  
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 600  
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 660  
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 720  
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 780  
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 840  
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 900  
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 960  
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 1020  
 cccaggatcc tgtgcaatgg ccctgggtgcc cttccacaac ctgggccttc tcatcggcct  
 1080  
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 1140  
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 1200  
 cgtggcggag cggctcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct  
 1260  
 cttccacacc tgccacagtg taggccagat tattgccaag cgcctcccc cagcccttca  
 1320  
 cgcgt  
 1325

&lt;210&gt; 144

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 144

Xaa Ala Trp Ile Cys Gln Leu Ser Leu Glu Leu Cys Arg Gln Leu Pro  
 1 5 10 15  
 Cys Tyr Asp Glu Ala Pro Gln Glu Lys Asn Phe Leu Tyr Lys Cys Ile  
 20 25 30  
 Gly Thr Thr Leu Gly Ala Ala Ser Ser Lys Glu Val Val Arg Lys His  
 35 40 45  
 Leu Gln Glu Leu Leu Glu Thr Ala Arg Tyr Gln Glu Glu Ala Glu Arg  
 50 55 60  
 Glu Gly Leu Ala Cys Cys Phe Gly Ile Cys Ala Ile Ser His Leu Glu  
 65 70 75 80  
 Asp Thr Leu Ala Gln Leu Glu Asp Phe Val Arg Ser Glu Val Phe Arg

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<210> 145
<211> 802
<212> DNA
<213> Homo sapiens
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494

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 360  
 ggtcattgtg cgatcaagct gccggggctct gtcagcgtgg tgaaccggtt atgtactggg  
 420  
 gttcgggtgg ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc  
 480  
 tggagaagcg ctgggtggcac atgcttgcca tcgtcatccc ggctgttttc atcgtcgccg  
 540  
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 600  
 tattgatctc cgttttatcg gctcctagca gccgtgggtca acgtatcgct atcaagcgat  
 660  
 acaggactcg tcgttcgcat cgttgtgtg ctgctgggaa acaatcccag cgatctactc  
 720  
 ggctaccgcc agacagttca ctcacaaccc ctcacgccgg cgcagacatc aaatcccatt  
 780  
 ctcgatagac ggcccacacc ac  
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<210> 146

<211> 151

<212> PRT

<213> Homo sapiens

<400> 146

Met	Lys	Val	Tyr	Ile	Thr	Leu	Val	Lys	Ala	Cys	Thr	Thr	Ser	Val	Gly
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Thr	Ile	Ser	Pro	Arg	Arg	Thr	Arg	His	His	Ala	Pro	Tyr	Leu	Asp	Arg
			20					25					30		
Met	Ser	Asp	Met	Ser	Met	Pro	Arg	Arg	Ala	Ala	Pro	Glu	Asp	Asp	Thr
		35					40					45			
Asp	Leu	Ala	Asp	Ala	Ala	Arg	Ser	Trp	Arg	Arg	Tyr	Leu	Ile	Leu	Val
	50					55					60				
Ile	Cys	Gly	Val	Ile	Val	Ala	Val	Leu	Gly	Leu	Gly	Ile	Phe	Gly	Tyr
65					70				75					80	
Leu	Ala	Trp	Trp	Ser	Leu	Cys	Asp	Gln	Ala	Ala	Gly	Val	Cys	Gln	Arg
			85					90					95		
Gly	Glu	Pro	Val	Met	Tyr	Trp	Cys	Ser	Val	Val	Ser	Leu	Ala	Ile	Leu
			100					105				110			
Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Gln	Ile	Trp	Leu	Glu	Lys	Arg	Trp
	115						120					125			
Trp	His	Met	Leu	Ala	Ile	Val	Ile	Pro	Ala	Val	Phe	Ile	Val	Ala	Gly
	130					135					140				
Ile	Phe	Trp	Leu	Ala	Val										
145					150										

<210> 147

<211> 368

<212> DNA

<213> Homo sapiens

<400> 147

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 120  
 attggtcaga aagtaccttg tgttcagtg acggggtcgg aaaagggtgct tcataaaaag  
 180  
 gattactggg atctagcaac acctatgcc aattgctggg gtacaacgga ccgaacagtt  
 240  
 attgctgatg cacgacgtac aatccccacc acggagtggg atatccttgc aagactacgt  
 300  
 ccacgcctag aagaggttcg caagcaacgt aatgatgtat tgctcctcaa cgaggaggat  
 360  
 ccccccta  
 368

<210> 148

<211> 117

<212> PRT

<213> Homo sapiens

<400> 148

Met	Thr	Leu	Leu	Ala	Leu	Val	Asp	Leu	Ser	Lys	Lys	Pro	Asp	Glu	Phe
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Thr	Gln	Trp	Ala	Leu	Val	Ala	Arg	Asp	Val	His	Asp	Ile	Pro	Gly	Leu
	20						25					30			
Arg	Lys	Val	Ile	Gly	Gln	Lys	Val	Pro	Cys	Val	Ala	Val	Thr	Gly	Ser
	35					40						45			
Glu	Lys	Val	Leu	His	Lys	Lys	Asp	Tyr	Trp	Asp	Leu	Ala	Thr	Pro	Met
	50					55					60				
Pro	Ile	Ala	Trp	Gly	Thr	Thr	Asp	Arg	Thr	Val	Ile	Ala	Asp	Ala	Arg
	65				70				75				80		
Arg	Thr	Ile	Pro	Thr	Thr	Glu	Trp	Asp	Ile	Leu	Ala	Arg	Leu	Arg	Pro
			85					90					95		
Arg	Leu	Glu	Glu	Val	Arg	Lys	Gln	Arg	Asn	Asp	Val	Leu	Leu	Leu	Asn
			100					105					110		
Glu	Glu	Asp	Pro	Pro											
			115												

<210> 149

<211> 407

<212> DNA

<213> Homo sapiens

<400> 149

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 120  
 gcggtggatg gtatcgtgta ccgaagtgcg gatgaaggca agtcgtgggc cccaattaag  
 180  
 gggcctgaac agggtcaggc gcaccttttc gtgctccatc cctacgacaa gactcaagcg  
 240  
 tatattctga cgcgcagcac tcagcattgg cgcacgtcga accgtggcga gacgtggcag  
 300

tcattctcaa cgctcatcc gcctacgacc ttgaaagcta tgcctctgga ctttcatccg  
 360  
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 407

<210> 150  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 150  
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 Val Thr His Phe Pro Asn Met Ala Ala Gln Ile Gln Tyr Phe Glu Asp  
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 Ser Ser Val Val Ile Trp His Asp Ala Val Asp Gly Ile Val Tyr Arg  
 35 40 45  
 Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln  
 50 55 60  
 Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala  
 65 70 75 80  
 Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly  
 85 90 95  
 Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys  
 100 105 110  
 Ala Met Pro Leu Asp Phe His Pro Thr His His Asp Trp Ile Leu Phe  
 115 120 125  
 Thr Gly Gln Ala Cys Thr Val  
 130 135

<210> 151  
 <211> 448  
 <212> DNA  
 <213> Homo sapiens

<400> 151  
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 60  
 gcttttcgag catccaggtc cccagcccca gctactggcg cgccccgagc ccctagggtgc  
 120  
 cagagcggtg gtcggccggg ctccctgccca gtctcggctc ctccctcctc cccaccagaa  
 180  
 ggaaaaactt gggcccttcg agaaccctgt ggaatgttct ttgtaatcaa ctgtacatcc  
 240  
 gcttcacagg caccggcctcg tgcaaaatcg cgggtttcgg ggccttggag caaattgcgc  
 300  
 ttgtcagcgg cgacgtcagg aggacaaggg gaggggttcg cggctgaaac tgcagcttcg  
 360  
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 448

<210> 152



<211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 152  
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 35 40 45  
 Cys Pro Val Ser Ala Pro Pro Ser Ser Pro Pro Glu Gly Lys Thr Trp  
 50 55 60  
 Ala Leu Arg Glu Pro Cys Gly Met Phe Phe Val Ile Asn Cys Thr Ser  
 65 70 75 80  
 Ala Ser Thr Ala Arg Pro Arg Ala Lys Ser Arg Val Ser Gly Pro Trp  
 85 90 95  
 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly  
 100 105 110  
 Phe Ala Ala Glu Thr Ala Ala Ser Gln His Arg Ala Ile Leu Gly Cys  
 115 120 125  
 Ser Pro Pro Arg Gly Ala His Gly Lys Pro Ala Pro Gly Gly Arg Gly  
 130 135 140  
 Cys Met Asp Ile Arg  
 145

<210> 153  
 <211> 440  
 <212> DNA  
 <213> Homo sapiens

<400> 153  
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 120  
 tgcattgggtc cgtgtatatg cgtgtatata tgcggggata tgtatatgtg tgtgtgtatg  
 180  
 aacaggtgta agtggggagc actcaggtgt gtctgtgtgt gtctgtgtac acgtgtgtaa  
 240  
 gtgggtgacc atgaaggggt gtgtgtgtcc gtgtgtaggt ttgcgtgcat gcacacatgc  
 300  
 atgtgtgtac tggggcatcc aagcccttgg tctccactcc attccaccct acgectacct  
 360  
 ccttgatctc tgcgccagc cttggctgtg ctcccctgct gtatgcacgt ggggtgtctgc  
 420  
 acgtgggtgt ctgcacgcgt  
 440

<210> 154  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

<400> 154  
 Gly Arg His Ala Gly Val Cys Pro Ser Val Cys Pro Trp Val His Val  
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 Cys Val Cys Ile Cys Gly Gly Thr Gly Val Cys Pro Ser Val Cys Met  
 20 25 30  
 Gly Pro Cys Ile Cys Val Tyr Ile Cys Gly Asp Met Tyr Met Cys Val  
 35 40 45  
 Cys Met Asn Arg Cys Lys Trp Gly Ala Leu Arg Cys Val Cys Val Cys  
 50 55 60  
 Ser Cys Thr Arg Val  
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<210> 155  
 <211> 344  
 <212> DNA  
 <213> Homo sapiens

<400> 155  
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 120  
 cgatcttcct cctcgatcac ctcgtttgaa gtggacaggg aacaaagaca ctgagacaac  
 180  
 gcgccgcagg aagtaaaaag ttcgctctcc gatcacggcc gtcgcgcgag tgcacaggga  
 240  
 gaactgggca cctcgcaagc tacgccaccg cgatccatgc ccccgcccgt atcttcgcc  
 300  
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 344

<210> 156  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 156  
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 20 25 30  
 Gln Arg His Ser Asp Asn Ala Pro Gln Glu Val Lys Ser Ser Leu Ser  
 35 40 45  
 Asp His Gly Arg Arg Ala Ser Ala Gln Gly Glu Leu Gly Thr Ser Gln  
 50 55 60  
 Ala Thr Pro Pro Arg Ser Met Pro Pro Pro Val Ser Ser Ala Ser Ser  
 65 70 75 80  
 Thr Ser Pro Leu Pro Ile Ser Ile Ile Ser Asp Leu  
 85 90

<210> 157  
 <211> 6816  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
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gaacaacaaa gtcaggcggt ttgcttttga gctcaagatg caggacaaaa gtagttatct  
120  
cttggcagca gacagtgaag tggaaatgga agaattggatc acaattctaa ataagatcct  
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900  
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960  
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1140  
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1980  
accagagcca cacaggaaga agtcgcgggtt aacgtgactc gggtcattat tcatgtgggt  
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2100  
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2160  
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2280  
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2580  
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2640  
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3180

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3660  
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3720  
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3780  
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3960  
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<211> 1572

<212> PRT

<213> Homo sapiens

<400> 158

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Asp	Phe	Arg	Lys	Pro	Glu	Lys	Met	Ala	Lys	Leu	Pro	Val	Ile	Leu	Gly
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Asn	Leu	Asp	Ile	Thr	Ile	Asp	Asn	Val	Ser	Ser	Asp	Phe	Pro	Asn	Tyr
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Val	Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys
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Thr	Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys
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His	Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro
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Lys	Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn
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Ile	Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln
	130					135					140				
Pro	Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg
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Ser	Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr
			165						170					175	
Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His
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Leu	Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly
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Ser	Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp
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225					230					235				240	
Pro	Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu
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505



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Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn
        740                745                750
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu
        755                760                765
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu
        770                775                780
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe
785                790                795                800
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg
        805                810                815
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly
        820                825                830
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
        835                840                845
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
        850                855                860
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
865                870                875                880
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
        885                890                895
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
        900                905                910
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
        915                920                925
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
        930                935                940
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
945                950                955                960
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
        965                970                975
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
        980                985                990
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
        995                1000                1005
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
        1010                1015                1020
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
1025                1030                1035                1040
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
        1045                1050                1055
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
        1060                1065                1070
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
        1075                1080                1085
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
        1090                1095                1100
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
1105                1110                1115                1120
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg

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1125      1130      1135
Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
1140      1145      1150
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1155      1160      1165
Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
1170      1175      1180
Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
1185      1190      1195      1200
Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
1205      1210      1215
Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
1220      1225      1230
Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
1235      1240      1245
Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
1250      1255      1260
Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
1265      1270      1275      1280
Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
1285      1290      1295
Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
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Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
1315      1320      1325
Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
1330      1335      1340
Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
1345      1350      1355      1360
Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
1365      1370      1375
Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
1380      1385      1390
Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
1395      1400      1405
Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
1410      1415      1420
Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
1425      1430      1435      1440
Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
1445      1450      1455
Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
1460      1465      1470
Tyr Pro Asp Asn Lys Val Lys Leu Lys Glu Val Phe Arg Gln Phe
1475      1480      1485
Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
1490      1495      1500
Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
1505      1510      1515      1520
Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu
1525      1530      1535
Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala
1540      1545      1550
Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser

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1560

1565

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<211> 540  
<212> DNA  
<213> Homo sapiens

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120  
agcatgggtca gcctcagtga gaggtggcca gtggggagtg gtggccactg tacacctggc  
180  
acagcccaga gatgcatgtg ccaactctgtt gtgtgcttca accaaggggc gctctggcag  
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300  
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<210> 160  
<211> 110  
<212> PRT  
<213> Homo sapiens

<400> 160  
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Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe  
20 25 30  
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Gly Thr Ser Gln Arg Ala  
35 40 45  
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly  
50 55 60  
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg  
65 70 75 80  
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro  
85 90 95  
Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe  
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<210> 161  
<211> 351  
<212> DNA  
<213> Homo sapiens

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 ccgcagggca tgcagaattt gtatgaccgt atcgagcgca tgagtcagct gggccccgag  
 240  
 tttgtggaca ttacgtggaa tgccgggggc cggacgtcgg atatgacgac gcagctggtc  
 300  
 aagacggtgc atgcgtactt tgggtgctgag acgtgcatgc atctgacgtg c  
 351

&lt;210&gt; 162

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 162

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Phe	Ala	Gly	Arg	Arg	Ala	Trp	Leu	Ala	Ala	Thr	Met	Lys	Gly	Asp	Asp
			20				25					30			
Ser	Ser	Lys	Ile	Thr	His	Lys	Ile	Ala	Arg	Ala	Lys	Arg	Glu	Gly	Arg
		35				40					45				
Val	Trp	Trp	Ser	Phe	Glu	Tyr	Phe	Pro	Pro	Arg	Thr	Pro	Gln	Gly	Met
	50					55				60					
Gln	Asn	Leu	Tyr	Asp	Arg	Ile	Glu	Arg	Met	Ser	Gln	Leu	Gly	Pro	Glu
65				70					75				80		
Phe	Val	Asp	Ile	Thr	Trp	Asn	Ala	Gly	Gly	Arg	Thr	Ser	Asp	Met	Thr
			85					90					95		
Thr	Gln	Leu	Val	Lys	Thr	Val	His	Ala	Tyr	Phe	Gly	Val	Glu	Thr	Cys
		100					105					110			
Met	His	Leu	Thr	Cys											
		115													

&lt;210&gt; 163

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 163

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 gacacctaca ccctgcgtca gcccatcggc gtatgcgcag gcatcactcc gttcaacttc  
 120  
 ccggcgatga ttccactgtg gatgttcccc atggcgattg cctgcggtaa cactttcgtg  
 180  
 ctcaaaccgt ccgaacaaga ccctctgtcg acgatgctgc tggtagaact ggcgctggaa  
 240  
 gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgac  
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<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

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			20					25					30		
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
		35					40					45			
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
	50					55					60				
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65				70						75				80	
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
			85					90					95		
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
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Val	Gly	Ser	Thr	Ala	Val	Gly	Thr								
			115				120								

<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

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120  
aagtttggca accgcaacgt cttcatgaag gacaacagct cttcttcag cacagactcc  
180  
cgctcccgct cctcctccag gtccccgacg cgccacttcc gcagaagtga ctcccactca  
240  
gactccgaca gtcctactc agggaatgag tgtcaccctg tgggccgcag gaaccgcgcc  
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 720  
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 728

<210> 166  
 <211> 242  
 <212> PRT  
 <213> Homo sapiens

<400> 166  
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 35 40 45  
 Met Lys Asp Asn Ser Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser  
 50 55 60  
 Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser  
 65 70 75 80  
 Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg  
 85 90 95  
 Arg Asn Pro Pro Pro Lys Gly Arg Gly Arg Gly Ala His Met Asp  
 100 105 110  
 Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro  
 115 120 125  
 Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro  
 130 135 140  
 Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly  
 145 150 155 160  
 His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser  
 165 170 175  
 Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val  
 180 185 190  
 Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala  
 195 200 205  
 Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe  
 210 215 220  
 Glu Lys Val Ala Val His Gly Gln Val Pro Leu Glu Arg Glu Ala Gly  
 225 230 235 240  
 Leu Arg

<210> 167  
 <211> 510  
 <212> DNA  
 <213> Homo sapiens

<400> 167  
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 120

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 180  
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 240  
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 420  
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 510

<210> 168  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 168  
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 Leu Ser Gln Pro Leu Leu Asp Gly Phe Ala Met Gly Ala Ser Val Thr  
 35 40 45  
 Ile Leu Thr Ser Gln Leu Lys His Leu Leu Gly Val Arg Ile Pro Arg  
 50 55 60  
 His Gln Gly Pro Gly Met Val Val Leu Thr Trp Leu Ser Leu Leu Arg  
 65 70 75 80  
 Gly Ala Gly Gln Ala Asn Val Cys Asp Val Val Thr Ser Thr Val Cys  
 85 90 95  
 Leu Ala Val Leu Leu Ala Ala Lys Glu Leu Ser Asp Arg Tyr Arg His  
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Ala	Thr	Ala	Gly	Pro	Arg	Ala	Gly	Ala	Gln	Asp	Ala	Leu	Pro	Arg	Ser

	115					120					125					
Ala	Ala	Pro	Pro	Val	Gln	Asn	Thr	Glu	Thr	Ala	Ala	Met	Thr	Thr	His	
	130					135					140					
Val	Thr	Leu	Glu	Asp	Ala	Leu	Ser	Asn	Val	Asp	Leu	Leu	Glu	Glu	Leu	
145					150					155					160	
Pro	Leu	Pro	Asp	Gln	Gln	Pro	Cys	Ile	Glu	Pro	Pro	Pro	Ser	Ser	Ile	
				165					170					175		
Met	Tyr	Gln	Ala	Asn	Phe	Asp	Thr	Asn	Phe	Glu	Asp	Arg	Asn	Ala	Phe	
			180					185					190			
Val	Thr	Gly	Ile	Ala	Arg	Tyr	Ile	Glu	Gln	Ala	Thr	Val	His	Ser	Ser	
	195						200				205					
Met	Asn	Glu	Met	Leu	Glu	Glu	Gly	His	Glu	Tyr	Ala	Val	Met	Leu	Tyr	
	210					215					220					
Thr	Trp	Arg	Ser	Cys	Ser	Arg	Ala	Ile	Pro	Gln	Val	Lys	Cys	Asn	Glu	
225					230					235					240	
Gln	Pro	Asn	Arg	Val	Glu	Ile	Tyr	Glu	Lys	Thr	Val	Glu	Val	Leu	Glu	
				245					250					255		
Pro	Glu	Val	Thr	Lys	Leu	Met	Asn	Phe	Met	Tyr	Phe	Gln	Arg	Asn	Ala	
			260					265					270			
Ile	Glu	Arg	Phe	Cys	Gly	Glu	Val	Arg	Arg	Leu	Cys	His	Ala	Glu	Arg	
	275						280				285					
Arg	Lys	Asp	Phe	Val	Ser	Glu	Ala	Tyr	Leu	Ile	Thr	Leu	Gly	Lys	Phe	
	290					295					300					
Ile	Asn	Met	Phe	Ala	Val	Leu	Asp	Glu	Leu	Lys	Asn	Met	Lys	Cys	Ser	
305					310					315					320	
Val	Lys	Asn	Asp	His	Ser	Ala	Tyr	Lys	Arg	Ala	Ala	Gln	Phe	Leu	Arg	
				325					330					335		
Lys	Met	Ala	Asp	Pro	Gln	Ser	Ile	Gln	Glu	Ser	Gln	Asn	Leu	Ser	Met	
			340					345					350			
Phe	Leu	Ala	Asn	His	Asn	Lys	Ile	Thr	Gln	Ser	Leu	Gln	Gln	Gln	Leu	
	355						360				365					
Glu	Val	Ile	Ser	Gly	Tyr	Glu	Glu	Leu	Leu	Ala	Asp	Ile	Val	Asn	Leu	
	370					375					380					
Cys	Val	Asp	Tyr	Tyr	Glu	Asn	Arg	Met	Tyr	Leu	Thr	Pro	Ser	Glu	Lys	
385					390					395					400	
His	Met	Leu	Leu	Lys	Val	Met	Gly	Phe	Gly	Leu	Tyr	Leu	Met	Asp	Gly	
				405					410					415		
Ser	Val	Ser	Asn	Ile	Tyr	Lys	Leu	Asp	Ala	Lys	Lys	Arg	Ile	Asn	Leu	
			420					425					430			
Ser	Lys	Ile	Asp	Lys	Tyr	Phe	Lys	Gln	Leu	Gln	Val	Val	Pro	Leu	Phe	
	435						440					445				
Gly	Asp	Met	Gln	Ile	Glu	Leu	Ala	Arg	Tyr	Ile	Lys	Thr	Ser	Ala	His	
	450					455					460					
Tyr	Glu	Glu	Asn	Lys	Ser	Arg	Trp	Thr	Cys	Thr	Ser	Ser	Gly	Ser	Ser	
465					470					475						



522

980 985 990  
 Pro Asn Tyr Cys Tyr Asn Gly Ser Thr Asn Arg Phe Val Arg Thr Val  
 995 1000 1005  
 Leu Pro Phe Ser Gln Glu Phe Gln Arg Asp Lys Gln Pro Asn Ala Gln  
 1010 1015 1020  
 Pro Gln Tyr Leu His Gly Ser Lys Ala Leu Asn Leu Ala Tyr Ser Ser  
 1025 1030 1035 1040  
 Ile Tyr Gly Ser Tyr Arg Asn Phe Val Gly Pro Pro His Phe Gln Val  
 1045 1050 1055  
 Ile Cys Arg Leu Leu Gly Tyr Gln Gly Ile Ala Val Val Met Glu Glu  
 1060 1065 1070  
 Leu Leu Lys Val Val Lys Ser Leu Leu Gln Gly Thr Ile Leu Gln Tyr  
 1075 1080 1085  
 Val Lys Thr Leu Met Glu Val Met Pro Lys Ile Cys Arg Leu Pro Arg  
 1090 1095 1100  
 His Glu Tyr Gly Ser Pro Gly Ile Leu Glu Phe Phe His His Gln Leu  
 1105 1110 1115 1120  
 Lys Asp Ile Val Glu Tyr Ala Glu Leu Lys Thr Val Cys Phe Gln Asn  
 1125 1130 1135  
 Leu Arg Glu Val Gly Asn Ala Ile Leu Phe Cys Leu Leu Ile Glu Gln  
 1140 1145 1150  
 Ser Leu Ser Leu Glu Glu Val Cys Asp Leu Leu His Ala Ala Pro Phe  
 1155 1160 1165  
 Gln Asn Ile Leu Pro Arg Val His Val Lys Glu Gly Glu Arg Leu Asp  
 1170 1175 1180  
 Ala Lys Met Lys Arg Leu Glu Ser Lys Tyr Ala Pro Leu His Leu Val  
 1185 1190 1195 1200  
 Pro Leu Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg  
 1205 1210 1215  
 Glu Gly Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met  
 1220 1225 1230  
 Phe Glu Val Ile Leu Thr Arg Ile Arg Ser Phe Leu Asp Asp Pro Ile  
 1235 1240 1245  
 Trp Arg Gly Pro Leu Pro Ser Asn Gly Val Met His Val Asp Glu Cys  
 1250 1255 1260  
 Val Glu Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile  
 1265 1270 1275 1280  
 Pro Val Gly Thr His Glu Phe Thr Val Glu Gln Cys Phe Gly Asp Gly  
 1285 1290 1295  
 Leu His Trp Ala Gly Cys Met Ile Ile Val Leu Leu Gly Gln Gln Arg  
 1300 1305 1310  
 Arg Phe Ala Val Leu Asp Phe Cys Tyr His Leu Leu Lys Val Gln Lys  
 1315 1320 1325  
 His Asp Gly Lys Asp Glu Ile Ile Lys Asn Val Pro Leu Lys Lys Met  
 1330 1335 1340  
 Val Glu Arg Ile Arg Lys Phe Gln Ile Leu Asn Asp Glu Ile Ile Thr  
 1345 1350 1355 1360  
 Ile Leu Asp Lys Tyr Leu Lys Ser Gly Asp Gly Glu Gly Thr Pro Val  
 1365 1370 1375  
 Glu His Val Arg Cys Phe Gln Pro Pro Ile His Gln Ser Leu Ala Ser  
 1380 1385 1390  
 Ser

<210> 177  
 <211> 417  
 <212> DNA  
 <213> Homo sapiens

<400> 177  
 acgcgtgatg tcacactgcc tctgccgctg ggtcctaatt cgattgcacg caccatggct  
 60  
 gcagttcgtg gcgcgcatag tttctggcat gcttcgcgca tcctggagac cgatccccgc  
 120  
 gctgccgtga aaccgcctaa aaatgtgaag cgattgccca aagccgtgtc cgtggagcaa  
 180  
 atgcaaaagc tccttgccat acccagtctt aagactccta ccggcctgcg taatcgagcg  
 240  
 atacttgagt tcttatatgc taccggcgcg cgcgtgagcg agatgctggc aacagacctg  
 300  
 gacgatatac acctgggcga aaaaccccgcg gatgaaaacg gggaatctat tgcacttccc  
 360  
 ggggtatgtgc gcctttttgg aaagggaggt aaagagcggt tagtcccttt gggatcc  
 417

<210> 178  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 178  
 Thr Arg Asp Val Thr Leu Pro Leu Pro Leu Gly Pro Asn Ser Ile Ala  
 1 5 10 15  
 Arg Thr Met Ala Ala Val Arg Gly Ala His Ser Phe Trp His Ala Ser  
 20 25 30  
 Arg Ile Leu Glu Thr Asp Pro Ala Ala Ala Val Lys Pro Pro Lys Asn  
 35 40 45  
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu  
 50 55 60  
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala  
 65 70 75 80  
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu  
 85 90 95  
 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu  
 100 105 110  
 Asn Gly Glu Ser Ile Ala Leu Pro Gly Tyr Val Arg Leu Phe Gly Lys  
 115 120 125  
 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser  
 130 135

<210> 179  
 <211> 362  
 <212> DNA  
 <213> Homo sapiens

<400> 179  
 acgcgtcgaa ggtgccggtg ggggcgatca ataacatcgc gcaatccctg gaagagcctc  
 60

aggtgattgc ccgtgggttg atggtggaag atcccgcac ccgaagaatc cgggaattcg  
 120  
 ccattggggc gggcagcccg aatccaaaat gtcggggcac gccagtgagg agtatggtaa  
 180  
 ggggcccggc ccgatgttgg nggcagcata cggatggaag tgctgggcga ggcctgggt  
 240  
 ttgccggcag agcaactggg gcagctcaag gcgggcgggg tgatcgagca gttggattga  
 300  
 gcaatggcgg ccgcgaagcc cgccatttac cttgatgact gtttagcgcg cggattcttt  
 360  
 aa  
 362

<210> 180  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Met Ala Gly Phe Ala Ala Ala Ile Ala Gln Ser Asn Cys Ser Ile Thr  
 1 5 10 15  
 Pro Pro Ala Leu Ser Cys Pro Ser Cys Ser Ala Gly Lys Pro Arg Arg  
 20 25 30  
 Ser Pro Ser Thr Ser Ile Arg Met Leu Pro Pro Thr Ser Val Pro Ala  
 35 40 45  
 Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala  
 50 55 60  
 Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe  
 65 70 75 80  
 His His Gln Pro Thr Gly Asn His Leu Arg Leu Phe Gln Gly Leu Arg  
 85 90 95  
 Asp Val Ile Asp Arg Pro His Arg His Leu Arg Arg  
 100 105

<210> 181  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

<400> 181  
 gcgttgatca tgtccgaccc aggcttgatc atgctggtac gccgtcactt cccgtgcatg  
 60  
 ccgattcact tgtcgggtaca ggccaatacg gtgaattggg ccagcgtcga gttctggcaa  
 120  
 cagcaaggta tctgccgggt aatcctgtcg cgggaattgt cactggaaga aatcggcgaa  
 180  
 atccgccaac aggtgccggc catggagctg gaagtgtttg tgcacgggtc cctgtacatg  
 240  
 gcctattccg ggcgctgttt gttgtccggc tatatgaaca agcgcgatgc caaccaa  
 297

<210> 182  
 <211> 99  
 <212> PRT

<213> Homo sapiens

<400> 182

Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His  
 1 5 10 15  
 Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn  
 20 25 30  
 Trp Ala Ser Val Glu Phe Trp Gln Gln Gln Gly Ile Cys Arg Val Ile  
 35 40 45  
 Leu Ser Arg-Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln  
 50 55 60  
 Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met  
 65 70 75 80  
 Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp  
 85 90 95  
 Ala Asn Gln

<210> 183

<211> 351

<212> DNA

<213> Homo sapiens

<400> 183

cgggacgtca ccatgaagcc gaccggctcg ggggatgtgg cgaacaaggt catcacccat  
 60  
 attccgttta acatcgtctc ccaggcgact catccattcc ttcgtacctt ggacgatgtc  
 120  
 aagcgcacatc ctttggcgac cgacgggctc ggccaccagg tctgtctcaa gggctaccag  
 180  
 gccgagggcc acgactacgc acaccccgcac tacggcggca acgtctccca ccgtgccggc  
 240  
 gggatgaagg atctcgagaa gtcaccgag tcgggcaggc agtggaacac cgatttcggc  
 300  
 attcacgtca acctggtgga gtcctatcct gaggcgaatc acttcggcga c  
 351

<210> 184

<211> 117

<212> PRT

<213> Homo sapiens

<400> 184

Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys  
 1 5 10 15  
 Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro  
 20 25 30  
 Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp  
 35 40 45  
 Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His  
 50 55 60  
 Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly  
 65 70 75 80  
 Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

85 90 95  
 Thr Asp Phe Gly Ile His Val Asn Leu Val Glu Ser Tyr Pro Glu Ala  
 100 105 110  
 Asn His Phe Gly Asp  
 115

<210> 185  
 <211> 396  
 <212> DNA  
 <213> Homo sapiens

<400> 185  
 cgcgtgggtc tcagtaaaga aaatttggtg cttagaggat gcaccattag aaacacagag  
 60  
 gctgttggtg gcatttggtt ttatgcaggc catgaaacca aagcaatgct gaacaacagt  
 120  
 gggccacggt ataagcgcag caaattagaa agaagagcaa acacagatgt cctctggtgt  
 180  
 gtcattgcttc tggtcataat gtgcttaact ggcgcagtag gtcattggaat ctggctgagc  
 240  
 aggtatgaaa agatgcattt tttcaatgtt cccgagcctg atggacatat catatcacca  
 300  
 ctgttggcag gattttatat gttttggacc gtgatcattt tgttacaggt cttgattcct  
 360  
 atttctctct atgtttccat cgaaattgtg aagctt  
 396

<210> 186  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 186  
 Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Leu Arg Gly Cys Thr Ile  
 1 5 10 15  
 Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu  
 20 25 30  
 Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys  
 35 40 45  
 Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu  
 50 55 60  
 Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser  
 65 70 75 80  
 Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His  
 85 90 95  
 Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile  
 100 105 110  
 Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu  
 115 120 125  
 Ile Val Lys Leu  
 130

<210> 187  
 <211> 423

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 187

cgagtgtca ccgctcagc cgtcatgcgt cccactgagg ctgttgctc tcggtcggca  
 60  
 gaacctcgac gagttcagcg gacccctggac cagcgcgagt gggctggcgt cttegttgct  
 120  
 gatgagcatc gtcgtttgct tggcacggtc ggcgatcaag aggtcatcga ggctgctcgc  
 180  
 cgcgagatc gcagtattgc tgacgcggtg gaaactaacg gcacccctcac ggcgcgacc  
 240  
 gacactccgt tgtccgagct cttcgtcccg accagcaacg ccagggtgcc gttggccgtt  
 300  
 gtcgacgagg acttccacct catgggtgtc atctctcggg tgaccctgct cgacgcgatg  
 360  
 tcacgagctc gcgacgaggc aggagaggga tctgtcatgt ccttgagaga caccggaag  
 420  
 ctt  
 423

&lt;210&gt; 188

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
1				5					10					15	
Ser	Arg	Ser	Ala	Glu	Pro	Arg	Arg	Val	Gln	Arg	Ile	Leu	Asp	Gln	Arg
		20						25					30		
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
	35					40						45			
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
	50				55						60				
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65				70					75					80	
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85					90					95		
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
		100						105					110		
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
	115					120						125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
	130					135					140				

&lt;210&gt; 189

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

ngatgggtta ccaacatatg cacgggttcga gcggcaatag ctccctcgggg gctggcagtg  
 60

aaatgtttga agatgccggc gtttcgggcc tcaacttggt tcgatgccgt ggttcaccg  
 120  
 atttcgccga tgcggctcat cgcacgggta agaagtttcg tccagataac ccaggacaga  
 180  
 gcaaggtata tcaggctcag aaccaggaaa agcaggggctt taccacagtg ccccatatag  
 240  
 accgcgctag ctacggcaaa aggcgcgccc agtgggggtcc aggacagcac tttcatggct  
 300  
 gaagggagcg catcccnagc ttcgcctagc cccagagcta acccagcgac cagtggacca  
 360  
 gcgccccatca tcagtaggaa ccctacgata atcagccctt gttttacccc tggaatggag  
 420  
 ctgatttcn  
 429

<210> 190  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 190  
 Met Met Gly Ala Gly Pro Leu Val Ala Gly Leu Ala Leu Gly Leu Gly  
 1 5 10 15  
 Glu Ala Xaa Asp Ala Leu Pro Ser Ala Met Lys Val Leu Ser Trp Thr  
 20 25 30  
 Pro Leu Gly Ala Pro Phe Ala Val Ala Ser Ala Val Tyr Met Gly His  
 35 40 45  
 Trp Gly Lys Ala Leu Leu Phe Leu Val Leu Ser Leu Ile Tyr Leu Ala  
 50 55 60  
 Leu Ser Trp Val Ile Trp Thr Lys Leu Leu Asn Arg Ala Met Ser Arg  
 65 70 75 80  
 Ile Gly Glu Ile Gly Gly Thr Thr Ala Ser Lys Gln Val Glu Ala Gly  
 85 90 95  
 Asn Ala Gly Ile Phe Lys His Phe Thr Ala Ser Pro Arg Gly Ala Ile  
 100 105 110  
 Ala Ala Arg Thr Val His Met Leu Val Asn His  
 115 120

<210> 191  
 <211> 4845  
 <212> DNA  
 <213> Homo sapiens

<400> 191  
 ccgcccgggg ccatggcgac actcagcttc gtcttcctgc tgctgggggc agtgtcctgg  
 60  
 cctccggctt ctgcctccgg ccaggagttc tggcccgagc aatcggcggc cgatattctg  
 120  
 tcggggggcg cttcccgag acggtatctt ctgtatgacg tcaaccccc ggaaggcttc  
 180  
 aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg  
 240  
 gaggagtggg tgcttgctct gcctccatgg ggccgctct atcactggca gagtcctgac  
 300



atccaccagg tccggattcc ctggtctgag ttttttgatc ttccaagtct caataaaaaac  
360  
atccccgtca tcgagtatga gcagttcatc gcagaatctg gtgggccctt tattgaccag  
420  
gtttacgtcc tgcaaagtta cgcagagggg tggaagaag ggacctggga agagaagggtg  
480  
gacgagcggc cgtgtattga tcagctcctg tactcccagg acaagcacga gtactacaga  
540  
ggatggtttt ggggttatga ggagaccagg ggtctaaacg tctcctgtct gtccgtccag  
600  
ggctcagcct ccatcgtggc gccctgctg ctgagaaaca catcagcccg gtccgtgatg  
660  
ttagacagag ccgagaacct acttcacgac cactatggag ggaaagaata ctgggatacc  
720  
cgtcgcagca tgggtgtttgc caggcacctg cgggagggtg gagacgagtt caggagcaga  
780  
catctcaact ccacggacga cgcagacagg atccccctcc aggaggactg gatgaagatg  
840  
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900  
gatttcatct ggggtcacag acaggatgta cccagtctgg aaggggccgt gaggaagatc  
960  
cgcagcctca tgaagacca ccggtgggac aagggtgtttg tggccacaga tgccgtcaga  
1020  
aaggaatatg aagagctaaa aaagctgtta cccgagatgg tgaggtttga acccactgg  
1080  
gaggagctgg agctctacaa ggacggaggc gttgcgatta ttgaccagtg gatctgcgca  
1140  
cacgccaggc gcctgccac gtcactgtcg gccgagagcg ggtcgggtgg ctttcaaagg  
1200  
ttcttctgtc ccaagtactc ggtgtcagag cagatggctg cctgtgttca cagtggctcat  
1260  
ttccatactg tttgcctcct cgtctgagtc tctgttagca tctggttcag tgtttccctg  
1320  
ggctgaagtt aattgttcat cttgccccct tagttctcat gcacagaatt cctccatagc  
1380  
aggctgttg catagctggc ctctctcag aacctcttct tgtgtcgcat tttcccatca  
1440  
ttcccggttt ctgccccctg ctgccccctg ccctgagagt tgcccgtgcc ctggacttgg  
1500  
gcatgtcctt gttgctgtgt tgttgagcat ccgtgagcgt ccccgaggcc gggagcgtgg  
1560  
gccctcgtgt gatcattctc gtggggctgc catgagcgtc cccaaggctg ggagcatggg  
1620  
ccctcgtgtg atcgttcttg tggggctgcc gtgagcgtcc ccgaggccgg gagcgtgggc  
1680  
cctcgtgtga tcattctcgt ggggctgcg tgagcgtccc agaggccggg agcgtgggcc  
1740  
ctgctgcag tcattcctct ggggttgctg tgggaggtac gcctgggect ctgttctcc  
1800  
aaagacctgc ctgccccctc gcataggaga tgaaggctgg ggttaggggtg aaacgggttg  
1860  
agttaaagtg aaaatgaaag tagaggggat gatcttccc gtgggttagca ctgtgcacac  
1920

gcgtgcgtct ctgtgggtta gtctgtctct ctctgcccc aggaatgctg agcgccctga  
1980  
gccggtgcct cttcacacat ctgctatttc ctgtggtgtt ctgggcatgg tgtataagac  
2040  
ccacagagge tccgggtgat gctgtctgct ggggtgtgggt ccctttccct gttaagcaga  
2100  
caggatgcag cgctgacttc ttaggtcagg gcggagggtg gcaggagccc agtcacgagc  
2160  
tcacccctgc ttctcagggtg tggccttggg attttgactg cgacctgggc ggtgctgtct  
2220  
ccgcagccca ggaagcctgc tgtggggagg ctctgcactg agctctcage ctctgcccc  
2280  
cagctgcgcg aagcgctcgg ccagctcac tgaagctgcc ctgcctccgg gccggcgcgg  
2340  
cctgctctgg caggcccttg tgtgtggggg ggtgaggggc tccccaccag tgctgcaccc  
2400  
cgcagcagca tacaggcctg tgtggcctgc tggccctgtg gctctgtgta cagcgctgtg  
2460  
catgttacat ttgctctgga aacatctctg gggtttgctt gttcacgaag ttcataagt  
2520  
gccgctggag agccagagac cagctgcgca ggagccggag gaacgggcag gccgctgacc  
2580  
tgaggtctgg agaaaccctt ggagaagggt gtccccacca gccatacag cgtgtgtgtg  
2640  
gagggggcct tgacctccgt gatgtctact gtgcctcagg ataaggaccc gccatgccct  
2700  
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2760  
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3300  
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3480  
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3540

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 4740  
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 4800  
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&lt;210&gt; 192

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 192

Pro Pro Gly Ala Met Ala Thr Leu Ser Phe Val Phe Leu Leu Leu Gly  
 1 5 10 15  
 Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro  
 20 25 30  
 Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

	35					40					45				
Tyr	Leu	Leu	Tyr	Asp	Val	Asn	Pro	Pro	Glu	Gly	Phe	Asn	Leu	Arg	Arg
	50					55					60				
Asp	Val	Tyr	Ile	Arg	Ile	Ala	Ser	Leu	Leu	Lys	Thr	Leu	Leu	Lys	Thr
65					70					75					80
Glu	Glu	Trp	Val	Leu	Val	Leu	Pro	Pro	Trp	Gly	Arg	Leu	Tyr	His	Trp
				85					90					95	
Gln	Ser	Pro	Asp	Ile	His	Gln	Val	Arg	Ile	Pro	Trp	Ser	Glu	Phe	Phe
			100					105					110		
Asp	Leu	Pro	Ser	Leu	Asn	Lys	Asn	Ile	Pro	Val	Ile	Glu	Tyr	Glu	Gln
		115					120					125			
Phe	Ile	Ala	Glu	Ser	Gly	Gly	Pro	Phe	Ile	Asp	Gln	Val	Tyr	Val	Leu
	130					135					140				
Gln	Ser	Tyr	Ala	Glu	Gly	Trp	Lys	Glu	Gly	Thr	Trp	Glu	Glu	Lys	Val
145					150					155					160
Asp	Glu	Arg	Pro	Cys	Ile	Asp	Gln	Leu	Leu	Tyr	Ser	Gln	Asp	Lys	His
				165					170					175	
Glu	Tyr	Tyr	Arg	Gly	Trp	Phe	Trp	Gly	Tyr	Glu	Glu	Thr	Arg	Gly	Leu
			180					185					190		
Asn	Val	Ser	Cys	Leu	Ser	Val	Gln	Gly	Ser	Ala	Ser	Ile	Val	Ala	Pro
		195					200					205			
Leu	Leu	Leu	Arg	Asn	Thr	Ser	Ala	Arg	Ser	Val	Met	Leu	Asp	Arg	Ala
	210					215					220				
Glu	Asn	Leu	Leu	His	Asp	His	Tyr	Gly	Gly	Lys	Glu	Tyr	Trp	Asp	Thr
225					230					235					240
Arg	Arg	Ser	Met	Val	Phe	Ala	Arg	His	Leu	Arg	Glu	Val	Gly	Asp	Glu
				245					250					255	
Phe	Arg	Ser	Arg	His	Leu	Asn	Ser	Thr	Asp	Asp	Ala	Asp	Arg	Ile	Pro
			260					265					270		
Phe	Gln	Glu	Asp	Trp	Met	Lys	Met	Lys	Val	Lys	Leu	Gly	Ser	Ala	Leu
	275						280					285			
Gly	Gly	Pro	Tyr	Leu	Gly	Val	His	Leu	Arg	Arg	Lys	Asp	Phe	Ile	Trp
	290					295					300				
Gly	His	Arg	Gln	Asp	Val	Pro	Ser	Leu	Glu	Gly	Ala	Val	Arg	Lys	Ile
305					310					315					320
Arg	Ser	Leu	Met	Lys	Thr	His	Arg	Leu	Asp	Lys	Val	Phe	Val	Ala	Thr
				325					330					335	
Asp	Ala	Val	Arg	Lys	Glu	Tyr	Glu	Glu	Leu	Lys	Lys	Leu	Leu	Pro	Glu
		340						345					350		
Met	Val	Arg	Phe	Glu	Pro	Thr	Trp	Glu	Glu	Leu	Glu	Leu	Tyr	Lys	Asp
	355						360					365			
Gly	Gly	Val	Ala	Ile	Ile	Asp	Gln	Trp	Ile	Cys	Ala	His	Ala	Arg	Cys
	370					375					380				
Leu	Pro	Thr	Ser	Leu	Ser	Ala	Glu	Ser	Gly	Ser	Gly	Gly	Phe	Gln	Arg
385					390					395					

<210> 193

<211> 350

<212> DNA

<213> Homo sapiens

&lt;400&gt; 193

gcccggcagc tggactgcgc catcatggcc gagcccttcc ccgacaccgg cctggccacg  
60  
gcgcagctgt acgacgagcc cttcgtcgtc ggcgtgcggg cgtcgcaccc gctggccgac  
120  
cgtgccagca tcagccccga ggagggtcaag ggcgagacca tgttgatgtt gggcacgggc  
180  
ccctggtttc cccggggcccg cgggtgggggt ttggcccga tttggcgcgt ttctccagcg  
240  
ccgttaaggg catacgccgc agtttcgagg gctcgtcgtt ggagaccatc aagcacatcg  
300  
tggttcggg catggcgtga cgggtgtgcc gcagctgtcc gtgccgcgcg  
350

&lt;210&gt; 194

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

Ala	Gly	Glu	Leu	Asp	Cys	Ala	Ile	Met	Ala	Glu	Pro	Phe	Pro	Asp	Thr
1				5					10					15	
Gly	Leu	Ala	Thr	Ala	Gln	Leu	Tyr	Asp	Glu	Pro	Phe	Val	Val	Ala	Leu
			20					25					30		
Arg	Ala	Ser	His	Pro	Leu	Ala	Asp	Arg	Ala	Ser	Ile	Ser	Pro	Glu	Glu
		35					40					45			
Val	Lys	Gly	Glu	Thr	Met	Leu	Met	Leu	Gly	Thr	Gly	Pro	Trp	Phe	Pro
	50				55					60					
Arg	Ala	Arg	Gly	Gly	Gly	Leu	Ala	Arg	Ile	Trp	Arg	Val	Ser	Pro	Ala
65				70					75					80	
Pro	Leu	Arg	Ala	Tyr	Ala	Ala	Val	Ser	Arg	Ala	Arg	Arg	Trp	Arg	Pro
			85						90					95	
Ser	Ser	Thr	Ser	Trp	Leu	Arg	Ala	Trp	Arg	Asp	Gly	Gly	Ala	Ala	Ala
			100					105					110		
Val	Arg	Ala	Ala												
			115												

&lt;210&gt; 195

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

acgcgtgaac gcgacggctt ggcgatcgga ggcgtcggcc ccgtcgttga gtgggcccgtt  
60  
gaaatggttc gcttcgacga aagcgagact ctcgaccgcc ttgcatcggg cgctccttgaa  
120  
ccagaacttg gcgacgattt ggccgccgtc ctgctcgatt ctcatcgggt tgctgtcatc  
180  
agcgagggat cgaactggct tgccctcgcta cccgtgatcg taggtcgcaa cacggaacag  
240  
tttcgcagca taccagacct tgcccgcgac cggatcgaca aactgcacca gttgagccat  
300

cgcgaaatag cacgaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcagggtcgg  
 360  
 cactgccacg gcgacgcaca cctcggcaac atcgatcatga ttgacggcaa gccgggtcctg  
 420  
 ttcgacgcga tcgaatttga tcctgatatc gcgacaacgg atgtgctgta cgatttcgcg  
 480  
 ttccctctga tggat  
 495

<210> 196

<211> 165

<212> PRT

<213> Homo sapiens

<400> 196

Thr	Arg	Glu	Arg	Asp	Gly	Leu	Ala	Ile	Gly	Gly	Val	Gly	Pro	Val	Val
1				5					10					15	
Glu	Trp	Ala	Val	Glu	Met	Val	Arg	Phe	Asp	Glu	Ser	Glu	Thr	Leu	Asp
			20					25					30		
Arg	Leu	Ala	Ser	Gly	Val	Leu	Glu	Pro	Glu	Leu	Gly	Asp	Asp	Leu	Ala
		35				40						45			
Ala	Val	Leu	Leu	Asp	Ser	His	Arg	Val	Ala	Val	Ile	Ser	Glu	Gly	Ser
50					55						60				
Asn	Trp	Leu	Ala	Ser	Leu	Pro	Val	Ile	Val	Gly	Arg	Asn	Thr	Glu	Gln
65					70					75				80	
Phe	Arg	Ser	Ile	Pro	Asp	Leu	Ala	Arg	Asp	Arg	Ile	Asp	Lys	Leu	His
				85				90					95		
Gln	Leu	Ser	His	Arg	Glu	Ile	Ala	Arg	Asn	Arg	Glu	Leu	Leu	Arg	Ala
			100					105					110		
Arg	Ala	Ala	Ser	Gly	Gln	Val	Arg	His	Cys	His	Gly	Asp	Ala	His	Leu
		115				120					125				
Gly	Asn	Ile	Val	Met	Ile	Asp	Gly	Lys	Pro	Val	Leu	Phe	Asp	Ala	Ile
130					135						140				
Glu	Phe	Asp	Pro	Asp	Ile	Ala	Thr	Thr	Asp	Val	Leu	Tyr	Asp	Phe	Ala
145					150					155					160
Phe	Pro	Leu	Met	Asp											
															165

<210> 197

<211> 402

<212> DNA

<213> Homo sapiens

<400> 197

caagcaatgc ttgacgcagt tgttgaatac ttaccagcac cgactgatat tccagcaatc  
 60  
 aaaggatatca atccagatga aactgaagggt gaacgtcacg caagcgatga tgagccattc  
 120  
 tcttcattag cattcaaaat tgcaactgac ccattcgtag gtaacttaac cttcttccgt  
 180  
 gtgtactcag gtgtaattaa ctctggtgat acagtattaa actctgtacg tcaaaaacgt  
 240  
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt  
 300

cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta  
360  
tgtgtgtcgc atgcaccaat cattcttgag cgtatggaat tc  
402

<210> 198

<211> 134

<212> PRT

<213> Homo sapiens

<400> 198

Gln Ala Met Leu Asp Ala Val Val Glu Tyr Leu Pro Ala Pro Thr Asp  
1 5 10 15  
Ile Pro Ala Ile Lys Gly Ile Asn Pro Asp Glu Thr Glu Gly Glu Arg  
20 25 30  
His Ala Ser Asp Asp Glu Pro Phe Ser Ser Leu Ala Phe Lys Ile Ala  
35 40 45  
Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe Arg Val Tyr Ser Gly  
50 55 60  
Val Ile Asn Ser Gly Asp Thr Val Leu Asn Ser Val Arg Gln Lys Arg  
65 70 75 80  
Glu Arg Phe Gly Arg Ile Val Gln Met His Ala Asn Lys Arg Glu Glu  
85 90 95  
Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala Ala Ile Gly Leu Lys  
100 105 110  
Asp Val Thr Thr Gly Glu Pro Leu Cys Ala Val Asp Ala Pro Ile Ile  
115 120 125  
Leu Glu Arg Met Glu Phe  
130

<210> 199

<211> 507

<212> DNA

<213> Homo sapiens

<400> 199

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60  
tattgcacaa agaccaagcg accctggacg ttctagacag aactctgcta cgaggcctga  
120  
caatagtga atccccgaga acccagctat ggaagggttt ccagatgctc gaaggcctgt  
180  
cataccagag gttagggttaa actgtatgga gactttcgag gtgaaagttg actcgccggt  
240  
aaagcctgct cctaaagagg atttagatct gatagatcta tcctcagatt caacctcggt  
300  
gcctgaaaaa cactctatac tctcaacctc cgacagcgac tctcttgat ttgagcctct  
360  
tcctctcttc agaatagtcg agagtgcga agaagaggag acgatgaacc aaggcgatga  
420  
cggccctccc ggtaaaaatg ctgcctcttc tccctccatc cccagccatc cctccgtcct  
480  
cagcctgagc acagctccgc ttgtaca  
507

<210> 200  
 <211> 153  
 <212> PRT  
 <213> Homo sapiens

<400> 200  
 Met Glu Gly Glu Glu Ala Ala Phe Leu Pro Glu Gly Pro Ser Ser Pro  
 1 5 10 15  
 Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu  
 20 25 30  
 Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile  
 35 40 45  
 Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg  
 50 55 60  
 Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr  
 65 70 75 80  
 Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu  
 85 90 95  
 Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu  
 100 105 110  
 Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu  
 115 120 125  
 Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser  
 130 135 140  
 His Arg Ser Met His Asp Phe Thr Arg  
 145 150

<210> 201  
 <211> 527  
 <212> DNA  
 <213> Homo sapiens

<400> 201  
 gatgtggcta ttatccctgt ttcccaggtg agaaacaggg tcagtgatag agctgggatg  
 60  
 tgtgcttgca ggctcaccag ccagtcacct cctcaccaag gatgatgttc tccgtggtga  
 120  
 gctggctcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat  
 180  
 cctttctccat ctctttggct agctgcaagt tctggagctg ctcgttgagg tctgtgatct  
 240  
 catccacctg ctggttgagc gtgcgcttga ggaaggccac aatctccttc ttgttattgg  
 300  
 ccagctgctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccacttcc  
 360  
 gctggtaccg ggctagccgg tcctccaggt ctcgatctg gatgtggtag aactccttca  
 420  
 tctccttggc cagaggcggc tccacggcca ccaccggctc cttcttgccc cctttcttct  
 480  
 tgacttcaag ctccttgccct gccttgctca cactcttttt gggaggc  
 527

<210> 202



<211> 70  
 <212> PRT  
 <213> Homo sapiens

<400> 202  
 Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro  
 1 5 10 15  
 Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly  
 20 25 30  
 Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr  
 35 40 45  
 Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro  
 50 55 60  
 Ser Cys Pro Leu Ser Ser  
 65 70

<210> 203  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<400> 203  
 ngtgcaccgg tggatcatgga caacgccgcc tacgtggtct acacctcggg atccaccggc  
 60  
 cgacccaagg gagttgtcgt caccacaccc ggactcgaca gcttcgcact cgaccagcag  
 120  
 cgtcgattcc acgcagatca ccaactctcga accctgcact tcgccacccc cagcttcgac  
 180  
 ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggt gatcgtcccc  
 240  
 accgacatct acggcgggcg cgaactggca agtctcatcc gccgcgaaca cgtcactcac  
 300  
 gcgt  
 304

<210> 204  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 204  
 Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser  
 1 5 10 15  
 Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu  
 20 25 30  
 Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His  
 35 40 45  
 Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe  
 50 55 60  
 Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro  
 65 70 75 80  
 Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu  
 85 90 95  
 His Val Thr His Ala

100

&lt;210&gt; 205

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 205

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nngaattcag caatgataac tggctcaatt gaaggtaaga caacaattga gggaattaat
60
gcacaattaa atacagtgtt aactttatct tcaccacaat caaaagataa agatttaatc
120
atgccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga
180
cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt
240
atcattcaaa gatttggacg gattgatcga attgggtcga agaataaatg tgtacaatta
300
gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt
356

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&lt;210&gt; 206

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 206

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Xaa Asn Ser Ala Met Ile Thr Gly Ser Ile Glu Gly Lys Thr Thr Ile
 1          5          10          15
Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro
          20          25          30
Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Glu Ile
          35          40          45
Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln
          50          55          60
Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg
65          70          75          80
Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys
          85          90          95
Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr
          100          105          110
Ile Asp Leu Lys Gly Arg
          115

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&lt;210&gt; 207

&lt;211&gt; 324

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

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acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
60
catgggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg
120

```

tgtgtgggtgt gstatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt  
 180  
 gtgcacatgt gcaactgtgtg gtgtgtatgc atgggtgtgtg cacgtgtgca ctgtgtatgc  
 240  
 atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtgggtgt  
 300  
 gstatgcatgg taatgtgcac gtgt  
 324

<210> 208  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 208  
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys  
 1 5 10 15  
 Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys  
 20 25 30  
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val  
 35 40 45  
 Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys  
 50 55 60  
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys  
 65 70 75 80  
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys  
 85 90 95  
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys  
 100 105

<210> 209  
 <211> 168  
 <212> DNA  
 <213> Homo sapiens

<400> 209  
 nnctccagag gttatgaggt tggaagcccg gtttttttca ggtgcagaaa aggctacat  
 60  
 attcaagggt ccacgactcg cacctgcctt gccaatataa catggagtgg gatacagacc  
 120  
 gaatgtatac ctcatgcctg cagacagcca gaaaccccg cacacgcg  
 168

<210> 210  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

<400> 210  
 Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg  
 1 5 10 15  
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn  
 20 25 30  
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35 40 45  
 Gln Pro Glu Thr Pro Ala His Ala  
 50 55  
 <210> 211  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens  
 <400> 211  
 tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgttgg aggcaatgtc  
 60  
 cagctggcag ctcagaccct tgcacacccat ggaggaagcc tcccaccga cctgcagttc  
 120  
 tcaggagagg actcctcccc cacaccgtcc acatccccat ctgactctgc agggacctct  
 180  
 agtgcctcga cagatgaaga catggagacg gaggtgttca acgaaatcct ggaggacatt  
 240  
 ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgct  
 300  
 gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gatc  
 354

<210> 212  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe  
 1 5 10 15  
 Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly  
 20 25 30  
 Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr  
 35 40 45  
 Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr  
 50 55 60  
 Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile  
 65 70 75 80  
 Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu  
 85 90 95  
 Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala  
 100 105 110  
 Xaa Lys Glu Gln Leu Ile  
 115

<210> 213  
 <211> 669  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tgttgagtc tattggggaa  
 60

gttgaacaaa acctggaagg gaaacagggtg tcatcactct catcaggagt catccaggaa  
 120  
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag  
 180  
 gccacccgtg agatgggtgac ccgattcatg gagacagcag acagtactac agcagcagtg  
 240  
 ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa  
 300  
 gaaaaggaga gctccctaaa gaagcttcta cccagggcag agatgtttga acacctctct  
 360  
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca  
 420  
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttgga aatggaagac  
 480  
 caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt  
 540  
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag  
 600  
 ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat  
 660  
 gaattccgg  
 669

<210> 214

<211> 223

<212> PRT

<213> Homo sapiens

<400> 214

Ile	Ala	Gln	Ser	Gln	Ser	Val	Gln	Glu	Ser	Leu	Glu	Ser	Leu	Leu	Gln
1				5				10						15	
Ser	Ile	Gly	Glu	Val	Glu	Gln	Asn	Leu	Glu	Gly	Lys	Gln	Val	Ser	Ser
		20					25					30			
Leu	Ser	Ser	Gly	Val	Ile	Gln	Glu	Ala	Leu	Ala	Thr	Asn	Met	Lys	Leu
		35				40					45				
Lys	Gln	Asp	Ile	Ala	Arg	Gln	Lys	Ser	Ser	Leu	Glu	Ala	Thr	Arg	Glu
	50					55				60					
Met	Val	Thr	Arg	Phe	Met	Glu	Thr	Ala	Asp	Ser	Thr	Thr	Ala	Ala	Val
65				70					75					80	
Leu	Gln	Gly	Lys	Leu	Ala	Glu	Val	Ser	Gln	Arg	Phe	Glu	Gln	Leu	Cys
			85					90					95		
Leu	Gln	Gln	Gln	Glu	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Leu	Leu	Pro	Gln
		100					105					110			
Ala	Glu	Met	Phe	Glu	His	Leu	Ser	Gly	Lys	Leu	Gln	Gln	Phe	Met	Glu
		115				120					125				
Asn	Lys	Ser	Arg	Met	Leu	Ala	Ser	Gly	Asn	Gln	Pro	Asp	Gln	Asp	Ile
	130				135					140					
Thr	His	Phe	Phe	Gln	Gln	Ile	Gln	Glu	Leu	Asn	Leu	Glu	Met	Glu	Asp
145				150				155						160	
Gln	Gln	Glu	Asn	Leu	Asp	Thr	Leu	Glu	His	Leu	Val	Thr	Glu	Leu	Ser
			165				170						175		
Ser	Cys	Gly	Phe	Ala	Leu	Asp	Leu	Cys	Gln	His	Gln	Asp	Arg	Val	Gln
		180					185					190			
Asn	Leu	Arg	Lys	Asp	Phe	Thr	Glu	Leu	Gln	Lys	Thr	Val	Lys	Glu	Arg

195                      200                      205  
 Glu Lys Asp Ala Ser Ser Cys Gln Glu Gln Leu Asp Glu Phe Arg  
 210                      215                      220  
  
 <210> 215  
 <211> 814  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 215  
 aaatttcgta cccgctccgg cacagtagca gcccttgacg atgtgagcct ggctattaag  
 60  
 agagggttcca tctcagccgt tatcgggcac tccggagccg gcaaattccac cctgggttcgc  
 120  
 ctcatcaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc  
 180  
 tcgcagctct cggacaaagc gatgcgcccg ctacgcgcag acatcgggat gatcttccaa  
 240  
 cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg  
 300  
 gctcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg  
 360  
 ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcgggtt  
 420  
 ggtattgccc gagcgctagc aactaaacca tcgattttgt tggctgacga gtccacctcg  
 480  
 gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa  
 540  
 ctaggggtga cggtcgtcgt catcaccac gagatggagg tcgtccgctc gattgcccag  
 600  
 caggtctcgg tactagcagc tggccatctc gtcgagtctg gaagcgcccg ccaggtcttc  
 660  
 gctcatccac agtcagagac caccacgcgt ttcttggcga cgattatcgg ccagcaccgg  
 720  
 agtggggagg aacaggcacg gttgcagtcg gaaaaccag atgcacgact cgtcgacgtc  
 780  
 agttcgggtg ccagtcactc gttcgggtgac gcgt  
 814

<210> 216  
 <211> 271  
 <212> PRT  
 <213> Homo sapiens

<400> 216  
 Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser  
 1                      5                      10                      15  
 Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly  
 20                      25                      30  
 Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro  
 35                      40                      45  
 Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser  
 50                      55                      60  
 Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln

```

65          70          75          80
Gln Phe Asn Leu Phe Gly Ser Arg Thr Ile Tyr Asp Asn Val Ala Tyr
          85          90          95
Pro Leu Lys Leu Ala His Trp Lys Lys Ala Asp Glu Lys Lys Arg Val
          100          105          110
Thr Glu Leu Leu Ser Phe Val Gly Leu Thr Ser Lys Ala Trp Asp His
          115          120          125
Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg
          130          135          140
Ala Leu Ala Thr Lys Pro Ser Ile Leu Leu Ala Asp Glu Ser Thr Ser
145          150          155          160
Ala Leu Asp Pro Glu Thr Thr Ala Asp Val Leu Ser Leu Leu Lys Arg
          165          170          175
Val Asn Ala Glu Leu Gly Val Thr Val Val Val Ile Thr His Glu Met
          180          185          190
Glu Val Val Arg Ser Ile Ala Gln Gln Val Ser Val Leu Ala Ala Gly
          195          200          205
His Leu Val Glu Ser Gly Ser Ala Arg Gln Val Phe Ala His Pro Gln
          210          215          220
Ser Glu Thr Thr Gln Arg Phe Leu Ala Thr Ile Ile Gly Gln His Pro
225          230          235          240
Ser Gly Glu Glu Gln Ala Arg Leu Gln Ser Glu Asn Pro Asp Ala Arg
          245          250          255
Leu Val Asp Val Ser Ser Val Ala Ser His Ser Phe Gly Asp Ala
          260          265          270

```

&lt;210&gt; 217

&lt;211&gt; 500

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 217

```

nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
60
agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
120
tttcctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
180
ctgttcacta tccaaggctc ggaccccagc ttgcagccct acctgctgat ggctcacttt
240
gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctctgg gttggagcgt
300
gatggcggtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
360
caggcccttg agctcctgct gatcaggaag tacatcccc gaagatcttt cttcatttct
420
ctgggccatg atgaggagtc atcagggaca ggggctcaga ggatctcagc cctgctacag
480
tcaaggggcg tccagctagc
500

```

&lt;210&gt; 218

&lt;211&gt; 166

&lt;212&gt; PRT

<213> Homo sapiens

<400> 218

```

Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
      20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
      35           40           45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
      50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
      85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
      100          105          110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile
      115          120          125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
      130          135          140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145          150          155          160
Ser Arg Gly Val Gln Leu
      165

```

<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

```

acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccatata
60
caagggtccgc acgctcccat gtccctcggt ttcgacagtt cttttgcgcc gcattatggc
120
gaagccgctcg agattgcgcc tgatatcaag cgcacacgg tcaacaaccc cagccccttc
180
acttttttcg gcaccaacag ttatctgatc ggccgcgata cgctggcatt gatcgatccc
240
ggtccgcttg acgaggccca tcacgcgggc ctgctgctg ccattgccgg ccggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgcgac ggttttgaaa
360
g
361

```

<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

```

Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```



```

      1           5           10           15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
      20           25           30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
      35           40           45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
      50           55           60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
      65           70           75           80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
      85           90           95
Ile Pro Val Ser Thr Arg
      100

```

<210> 221  
 <211> 401  
 <212> DNA  
 <213> Homo sapiens

```

<400> 221
agatctctgt gtcgtcggct gcaaagagga tgagcccaga tgcataatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagcccaca ctgctgcagc acacctcgct
120
gcagctctgg ttctctctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgctggc ccagtgaacca cccccacagg gcataaccctc ctacagagca
240
ttcccaaaaa aggctagagt agacaccagg ctgctccgta gggggcctcc accccattct
300
ccaaggctc caccagggga cgctgggtga accagcatcc aggcctggcc cacctccctg
360
ctcagagtcc atgttctgtg acaagggtgg caactgggat t
401

```

<210> 222  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

```

<400> 222
Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
1           5           10           15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
      20           25           30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
      35           40           45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
      50           55           60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
      65           70           75           80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
      85           90           95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```

100 105 110  
 Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser  
 115 120  
 <210> 223  
 <211> 331  
 <212> DNA  
 <213> Homo sapiens  
 <400> 223  
 tcatgaaatc tgtgggcagt gacccaggag ggtatgggca ggcccaacca ggttgggtgtg  
 60  
 cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag  
 120  
 aaccaagcca ggctgcatgc aggaggttgg cacgtgaacg ctgcaggtgt tgccggcagc  
 180  
 cgtgggtgcct ggcagatagt gttcgacccc cnaggacctt cttgctgggc agcccagtc  
 240  
 aaaagctgtt cccgettaag ccacccccac cgccttggcc acacctggca catgggtgaa  
 300  
 gcaagggcac ttcccggggc ttcctgttcc c  
 331

<210> 224  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 224  
 Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly  
 1 5 10 15  
 Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Lys Val  
 20 25 30  
 Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His  
 35 40 45  
 Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser  
 50 55 60  
 Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly  
 65 70 75 80  
 Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly  
 85 90 95  
 Ser Leu Pro Thr Asp Phe Met  
 100

<210> 225  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<400> 225  
 tgatcacggg cgtgagccac cagcccagca tcccttgcct ttcattcgca cctccacctc  
 60  
 cagaatgacc ctcatccct cctgcacaga cgggtgacagc agtaactcct acaaacacca  
 120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct  
 180  
 caaatcctcc aggggtgcct gctatggggg agggaggcac actttgcttg gctctcaagg  
 240  
 cctcagccag ccgggtccaa accaactccc agcctggcct caccatccca ccgccaacc  
 300  
 tttgctcaca ctggcccctc ttcctggaac atgggcctn  
 339

<210> 226

<211> 91

<212> PRT

<213> Homo sapiens

<400> 226

Met	Thr	Leu	Ile	Pro	Ser	Cys	Thr	Asp	Gly	Asp	Ser	Ser	Asn	Ser	Tyr
1				5					10					15	
Lys	His	His	Gln	Thr	Asp	Leu	Gln	Glu	Gln	Arg	Asn	Ser	Gln	Ser	Arg
			20					25					30		
Phe	His	Pro	Arg	Arg	Ala	Leu	Lys	Ser	Ser	Arg	Ala	Ala	Cys	Tyr	Gly
		35					40					45			
Gly	Gly	Arg	His	Thr	Leu	Leu	Gly	Ser	Gln	Gly	Leu	Ser	Gln	Pro	Gly
	50					55					60				
Pro	Asn	Gln	Leu	Pro	Ala	Trp	Pro	His	His	Pro	Thr	Ala	Lys	Pro	Leu
65					70					75				80	
Leu	Thr	Leu	Ala	Pro	Leu	Pro	Gly	Thr	Trp	Ala					
				85						90					

<210> 227

<211> 353

<212> DNA

<213> Homo sapiens

<400> 227

gtcgaccctc tcgattgtgg cgaactccat ggctgctgcg ggctgctgta ggctctcgag  
 60  
 tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgctgcttct tggatggttc  
 120  
 gggcaactcc tcgggggatt cgagcagttc ttggcgcaac tgctctggcg tcatcccgga  
 180  
 ggccaggccg acaagtgtcg cctcctgcca cccgctgagc gacgctgcca tgttgagtac  
 240  
 ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgctca ggccgagaga  
 300  
 cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg  
 353

<210> 228

<211> 102

<212> PRT

<213> Homo sapiens

<400> 228

Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

```

      1           5           10           15
Leu Thr Ser Glu Asp Ala Val Leu Asn Met Ala Ala Ser Leu Ser Gly
      20           25           30
Trp Gln Glu Ala Ala Leu Val Gly Leu Ala Ser Gly Met Thr Pro Glu
      35           40           45
Gln Val Arg Gln Glu Leu Leu Glu Ser Pro Glu Glu Leu Pro Glu Pro
      50           55           60
Ser Lys Lys Gln His Gly His Ala Ala Ser Pro Arg Glu Pro Asp Val
65           70           75           80
Glu Leu Leu Glu Ser Leu Arg Arg Pro Ala Ala Ala Met Glu Phe Ala
      85           90           95
Thr Ile Glu Gly Val Asp
      100

```

&lt;210&gt; 229

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 229

```

nnggctaggg acacggcctc ctcctcaaca ggcagtgcct gtgcaggctc aggggcatca
60
tcaaagataa cacagggctg gtcaggggct gctggctgct cctgccccag gactggctcc
120
aggatgggca aggctgcctc cctggtagcc agggggagag ggggaaggag caccagggag
180
tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
240
agtaaagtgt ctgccccagg ggtgctcaca gcccaggacc gggtagttgg aaagccagcc
300
cagcttggca ctcagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
360
gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaag
420
agagattcac tgggtaccta cagtagtcga gatgtaagcc ttggggactg ggaatttggg
480
aagagagatt ctctgggtgc ttatgccagc caagatgcca acgagcaggg ccaagatttg
540
gggaagagg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
600
tttcagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa
660
caggagtttg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc
720
cttgacgccc aggacagaag ctt
743

```

&lt;210&gt; 230

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 230

```

Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

```

```

      1           5           10           15
Ser Gly Ala Ser Ser Lys Ile Thr Gln Gly Trp Ser Gly Ala Ala Gly
      20           25           30
Cys Ser Cys Pro Arg Thr Gly Ser Arg Met Gly Lys Ala Ala Ser Leu
      35           40           45
Val Ala Arg Gly Arg Gly Glu Gly Ser Thr Arg Glu Trp Ala Ser Arg
      50           55           60
Cys Gly Ile Gly Gln Glu Glu Met Glu Ala Ser Ser Ser Gln Asp Gln
      65           70           75           80
Ser Lys Val Ser Ala Pro Gly Val Leu Thr Ala Gln Asp Arg Val Val
      85           90           95
Gly Lys Pro Ala Gln Leu Gly Thr Gln Arg Ser Gln Glu Ala Asp Val
      100          105          110
Gln Asp Trp Glu Phe Arg Lys Arg Asp Ser Gln Gly Thr Tyr Ser Ser
      115          120          125
Arg Asp Ala Glu Leu Gln Asp Gln Glu Phe Gly Lys Arg Asp Ser Leu
      130          135          140
Gly Thr Tyr Ser Ser Arg Asp Val Ser Leu Gly Asp Trp Glu Phe Gly
      145          150          155          160
Lys Arg Asp Ser Leu Gly Ala Tyr Ala Ser Gln Asp Ala Asn Glu Gln
      165          170          175
Gly Gln Asp Leu Gly Lys Arg Asp His His Gly Arg Tyr Ser Ser Gln
      180          185          190
Asp Ala Asp Glu Gln Asp Trp Glu Phe Gln Lys Arg Asp Val Ser Leu
      195          200          205
Gly Thr Tyr Gly Ser Arg Ala Ala Glu Pro Gln Glu Gln Glu Phe Gly
      210          215          220
Lys Ser Ala Trp Ile Arg Asp Tyr Ser Ser Gly Gly Ser Ser Arg Thr
      225          230          235          240
Leu Asp Ala Gln Asp Arg Ser
      245

```

&lt;210&gt; 231

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 231

```

acgcgttggc caccgagagg ctggcgaggg tgtgcagcac ggcgcagtgt ggcagggctc
60
caggggtgcag cctgcgcagc agctcctcca tcaccttgcg gatgaactgt cttcccacgg
120
ccaccaggac gccactcgcc gcctgctgcc agtcccagac caggtccttc gtcttggtca
180
tctcgctgga ggccaggagg atgatggtgc tggtgtgtgc cttgtccagc tcaactggcg
240
gactgtcag gacctctcc atggcctca ggaccgctgc tcggtatggg tgtgccagct
300
tgtcatgctg ccgcagatac tcctcgagg cacggagcgt ctccaccctg ctggacgcca
360
tcaccgataa ggacccctg gtgcaggagc aggtctgcag tgccctgtgc tcctcgggg
420
aggtgcggcc g
431

```

<210> 232  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 232  
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu  
 1 5 10 15  
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg  
 20 25 30  
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp  
 35 40 45  
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr  
 50 55 60  
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val  
 65 70 75 80  
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg  
 85 90 95  
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu  
 100 105 110  
 Ala Ser Leu Ser Val Ala Asn Ala  
 115 120

<210> 233  
 <211> 606  
 <212> DNA  
 <213> Homo sapiens

<400> 233  
 acgcgttcag ggatgccaga aatctaactg ggtaataaaa agctgggaga acattccaga  
 60  
 aagggtgggca cccttagcat tcccaaaaag caccagccct cctcatcctt ccagcttct  
 120  
 gtgctggaat gcacccccat cggaaggct cgaaaactca ggacacatta ggatcacctg  
 180  
 gaaagcattt gtcaaaacgc atctccctgc gggtcagggt ccaagttaaa atcaaacttc  
 240  
 aggtgatgct gactcaggtg gctccagaaa cacctgggga agcagcactt tggaggctgc  
 300  
 ctctcacatc caccacacag caagtgggca gggagctagg taaatctcct tcccagttga  
 360  
 gaaggggctc ggagcaggca cagagaagag atacccttag aatgcaagtt gttcagctgc  
 420  
 gaaagtccag cctgcaggct tcttgggcaa gctagtgggc tgaagtatgc cacagcaaca  
 480  
 ggcttctaga gccggctgcc cagctcctac tctgcctctg ccactcactg actgtgtggt  
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 acgcgt  
 606

<210> 234

<211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 234

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Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser
 1             5             10             15
Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln
      20             25             30
Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr
      35             40             45
Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln
      50             55             60
Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly
65             70             75             80
Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln
      85             90             95
Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser
      100             105

```

<210> 235  
 <211> 328  
 <212> DNA  
 <213> Homo sapiens

<400> 235

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ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atgggtcaag
180
aaagaggaaa aagaagggca acttcaggat taaccactgg ggacctgaac ctaactgaaa
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acattttctca aggagataga ataagtgaaa gaaaattgga tttattgagc ctcaaaaata
300
tgagtgaagc acaatcaaag aatgaatt
328

```

<210> 236  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 236

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Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln
 1             5             10             15
Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu
      20             25             30
Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln
      35             40             45
Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu
      50             55             60
Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

```

65                      70                      75                      80  
Leu Asp Leu Leu Ser Leu Lys Asn Met Ser Glu Ala Gln Ser Lys Asn  
                              85                      90                      95

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<210> 237
<211> 2059
<212> DNA
<213> Homo sapiens
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<400> 237

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120					
gatgtcagac	tgcacatgaa	atcgggttacg	gtaccccagg	atcatcgcta	ccgagtacac
180					
ccgaacagc	acccgctggg	cgccgatcag	cgtgaggag	tgccccacca	gtggcacttt
240					
tcttagatag	cggaacccat	ccaccacatc	cccagtcacc	gttctcatcg	tccgggaacg
300					
atccaccagt	ggcggcccaa	gctcccgcag	tgaaaactgc	agcccctagg	cgaccgagac
360					
tgcgaagagg	gctgcggaga	tgcagaaaat	gatcgtgtcg	gcgtgggtgca	caggaatatg
420					
gcgtccggca	atcatgcgca	ctgctgcagc	aacaaccgca	ccgatcatga	gccttagcgg
480					
ccaatcgttg	gcatgattga	cgatgccgtc	aggtagtcgc	gcttgctgat	ggtgtattcc
540					
aaccagcga	ccaaggcggg	gagcaaaaac	cggttcaggc	tcatcgcgat	gagcaaccca
600					
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660					
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720					
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780					
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840					
gccagaccag	gctccttggg	gagaagacca	ccacagcggc	agctttccca	gtagcccttt
900					
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960					
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1020					
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1080					
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1140					
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1200					
ctagacatca	atgcctggat	ccttcagccg	gccctgccct	cctttaggag	acaggagtc
1260					



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 1380  
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 1920  
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 2040  
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 2059

&lt;210&gt; 238

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 238

Ala	Glu	Gln	Lys	Phe	Cys	Ala	Arg	Leu	Pro	Pro	Ser	Pro	Pro	Gly	His
1				5					10					15	
Val	Leu	Asp	Gly	Pro	Cys	Ser	Cys	Gly	Ser	Trp	Val	Ser	Ser	Glu	Leu
		20						25					30		
Asp	Ile	Asn	Ala	Trp	Ile	Leu	Gln	Pro	Ala	Leu	Pro	Ser	Phe	Arg	Arg
		35					40					45			
Gln	Glu	Ser	Pro	Gly	His	Ser	Pro	Pro	Gly	Pro	Pro	Gln	Glu	Gly	Met
		50				55				60					
Lys	Gly	Met	Pro	Ser	Ser	Leu	Val	Pro	Arg	Ala	Gln	Pro	Ser	Pro	Ser
65					70				75					80	
Pro	Pro	Gly	Gln	Gly	Gln	Cys	Gly	Ile	Phe	Arg	Phe	Arg	Pro	Leu	Trp
				85				90						95	
Ala	Glu	Pro	Pro	Cys	Glu	Cys	Ser	Tyr	Cys	Leu	Cys	Val	Ala	Val	Thr
			100					105					110		
Ser	Ile	Cys	Leu	Leu	Leu	Ile	Cys	Gln	Pro	Ile	Ala	Ala	Gly	Ser	Thr
			115				120						125		

Phe

<210> 239  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<400> 239  
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 120  
 ggtcagctgc ccttcctcca cttctgcttc tcggcggttac cccataccgt attggccgcg  
 180  
 tgttcacctt tgaatgcagc catgtcgtcg tctccgtatc gaaatgatgt gccatcgaag  
 240  
 atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgcgccac acgaaacgcc  
 300  
 cagcgcaacc gtgtcctcgc acgatacgaa gtgcttgggt atctcagctc tggtagctat  
 360  
 ggtcgtgtat ataaagcaaa ggaacttn  
 388

<210> 240  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 240  
 Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly  
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 Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val  
 20 25 30  
 Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Pro Tyr  
 35 40 45  
 Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala  
 50 55 60  
 Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val  
 65 70 75 80  
 Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly  
 85 90 95  
 Arg Val Tyr Lys Ala Lys Glu Leu  
 100

<210> 241  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 241  
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 gatgctgctt ccagggcggg cctgggggaa acatcggcct tcccaggcac ccttagccccg  
 120  
 tcccatctgg gggcccttag cacagtcctt gggaccccac atgctgcctt tcaggctgat  
 180

gtgggcaaac tcggcagccc agcctactcc cgggccatgg gccaccatct cagcttcctt  
 240  
 ggggctaagc cgtgtgctct gaatcaaaag cagtagtggc atcggcggca ctggcgccat  
 300  
 gggaaacggg ttgacttgca caaccagcac  
 330

<210> 242  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 242  
 Met Ala Pro Val Pro Pro Met Pro Leu Leu Leu Leu Ile Gln Ser Thr  
 1 5 10 15  
 Arg Leu Ser Pro Arg Glu Ala Glu Met Val Ala His Gly Pro Gly Val  
 20 25 30  
 Gly Trp Ala Ala Glu Phe Ala His Ile Ser Leu Lys Gly Ser Met Trp  
 35 40 45  
 Gly Pro Arg Asp Cys Ala Lys Gly Pro Gln Met Gly Arg Ala Lys Gly  
 50 55 60  
 Ala Trp Glu Gly Arg Cys Phe Pro Gln Ala Arg Pro Gly Ser Ser Ile  
 65 70 75 80  
 Pro Arg Ser Glu Ala Ser Ser Thr Ala Ser Val Pro Ala Ala Phe Asn  
 85 90 95  
 Ser Ala Pro Arg  
 100

<210> 243  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 243  
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 120  
 cccgtactgc tacacatgct agatattctc ccttccttgc ggactacagt ggtgatgggtg  
 180  
 caggcagaag tagccgatcg attggctgcc acaccaggca gccgcattta cggtgtcccc  
 240  
 agcgtcaaag tcaactttta cgggactgtc tcgcgtgcgg gagcaattgg acgcaatgtc  
 300  
 ttctggccgg ctcccaatgt tgattctggn  
 330

<210> 244  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 244  
 Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

```

      1           5           10           15
Glu Glu Ile Leu His Thr Gly His Pro Ala Pro Thr Ala Leu Val Ala
      20           25           30
Asn Leu Pro Tyr Asn Val Ala Val Pro Val Leu Leu His Met Leu Asp
      35           40           45
Ile Leu Pro Ser Leu Arg Thr Thr Val Val Met Val Gln Ala Glu Val
      50           55           60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
      65           70           75           80
Ser Val Lys Val Asn Phe Tyr Gly Thr Val Ser Arg Ala Gly Ala Ile
      85           90           95
Gly Arg Asn Val Phe Trp Pro Ala Pro Asn Val Asp Ser Gly
      100           105           110

```

&lt;210&gt; 245

&lt;211&gt; 355

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 245

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tctagatcct gaatcaccca cctcctagtt tcggattcac ctccgccggc gtcacctgaa
60
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120
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240
ganttggaac ccacagcatc gaatttgtcc agaaggaagt ggtcgttggt gagggatttg
300
ccccattcaa tacgcgcata ttcccgggaag cgcgcctcta ttgcggccaa cgcgt
355

```

&lt;210&gt; 246

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 246

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Met Arg Val Leu Asn Gly Ala Ile Pro Ser Pro Thr Thr Thr Ser Phe
      1           5           10           15
Trp Thr Asn Ser Met Leu Trp Leu Pro Xaa Pro Pro Thr Ala Trp Thr
      20           25           30
Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
      35           40           45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
      50           55           60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
      65           70           75           80
Ile Arg Ala Arg His Cys Phe Gln Val Thr Pro Ala Glu Val Asn Pro
      85           90           95
Lys Leu Gly Gly Gly
      100

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<210> 247  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 247  
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 60  
 gcctgggaca ccagcgtcgt gtccgagatc aagatgggag acaggtacga gacggtcagg  
 120  
 ttcttccact gctacaagcg cggagtggac cgcgtgttcg ttgaccaccc actgttctctg  
 180  
 gagagggttt ggggaaagac cgaggagaag atctacgggc ctgacgctgg aacggactac  
 240  
 agggacaacc agctgcgggt cagcctgcta tgccaggcag cacttgaagc tccaaggatc  
 300  
 ctgagcctca acaacaaccc atacttctcc gga  
 333

<210> 248  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 248  
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 Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys Met  
 20 25 30  
 Gly Asp Arg Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg Gly  
 35 40 45  
 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp  
 50 55 60  
 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr  
 65 70 75 80  
 Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu  
 85 90 95  
 Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser Gly  
 100 105 110

<210> 249  
 <211> 5503  
 <212> DNA  
 <213> Homo sapiens

<400> 249  
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 120  
 tcgccaacgca ccgcatgccca cctgaacccc agccccgatg gtgaggccta cacactggct  
 180  
 tcgagaccac ccgtccgcct caatgatgtc atgctcaggc tggtgacgga gctgcgctgg  
 240

cagaagttcg tcatgttcta cgacagcgag tatgatatcc gtgggcttca aagctttctg  
300  
gaccaggcct cgcggctggg ccttgacgtc tctttacaaa aggtggacaa gaacattagc  
360  
cacgtattca ccagcctgtt caccacgatg aagacagagg agctgaatcg ctaccgggac  
420  
acgcttcgcc gcgccatcct gctgctcagc ccacagggag cccactcctt catcaacgag  
480  
gccgtggaga ccaacctggc ttccaaggac agccactggg tctttgtgaa tgaggaaatc  
540  
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600  
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1560  
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1860

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1920  
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1980  
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2580  
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2700  
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2940  
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4200  
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4260  
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4380  
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4440  
catctgtcac tgaaggaggt ggagctccca cagccagcag taatcaggga gctgagagcc  
4500  
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4560  
gagtttctag agagatgtat ttatgagggt gataactagc ccaggattga tttctttcct  
4620  
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4680  
gcactgtggg gaagagagtg tttataatta tgttatttat tgctggatgc tgagaatggt  
4740  
ctgatattcg tgctacctag gcaatccatt gacatttctc caatcagagc atgtggacct  
4800  
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4860  
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4920  
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4980  
tcctcattgc cccctgagat ggctgtctt ctggggtata gcttggatgt cttcttggat  
5040  
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5100



gcctgtgtgt gtgtgtttgt gtgtgtgtgt gtgtgtgaga gagagagaga gagagagaga  
 5160  
 gaccagcatc ttcaagagaa gtattctgct tatacaaaat ccttaacacc tcatggtgtt  
 5220  
 attcttcacc atgtttatat atatatatat atattttttt ttttttttag aattttctac  
 5280  
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 5340  
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 5400  
 gatttataac tctgtttaga ctattccata catttttaggt atattttgtg ccttcagaca  
 5460  
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 5503

<210> 250

<211> 927

<212> PRT

<213> Homo sapiens

<400> 250

Met	Thr	Gln	Gly	Ile	Leu	Ala	Leu	Val	Thr	Ser	Thr	Gly	Cys	Ala	Ser
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Ala	Asn	Ala	Leu	Gln	Ser	Leu	Thr	Asp	Ala	Met	His	Ile	Pro	His	Leu
		20						25					30		
Phe	Val	Gln	Arg	Asn	Pro	Gly	Gly	Ser	Pro	Arg	Thr	Ala	Cys	His	Leu
	35						40					45			
Asn	Pro	Ser	Pro	Asp	Gly	Glu	Ala	Tyr	Thr	Leu	Ala	Ser	Arg	Pro	Pro
	50				55					60					
Val	Arg	Leu	Asn	Asp	Val	Met	Leu	Arg	Leu	Val	Thr	Glu	Leu	Arg	Trp
65				70					75					80	
Gln	Lys	Phe	Val	Met	Phe	Tyr	Asp	Ser	Glu	Tyr	Asp	Ile	Arg	Gly	Leu
		85					90						95		
Gln	Ser	Phe	Leu	Asp	Gln	Ala	Ser	Arg	Leu	Gly	Leu	Asp	Val	Ser	Leu
		100					105						110		
Gln	Lys	Val	Asp	Lys	Asn	Ile	Ser	His	Val	Phe	Thr	Ser	Leu	Phe	Thr
	115					120						125			
Thr	Met	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Tyr	Arg	Asp	Thr	Leu	Arg	Arg
	130				135					140					
Ala	Ile	Leu	Leu	Leu	Ser	Pro	Gln	Gly	Ala	His	Ser	Phe	Ile	Asn	Glu
145				150					155					160	
Ala	Val	Glu	Thr	Asn	Leu	Ala	Ser	Lys	Asp	Ser	His	Trp	Val	Phe	Val
		165					170						175		
Asn	Glu	Glu	Ile	Ser	Asp	Pro	Glu	Ile	Leu	Asp	Leu	Val	His	Ser	Ala
	180						185					190			
Leu	Gly	Arg	Met	Thr	Val	Val	Arg	Gln	Ile	Phe	Pro	Ser	Ala	Lys	Asp
	195					200						205			
Asn	Gln	Lys	Cys	Thr	Arg	Asn	Asn	His	Arg	Ile	Ser	Ser	Leu	Leu	Cys
	210					215					220				
Asp	Pro	Gln	Glu	Gly	Tyr	Leu	Gln	Met	Leu	Gln	Ile	Ser	Asn	Leu	Tyr
225				230					235					240	
Leu	Tyr	Asp	Ser	Val	Leu	Met	Leu	Ala	Asn	Ala	Phe	His	Arg	Lys	Leu
		245					250						255		
Glu	Asp	Arg	Lys	Trp	His	Ser	Met	Ala	Ser	Leu	Asn	Cys	Ile	Arg	Lys

563

```

      690              695              700
Arg Ile Leu Glu Leu Gln Asp Thr Gly Asp Leu Asp Val Leu Lys Gln
705              710              715              720
Lys Trp Trp Pro His Met Gly Arg Cys Asp Leu Thr Ser His Ala Ser
      725              730              735
Ala Gln Ala Asp Gly Lys Ser Leu Lys Leu His Ser Phe Ala Gly Val
      740              745              750
Phe Cys Ile Leu Ala Ile Gly Leu Leu Ala Cys Leu Val Ala Ala
      755              760              765
Leu Glu Leu Trp Trp Asn Ser Asn Arg Cys His Gln Glu Thr Pro Lys
      770              775              780
Glu Asp Lys Glu Val Asn Leu Glu Gln Val His Arg Arg Met Asn Ser
785              790              795              800
Leu Met Asp Glu Asp Ile Ala His Lys Gln Ile Ser Pro Ala Ser Ile
      805              810              815
Glu Leu Ser Ala Leu Glu Met Gly Gly Leu Ala Pro Thr Gln Thr Leu
      820              825              830
Glu Pro Thr Arg Glu Tyr Gln Asn Thr Gln Leu Ser Val Ser Thr Phe
      835              840              845
Leu Pro Glu Gln Ser Ser His Gly Thr Ser Arg Thr Leu Ser Ser Gly
      850              855              860
Pro Ser Ser Asn Leu Pro Leu Pro Leu Ser Ser Ser Ala Thr Met Pro
865              870              875              880
Ser Met Gln Cys Lys His Arg Ser Pro Asn Gly Gly Leu Phe Arg Gln
      885              890              895
Ser Pro Val Lys Thr Pro Ile Pro Met Ser Phe Gln Pro Val Pro Gly
      900              905              910
Gly Val Leu Pro Glu Ala Leu Asp Thr Ser His Gly Thr Ser Ile
      915              920              925

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<210> 251  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

```

<400> 251
nngatcagcc gcggggtccg cgccctcgat tcggcggtgg agaccgagag tctgcgtgag
60
gacgtcaacg cgtcgaacg gctgcggttg gccgtgcgcg ccagcgtggt catcctcacc
120
gagtaccacc attcggtagc cctgctgctg cgggtgcgcg ggaactcacc tctggaacga
180
gaggeccctcg aggcccgccg ccgtatcgat gcgaagggttc ccgctctcgt cgagagcgcc
240
atcgccgagg gtggtctgcg ctcggatttc actcccgggc tcatcacgcg t
291

```

<210> 252  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

```

<400> 252
Xaa Ile Ser Arg Gly Val Arg Ala Leu Asp Ser Ala Val Glu Thr Glu

```

```

      1             5             10             15
Ser Leu Arg Glu Asp Val Asn Ala Leu Glu Arg Leu Arg Leu Ala Val
      20             25             30
Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
      35             40             45
Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
      50             55             60
Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
      65             70             75             80
Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
      85             90             95
Arg

```

<210> 253  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

```

<400> 253
gtgcacggat gggagcgctc gcgcgcgtgc tggcgcttc acagcccggc gagcggcgtg
60
cgctcacggg cctgtaccga ccgatctcgc aaccttcgc agaccgatcc accaaccggc
120
cccacatgtc ggcagtgatg gcgggcacct tgcgggagaa ggccgggaag gtcgagcgag
180
ccaatgaccg tcgcacggtc ggcacgctcc acgagcggga cgagaagctc gcggcaggac
240
gtcactcgt cgcggtgtcc tccgcggtct ccatcacgt ccctgcgaca tggaacgccc
300
acgacttcgg acggcgactc gacgcgt
327

```

<210> 254  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

```

<400> 254
Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
1             5             10             15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
      20             25             30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
      35             40             45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
      50             55             60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
      65             70             75             80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
      85             90             95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
      100             105

```

<210> 255  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

<400> 255  
 ctagaaatgg ctggctacga atacatggaa gctgaaaata gccacaagc ccacgaaatt  
 60  
 atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc  
 120  
 atcgagctaa ctctgcgtt aaagaaagac agcacgacag cagaaatccc tgttatttta  
 180  
 ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac  
 240  
 tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc  
 300  
 cgagcgactc cacaaggtat tgatgatcct attgaaattg atggtttaac gcttgatccc  
 360  
 attagccaac gc  
 372

<210> 256  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 256  
 Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln  
 1 5 10 15  
 Ala His Glu Ile Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp  
 20 25 30  
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys  
 35 40 45  
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Leu Thr Ala Lys  
 50 55 60  
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp  
 65 70 75 80  
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys  
 85 90 95  
 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu  
 100 105 110  
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg  
 115 120

<210> 257  
 <211> 639  
 <212> DNA  
 <213> Homo sapiens

<400> 257  
 nnacgcgtag cggctcgaggt tgcggacacc atgcccgaa cggcctgct cgccatcgag  
 60  
 gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgccgaa  
 120

cggttcgggc tcggcggcat cttcttcggt ctaccgacga tggccacgtc caatcccatg  
 180  
 ttcgggtcgag ttcgggaatg gctggacgct gtgccagcca aggaccgctc aagcatttcc  
 240  
 ctgggtcact cgaaagctgg actcaacgag gagtaccagc agctcatgcc gtggaacgcc  
 300  
 accatggccg tctacgacga aggtgccggc acgcagcgtg aagcttcggc gatcgtccat  
 360  
 gagtggttct tgggcccga ggcgcgcatc ctggccgacc acgtcgtcgg gaccatcgac  
 420  
 caggcactgt tcaccggtct caaagccaag catgtggtgt tacgccacct cggctctggcg  
 480  
 agcaaggtcg tcatcattga tgaggtccac gccgccgacg tctatatgcy cgaatacctc  
 540  
 aaggtcgtcc tcgaatggct cgggccttac cgcacgccag tcatcctcat gtccgcgacg  
 600  
 ctgccaccgg cccaacgtca tgaactcgcg ctacggtac  
 639

&lt;210&gt; 258

&lt;211&gt; 213

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 258

Xaa	Arg	Val	Ala	Val	Glu	Val	Ala	Asp	Thr	Met	Pro	Glu	Pro	Gly	Leu
1				5					10					15	
Leu	Ala	Ile	Glu	Ala	Pro	Met	Gly	His	Gly	Lys	Thr	Glu	Ala	Ala	Leu
		20						25					30		
Met	Cys	Ala	Gln	Val	Leu	Ala	Glu	Arg	Phe	Gly	Leu	Gly	Gly	Ile	Phe
	35						40					45			
Phe	Gly	Leu	Pro	Thr	Met	Ala	Thr	Ser	Asn	Pro	Met	Phe	Gly	Arg	Val
50						55					60				
Arg	Glu	Trp	Leu	Asp	Ala	Val	Pro	Ala	Lys	Asp	Pro	Ser	Ser	Ile	Ser
65				70						75				80	
Leu	Ala	His	Ser	Lys	Ala	Gly	Leu	Asn	Glu	Glu	Tyr	Gln	Gln	Leu	Met
				85					90					95	
Pro	Trp	Asn	Ala	Thr	Met	Ala	Val	Tyr	Asp	Glu	Gly	Ala	Gly	Thr	Gln
		100					105					110			
Arg	Glu	Ala	Ser	Ala	Ile	Val	His	Glu	Trp	Phe	Leu	Gly	Arg	Lys	Arg
	115						120					125			
Ala	Ile	Leu	Ala	Asp	His	Val	Val	Gly	Thr	Ile	Asp	Gln	Ala	Leu	Phe
130						135					140				
Thr	Gly	Leu	Lys	Ala	Lys	His	Val	Val	Leu	Arg	His	Leu	Gly	Leu	Ala
145				150						155				160	
Ser	Lys	Val	Val	Ile	Ile	Asp	Glu	Val	His	Ala	Ala	Asp	Val	Tyr	Met
				165					170					175	
Arg	Glu	Tyr	Leu	Lys	Val	Val	Leu	Glu	Trp	Leu	Gly	Ala	Tyr	Arg	Thr
	180						185					190			
Pro	Val	Ile	Leu	Met	Ser	Ala	Thr	Leu	Pro	Pro	Ala	Gln	Arg	His	Glu
	195						200					205			
Leu	Ala	Leu	Ala	Tyr											
210															

<210> 259  
 <211> 252  
 <212> DNA  
 <213> Homo sapiens

<400> 259  
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg  
 60  
 ncatgggtgtg tgcacgtgtg cnactgtgta tgcattgtaa tgtgcacgtg tgcactgtgtg  
 120  
 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtggggg gtatgcatgg  
 180  
 tgtgtgcaca tgagcactgt gtgggtgtgta tgcattggtgn ggtgcacgtg tgcactgtgtg  
 240  
 atgcaatggt gt  
 252

<210> 260  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<400> 260  
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys  
 1 5 10 15  
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met  
 20 25 30  
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val  
 35 40 45  
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met  
 50 55 60  
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys  
 65 70 75 80  
 Met Gln Trp Cys

<210> 261  
 <211> 1202  
 <212> DNA  
 <213> Homo sapiens

<400> 261  
 gctagcccg tgcggttcgt cgtcgatttg ctggcggcag tcccctcgat cgtcttcggt  
 60  
 ctgtggggcg gcatcgcttt cggatcgctg ggaatcatca acggttacgc gggggcctta  
 120  
 ttcaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtgggc ctcggctact  
 180  
 ggcaagggtc accttgccag tctcgtcctg gccatcatga tcctgccaat tatcactgct  
 240  
 gttagcccg acgtcatgcc ccgaacgcc catgatcaag tcgaggccgc gtcgcacctc  
 300  
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtccggcatc  
 360

atttccggat ccatgttggg tctaggacgc gccctcggcg agaccctggc tgtcacccctc  
 420  
 atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc  
 480  
 ggtggtgaga cattcgcgctc gaagattgcc ggtaacttct ccgaggccat tagcgatccc  
 540  
 acctcgctgg gtgccctcgt ggcgtcggcc ctggccctgt tcgtcattac cttcgtggtc  
 600  
 aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accaccctg  
 660  
 accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgtctg  
 720  
 gtaaacggac tatcaagagc ggctgcgcct caacattcat gatcgtggcc accgtactgg  
 780  
 ctgttatccc actggcctgg ctgctcttcg cggcgcgccg gcgcggcatc ggatcactat  
 840  
 tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg  
 900  
 ccateccagc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggta  
 960  
 cgatcgctct gatgaccgcg atcttcctag tcgagtacgc ccgcggaact aagatcgcca  
 1020  
 aggtcattag cttcgccgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct  
 1080  
 tcgtcttcgc cgtagtcgtt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt  
 1140  
 tggccctcat gatcctcatg gttccgacgg tgctgcgatc aaccgaggaa atgctcaagc  
 1200  
 tt  
 1202

&lt;210&gt; 262

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 262

Ala	Ser	Pro	Val	Ala	Phe	Val	Val	Asp	Leu	Leu	Ala	Ala	Val	Pro	Ser
1				5				10						15	
Ile	Val	Phe	Gly	Leu	Trp	Gly	Gly	Ile	Val	Phe	Gly	Ser	Ser	Gly	Ile
			20					25					30		
Ile	Asn	Gly	Tyr	Ala	Gly	Ala	Leu	Phe	Lys	Ala	Leu	Gly	Trp	Ile	Pro
			35				40					45			
Ile	Phe	Ser	Glu	Asp	Pro	Ser	Trp	Ser	Ser	Ala	Thr	Gly	Thr	Val	Tyr
			50				55				60				
Leu	Ala	Ser	Leu	Val	Leu	Ala	Ile	Met	Ile	Leu	Pro	Ile	Ile	Thr	Ala
65					70					75				80	
Val	Ser	Arg	Asp	Val	Met	Pro	Arg	Thr	Pro	His	Asp	Gln	Val	Glu	Ala
				85					90					95	
Ala	Leu	Ala	Leu	Gly	Ser	Thr	Arg	Trp	Glu	Val	Ile	Lys	Leu	Ala	Val
			100					105					110		
Phe	Pro	His	Ser	Arg	Ser	Gly	Ile	Ile	Ser	Gly	Ser	Met	Leu	Gly	Leu
			115				120					125			
Gly	Arg	Ala	Leu	Gly	Glu	Thr	Leu	Ala	Val	Thr	Leu	Ile	Leu	Gln	Thr



130                      135                      140  
 Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val  
 145                      150                      155                      160  
 Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala  
                     165                      170                      175  
 Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala  
                     180                      185                      190  
 Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala  
                     195                      200                      205  
 Ala Lys Gly Val Lys Arg  
 210

<210> 263  
 <211> 424  
 <212> DNA  
 <213> Homo sapiens

<400> 263  
 acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgccg tgaactttcc  
 60  
 gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgag aacgtacctc ggaagacgtt  
 120  
 gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg  
 180  
 tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaag  
 240  
 gcttatatgg cctcgccatt ccgtgccaat ttggacctgg cataccatc ttcgacgcca  
 300  
 caggcccagt cccagccggc gatgccgccg tgggagacag ggacctcagc cagtagcatg  
 360  
 gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac  
 420  
 gann  
 424

<210> 264  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 264  
 Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile  
 1                      5                      10                      15  
 Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His  
                     20                      25                      30  
 Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn  
                     35                      40                      45  
 Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro  
                     50                      55                      60  
 Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp  
 65                      70                      75                      80  
 Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln  
                     85                      90                      95  
 Lys His Xaa

<210> 265  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 265  
 ncgtacggcc ctggcgccg catggacgag ggataccatt ccggcatgac ggtgccgggt  
 60  
 gccttcgact ccctcatcgg caagctcatc atcactgggtg atagccgtga gcaagccctg  
 120  
 gctcgagctg cccgcgccct cgacgaaatc gtcacgacg gcatgccgac ggtcattccc  
 180  
 tttcaccagg cgggtggttca cgacccggct ttcactgccg ccgacgggtg cttcggcgctc  
 240  
 tttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg  
 300  
 ggcgagtctg ccaattccga gcctcctcgt gaggtcgtcg tcgaggtcaa cggtaaacgc  
 360

<210> 266  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 266  
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met  
 1 5 10 15  
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr  
 20 25 30  
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Arg Ala Leu Asp  
 35 40 45  
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala  
 50 55 60  
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val  
 65 70 75 80  
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr  
 85 90 95  
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val  
 100 105 110  
 Val Val Glu Val Asn Gly Lys Arg  
 115 120

<210> 267  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 267  
 naccctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg  
 60  
 ttaacgcatac ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg  
 120

ctagatctcg ggcaccttca ccctagtcgg cggggactcg tcactatcac cacaactgtc  
 180  
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa  
 240  
 aaacttttcg aagctcgcga ttaccgccag attccgatgc ttgcatcacg tcatggctgg  
 300  
 acagctccat tcattggtga gaccggcgca gcccatgcca tcgaggatgc gatgggcatt  
 360  
 accatcccaa ctgcgctggc atggatacga accctgctcg ctgagttcag cagaatcacc  
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<210> 268

<211> 157

<212> PRT

<213> Homo sapiens

<400> 268

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Gly	Ser	Met	Pro	Leu	Thr	His	Pro	Ser	Gln	Ser	Thr	Asp	Gly	Asp	Pro
			20					25					30		
Gly	Lys	Lys	Tyr	Glu	Val	Thr	Trp	Leu	Asp	Leu	Gly	His	Leu	His	Pro
		35					40					45			
Ser	Arg	Pro	Gly	Leu	Val	Thr	Ile	Thr	Thr	Thr	Val	Asp	Asp	Asp	Val
	50					55					60				
Ile	Thr	Ser	Ser	Gln	Val	Asn	Val	Gly	Asn	Leu	His	Arg	Gly	Asp	Glu
65				70					75					80	
Lys	Leu	Phe	Glu	Ala	Arg	Asp	Tyr	Arg	Gln	Ile	Pro	Met	Leu	Ala	Ser
			85					90						95	
Arg	His	Gly	Trp	Thr	Ala	Pro	Phe	Ile	Gly	Glu	Thr	Gly	Ala	Ala	His
		100						105					110		
Ala	Ile	Glu	Asp	Ala	Met	Gly	Ile	Thr	Ile	Pro	Thr	Arg	Val	Ala	Trp
		115					120					125			
Ile	Arg	Thr	Leu	Leu	Ala	Glu	Phe	Ser	Arg	Ile	Thr	Ser	His	Phe	Thr
	130					135					140				
Phe	Leu	Ser	Trp	Val	Gly	His	His	Cys	Asp	Asp	Ala	Gly			
145					150						155				

<210> 269

<211> 387

<212> DNA

<213> Homo sapiens

<400> 269

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 120  
 tttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct  
 180  
 tgttcgttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat  
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatggtat tcgcttagaa  
 300  
 ccgggcggttc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc  
 360  
 tcgggggttat tggttcaaact actacgc  
 387

<210> 270  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<400> 270  
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 Glu Val Ile Ala Asp Met Thr Val Ile Asn Pro Phe Asp Phe Phe Val  
 20 25 30  
 Glu Ser Tyr Ala Glu Asp Tyr Pro Phe Ala Tyr Asp Lys Ala Leu Lys  
 35 40 45  
 Lys Glu Leu Glu Pro Tyr Leu Gln Val Ser Glu Pro Cys Ser Leu Leu  
 50 55 60  
 Asp Lys Trp Leu Ser Gly Val Asp Arg Glu Lys Thr Pro Ile Asn Asp  
 65 70 75 80  
 Phe Leu Val Ala Ile Asn Ser Arg Leu Ala Gly Asp Ile Gly Tyr Gly  
 85 90 95  
 Ile Arg Leu Glu Pro Gly Val Gln Ser Pro Glu Glu Thr Leu Thr Leu  
 100 105 110  
 Met Lys Gly Ser Cys Arg Asp Thr Ser Gly Leu Leu Val Gln Ile Leu  
 115 120 125  
 Arg

<210> 271  
 <211> 443  
 <212> DNA  
 <213> Homo sapiens

<400> 271  
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 60  
 caccgccgag tgggtttggt aaccagccca cacctgcagc gcgttactga gcgcacgagc  
 120  
 attgatggcc agccattca ccgcgcgat tatgtacgca tctggcacga gattaagcca  
 180  
 tttgtggaat tggctgatgc cgaatcggac gtgcctatgt ctaagttcga ggtcttcgtg  
 240  
 ggctgtcct atgtgcggt tgcgcagcc ccgggggacg tcgctgtcgt cgaagtcggc  
 300  
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattaccccg  
 360  
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 420  
 gctggcatta ttaagccacg cgt  
 443

<210> 272  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<400> 272  
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 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu  
 20 25 30  
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro  
 35 40 45  
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met  
 50 55 60  
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val  
 65 70 75 80  
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val  
 85 90 95  
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn  
 100 105 110  
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr  
 115 120 125  
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile  
 130 135 140  
 Lys Pro Arg  
 145

<210> 273  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens

<400> 273  
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 aagagaagcc aaagcccccc cccccacct caaaggctcg gaagtctggc atccctactt  
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 180  
 tgctgcctga gaactggcct ccagccggtg tcttcattcc atggggctcc ctgctgactg  
 240  
 catttcctga tctgggatga tgtttaccag cccaaaacca gtcattgttct tccaaaagct  
 300  
 tctctttgat agaattttga ggccatgcc cctcccttcc agtccacatg gaattccaga  
 360  
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaattgca  
 420  
 gcctgtacgg cagagacatg gtggtctgca caagcctgga caagttcttc catattgatg  
 480  
 gtgggagcaa ccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaagc  
 540  
 tgtgcttgag acttaggtac ttttctcagc tggacacact gatcccatcc catattgcat  
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg  
 660  
 tctattgtat ctcctttgag gaaaagaaca cacattttta atggagattg gctgctttca  
 720  
 ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt  
 780  
 ccaccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac  
 840  
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 864

<210> 274

<211> 116

<212> PRT

<213> Homo sapiens

<400> 274

Met	Trp	Thr	Gly	Arg	Glu	Val	Ala	Trp	Pro	Gln	Asn	Ser	Ile	Lys	Glu
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Lys	Leu	Leu	Glu	Glu	His	Asp	Trp	Phe	Trp	Ala	Gly	Lys	His	His	Pro
			20					25					30		
Arg	Ser	Gly	Asn	Ala	Val	Ser	Arg	Glu	Pro	His	Gly	Met	Arg	Thr	Pro
		35					40					45			
Ala	Gly	Gly	Gln	Phe	Ser	Gly	Ser	Ser	Cys	Leu	Arg	His	Ser	Val	Leu
	50					55					60				
Gln	Gly	Gly	Gln	Asp	Pro	Tyr	Trp	Asp	Pro	Gly	Ser	Glu	Val	Gly	Met
65				70					75					80	
Pro	Asp	Phe	Arg	Ala	Phe	Glu	Val	Gly	Gly	Gly	Gly	Phe	Gly	Phe	Ser
			85					90					95		
Ser	Thr	Ala	Gly	Ser	Glu	Leu	Gln	Ser	Arg	Thr	Gln	Asn	Leu	Lys	
			100				105					110			
Gln	Ser	Tyr	Phe												
			115												

<210> 275

<211> 911

<212> DNA

<213> Homo sapiens

<400> 275

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 ttattttcag gaatgaaagg aattaccacg cttctgctt ttatacctac agctgaaagt  
 120  
 aattcctttc agcctcaggt gaagactttg ccattctcaa ttgatgctaa acagcagttg  
 180  
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccttt gccaggagaa  
 240  
 tctgcagcaa aaaagtcaga aagtgtaca agcaatggag tgactaatct tcctaattga  
 300  
 aatccttcaa tcctttctcc tcaacctatt ggtatcgttg tggcagctgt ccctagtccc  
 360  
 attccggctc agcggactag gcaattggta acttcaccga gtccaatgag ttcttctnga  
 420

cggcaaagtt cttccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca  
 480  
 ggacacaaag actccccaga acgttccagc agtcctgggtg ggaatcggtc tgcccggaac  
 540  
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgtcttcca  
 600  
 actactgtcc tctttactag tagtcccatc aaaactgctg ttgtaccgcg ttcacacatg  
 660  
 agttctctaa atgtgggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc  
 720  
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt  
 780  
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctctggggtc caggagcagc  
 840  
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 900  
 catcctgtac a  
 911

<210> 276

<211> 279

<212> PRT

<213> Homo sapiens

<400> 276

Met	Lys	Gly	Ile	Thr	Gln	Pro	Ser	Ala	Phe	Ile	Pro	Thr	Ala	Glu	Ser
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Asn	Ser	Phe	Gln	Pro	Gln	Val	Lys	Thr	Leu	Pro	Ser	Pro	Ile	Asp	Ala
			20					25					30		
Lys	Gln	Gln	Leu	Gln	Arg	Lys	Ile	Gln	Lys	Lys	Gln	Gln	Glu	Gln	Lys
			35				40						45		
Leu	Gln	Ser	Pro	Leu	Pro	Gly	Glu	Ser	Ala	Ala	Lys	Lys	Ser	Glu	Ser
			50				55					60			
Ala	Thr	Ser	Asn	Gly	Val	Thr	Asn	Leu	Pro	Asn	Gly	Asn	Pro	Ser	Ile
65					70					75				80	
Leu	Ser	Pro	Gln	Pro	Ile	Gly	Ile	Val	Val	Ala	Ala	Val	Pro	Ser	Pro
				85				90						95	
Ile	Pro	Val	Gln	Arg	Thr	Arg	Gln	Leu	Val	Thr	Ser	Pro	Ser	Pro	Met
			100					105					110		
Ser	Ser	Ser	Xaa	Arg	Gln	Ser	Ser	Ser	Pro	Gln	Cys	Thr	Gly	Gly	His
			115				120					125			
Ser	Ala	His	Ala	Val	Cys	Glu	Thr	Gly	Thr	Lys	Asp	Ser	Pro	Glu	Arg
			130				135				140				
Ser	Ser	Ser	Pro	Gly	Gly	Asn	Arg	Ser	Ala	Arg	His	Arg	Tyr	Pro	Gln
145					150					155				160	
Ile	Leu	Pro	Lys	Pro	Ala	Asn	Thr	Ser	Ala	Leu	Thr	Ile	Arg	Ser	Pro
				165				170					175		
Thr	Thr	Val	Leu	Phe	Thr	Ser	Ser	Pro	Ile	Lys	Thr	Ala	Val	Val	Pro
			180					185					190		
Ala	Ser	His	Met	Ser	Ser	Leu	Asn	Val	Val	Lys	Met	Thr	Thr	Ile	Ser
			195				200					205			
Leu	Thr	Pro	Ser	Asn	Ser	Asn	Thr	Pro	Leu	Lys	His	Ser	Ala	Ser	Val
210					215					220					
Ser	Ser	Ala	Thr	Gly	Thr	Thr	Glu	Glu	Ser	Arg	Ser	Val	Pro	Gln	Ile

<400> 278															
Met	Ser	Glu	Val	Pro	Asp	Glu	Leu	Val	Val	Leu	Arg	Gly	Ala	Ile	Asp
1				5					10					15	
Asn	Met	Asp	Ala	Leu	Ile	His	Leu	Leu	Ala	Glu	Arg	Phe	Arg	Ile	
			20				25					30			
Thr	Arg	Glu	Val	Gly	Arg	Leu	Lys	Ala	Glu	Cys	Gly	Leu	Pro	Pro	Ala
		35				40					45				
Asp	Pro	Ala	Arg	Glu	Ala	Glu	Gln	Ile	Ala	Arg	Leu	Arg	Gln	Leu	Ala
	50					55				60					
Val	Glu	Ser	Asn	Leu	Asp	Pro	Glu	Phe	Ala	Gln	Lys	Val	Ile	Thr	Phe
65				70					75					80	
Ile	Val	Ala	Glu	Val	Val	Arg	His	His	Glu	Ala	Ile	Ala	Asp	Asp	Ser



85 90 95  
 Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly  
 100 105 110  
 Ser Gly Ser  
 115

<210> 279  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<400> 279  
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 60  
 taccacaatc cttaaaaaga aaagaaagaa aggcatatgg aacccttagt taccttcat  
 120  
 ccagcttcaa aattgtcagt gcatgggtcaa tcttgtctta tctgcccctc acccaccctt  
 180  
 ttccagaaag aagaccaga ggattccaca tctgcctgga aaccacgacc agtctcgact  
 240  
 ggaagtgttt gttaatgttg catgtattca taaaacctct aggcatttct agtgtccctc  
 300  
 agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt  
 348

<210> 280  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 280  
 Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr  
 1 5 10 15  
 Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp  
 20 25 30  
 Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg  
 35 40 45  
 Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp  
 50 55 60  
 Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser  
 65 70 75 80  
 Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu  
 85 90 95  
 Pro Lys Ile

<210> 281  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

<400> 281  
 agatctgcgc agatcgataa tggattaaag actcttgacg ctggagtcac cgagatgaac  
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aacaaggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccaggtg  
120  
aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag  
180  
acgcgcgtgg gtgcccaggc gattaccggc gctgctcaaa atgtcatggc tgattcccaa  
240  
gctgtcaact cagccatggg tccgcttatt aataacgtga caaagaatct tcctaccttg  
300  
caaaaacagg ccaggaatct cgtgtcagtg aacgggtaccc tgcagaaccc caacggtgat  
360  
tctgtcatta agattcaaca gacc  
384

<210> 282

<211> 110

<212> PRT

<213> Homo sapiens

<400> 282

Met	Asn	Asn	Lys	Val	Leu	Gly	Ala	Thr	Lys	Ala	Val	Gly	Asp	Ser	Thr
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Thr	Thr	Val	Asn	Gln	Val	Asn	Ser	Ala	Leu	Gly	Xaa	Ala	Asp	Ser	Ala
		20						25				30			
Ala	Glu	Lys	Thr	Ser	Ser	Ala	Val	Thr	Gln	Thr	Arg	Val	Gly	Ala	Gln
	35					40					45				
Ala	Ile	Thr	Gly	Ala	Ala	Gln	Asn	Val	Met	Ala	Asp	Ser	Gln	Ala	Val
	50					55				60					
Asn	Ser	Ala	Met	Val	Pro	Leu	Ile	Asn	Asn	Val	Thr	Lys	Asn	Leu	Pro
65				70						75				80	
Thr	Leu	Gln	Lys	Gln	Ala	Arg	Asn	Leu	Val	Ser	Val	Asn	Gly	Thr	Leu
		85						90				95			
Gln	Asn	Pro	Asn	Gly	Asp	Ser	Val	Ile	Lys	Ile	Gln	Gln	Thr		
		100						105				110			

<210> 283

<211> 426

<212> DNA

<213> Homo sapiens

<400> 283

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120  
ggaagcgtag tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc  
180  
tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga  
240  
tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta  
300  
cgcatcaagg aagtcttgca tgaaaaaggg gtcattgtgc cttccacgct gcgcttgatc  
360  
cgcaacgcgg tgcccaccac ctgccaaatt accatgctca agcctgatac cgaattgtcg  
420

gagaga  
426

<210> 284  
<211> 142  
<212> PRT  
<213> Homo sapiens

<400> 284  
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys  
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20 25 30  
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu  
35 40 45  
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu  
50 55 60  
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg  
65 70 75 80  
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu  
85 90 95  
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met  
100 105 110  
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys  
115 120 125  
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg  
130 135 140

<210> 285  
<211> 345  
<212> DNA  
<213> Homo sapiens

<400> 285  
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cgatttctca gaaatctaca aacgtcagaa ctcgatcttc ggcgatgtaa ggaataactt  
120  
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggt gtattgcgca agatttcact  
180  
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc  
240  
gcatttcgaa ctcgtcggtt tgtttgaca accctggggt tatacttcgg acaattcaca  
300  
ctacggcatc ccgctccgca atgaaatcgt aattgggttct attcn  
345

<210> 286  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 286  
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

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      20             25             30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu
      35             40             45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly
      50             55             60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu
      65             70             75             80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile
      85             90             95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile
      100             105

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&lt;210&gt; 287

&lt;211&gt; 1379

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 287

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120
gtttttgcagg tcaegggccag gggctttggg ccgctgttac agtttgcta cactgccaag
180
ctgttactca gcagagaaaa catccgcgag gtcattccgct gtgctgagtt cctgcgcatg
240
cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
300
ggcctgtttg tgtgccggaa ggatgctgctg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
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480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac cccagataca agaaatacca gcttgcatgt
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagttag
720
ccgcccagtg aagagaatga ggaagagagc atcacgctct gcctgtctgg agatgagcct
780
gacgccaagg acagagcggg ggatgtcgag atggaccgga aacagcccag ccctgcccct
840
acccccacgg cccagctgg ggcgcctgc ctggagagat ccaggagcgt ggcctcgccc
900
tctgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtctgg cctgcccagt
960
acatctcagc agcactttgc caggagtcca gcctgccctt ttgacaaggg gatcactcag
1020

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ggtgacctta aaactgacta cacccttttc acaggaatt atggacagcc ccacgtgggc  
 1080  
 cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct  
 1140  
 ctctgtaaac aggagggaga gctggaccgg aggagcgtga tcttctctc cagcgcttgt  
 1200  
 gaccaagtga gcacctcggg gcattcttat tctggggtga gcagtttga caaagacctc  
 1260  
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 1320  
 gcctactccc acggtgggct gatggccgac cacttgccag gaaggatgcg gcccaacac  
 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
1				5					10					15	
Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25				30			
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35				40					45				
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
	50					55					60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
65				70					75					80	
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
			85					90				95			
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105				110			
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
		115				120						125			
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
	130					135					140				
Thr	Asp	Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro
145				150					155					160	
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
			165					170					175		
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180				185						190			
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
		195				200					205				
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu	
	210					215				220					
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
225				230				235						240	
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
			245					250				255			
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
		260				265						270			
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

```

<400> 289
ngcattaccg ggctgaagac ggggtgctcat gacctcaacg atataggcta ttgctagaac
60
cacgccggcc cacgccgcgc aaagcgcaga cacggcacca ggaggggtca catggctgat
120
agcaagtcga aggcgaagga cgagcgcact gccgatgaga tcaggcgggga tattgcagcg
180
acccgtgctt gcctggcagc cgggggtggag aacctcgtgg aggaggtgca tccggcaacc
240
ctcaagcgtg aagcatctga tcgtgcccggt gattttgtgc aggggtgagtt tgatcaggtc
300
aagagccagg tcaaagatga gaaatggtgg cgcgtcgagc ggatcgcgat ggccgcagga
360
gtgctcgctg ccggcgctcg cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg
420
ggcgctaccg ctcgtcgcaa gcttgagaag ctgcagcttt ctcaggcgaa gcggggttca
480
aaagatgcca agcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc
540
ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac
600
cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccggggcg
660
tgagaacagt gccgcctagc aaacagcggg cacagcgcaa aacaggtttg gctccgaccc
720
atggtggacc ggagccaaac tgtgttaccg catcatttga taccgccagc agccaggcct
780
gcgacaatgc gacgctggaa taccagcacc atgatgacta gt
822

```

<210> 290  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 290  
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu  
 1 5 10 15  
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val  
 20 25 30  
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala  
 35 40 45  
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys  
 50 55 60  
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met  
 65 70 75 80  
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg  
 85 90 95  
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu  
 100 105 110  
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln  
 115 120 125  
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly  
 130 135 140  
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser  
 145 150 155 160  
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg  
 165 170 175  
 Ala Gln Ala Ala Ala Gly Ala  
 180

<210> 291  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 ctccacgccg acaagactta cgacgggcgt cgctgccggg ctgagtgccg ggccccgtcc  
 60  
 atcaccccc gcatcgctcg ccgcggcgtg gagaccagcg agcgcttgagg ccggtatcgc  
 120  
 tgggtcgctg agcgcacctt cgctggctc aaccgcttcc ggcgctcgc catcgctac  
 180  
 gagcggcgtg ctgacatcca cgaagccttc gtgatcctcg gctgcgcct catctgcctc  
 240  
 aaccagatca gacggttttg ttaggtgctg taaagggaga atggctgcag ctgggctatc  
 300  
 tgctccctcg tcaaccagaa acaggctgct catcctcact caacaacgcg t  
 351

<210> 292  
 <211> 87  
 <212> PRT

<213> Homo sapiens

<400> 292

```

Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1           5           10          15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
          20          25          30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
          35          40          45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
          50          55          60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
65           70           75           80
Asn Gln Ile Arg Arg Phe Cys
          85

```

<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

```

nncttcacca caccggccat caacgcacct cctcgtgata acttgacctt ctgccgaacc
60
ggttaatcag tttagtggcg aggcattgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcattgtt ctgtcgggtca cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaagggt
240
gcgaagactt tcgatgttcc agtgtgcgtc atagctgggt cggggacagg taaaactcgt
300
gctgtcactc atcgcatctg ctacggtgca gcgacaggca agcttgatcc gcgtcgatcc
360
ctcgcgggtca cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
420
gggggtgttg gtgtgcaggc tcgcactatt cattctgcgg cgttgcggca gatcaagttt
480
ttctggcctc gtgcatataa ctgtgagttg ccaccggtga gtgattctcg tttctcgatg
540
gtggcggaga cgacccatcg cattggtctg ggcaatgaca aggcgtgct gcgcgacttg
600
tccgccgaga tctcgtgggc gaaggctctc aatgtgccga ctgatcaata cgcatcctg
660
gctaggggcg aaggtcgggt ggtggcggga gtttcggcaa ctgacgtagg acgcgt
716

```

<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

```

Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```



```

      1           5           10           15
Thr Ala Asp Ala Ile Leu Ala Ala Leu Asp Leu Asn Arg Phe Lys Val
      20           25           30
Ala Lys Thr Phe Asp Val Pro Val Cys Val Ile Ala Gly Ala Gly Thr
      35           40           45
Gly Lys Thr Arg Ala Val Thr His Arg Ile Ala Tyr Gly Ala Ala Thr
      50           55           60
Gly Lys Leu Asp Pro Arg Arg Thr Leu Ala Val Thr Phe Thr Thr Lys
      65           70           75           80
Ala Ala Gly Thr Met Arg Gly Arg Leu Ala Asp Leu Gly Val Val Gly
      85           90           95
Val Gln Ala Arg Thr Ile His Ser Ala Ala Leu Arg Gln Ile Lys Phe
      100          105          110
Phe Trp Pro Arg Ala Tyr Asn Cys Glu Leu Pro Pro Val Ser Asp Ser
      115          120          125
Arg Phe Ser Met Val Ala Glu Thr Thr His Arg Ile Gly Leu Gly Asn
      130          135          140
Asp Lys Ala Leu Leu Arg Asp Leu Ser Ala Glu Ile Ser Trp Ala Lys
      145          150          155          160
Val Ser Asn Val Pro Thr Asp Gln Tyr Ala Ser Leu Ala Arg Ala Glu
      165          170          175
Gly Arg Val Val Ala Gly Val Ser Ala Thr Asp Val Gly Arg
      180          185          190

```

&lt;210&gt; 295

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 295

```

ttcatatcag gcagtagccg agtccatgag atcaacaacg tcagcgtatc tttcacccat
60
tctggagtgc accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctgggc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gatcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttccag
240
gacgacaacc tcacgctga gttgaccaat accgagaata ttgcgctacc cctgtgggag
300
cagggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgag aaaactagga
360
atcgagtcac tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
417

```

&lt;210&gt; 296

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 296

```

Phe Ile Ser Gly Ser Thr Arg Val His Ala Ile Asn Asn Val Ser Val
      1           5           10           15
Ser Phe Thr His Ser Gly Val His Leu Leu Met Gly Glu Ser Gly Ser

```

```

                20                25                30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
                35                40                45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
                50                55                60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
65                70                75                80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
                85                90                95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
                100                105                110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
                115                120                125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
                130                135

```

&lt;210&gt; 297

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 297

```

tacaccatcg gtgaccagat tgtcgaagct ctgcaggtgc actcgaagat gtccgacaag
60
gacgcttggg cgcgtgccat cgagctgctc gacttggtgg ggattccgaa tcccaggtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccctcgac
240
gtgaccatcc aggcccagat tctcgatttg ctgcgcgtag cccagcgtga aacccatgcg
300
ggcgtcggtta tgatcaccca cgacctcggt gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

```

&lt;210&gt; 298

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 298

```

Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
1                5                10                15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
                20                25                30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
                35                40                45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
50                55                60
Asn Asp Pro Asp Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
65                70                75                80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Arg Val Ala Gln Arg

```

```

      85              90              95
Glu Thr His Ala Gly Val Val Met Ile Thr His Asp Leu Gly Val Val
      100              105              110
Ala Gly Leu Ala Asp Arg Val Ala Val Met Tyr Ala Gly Arg
      115              120              125

```

<210> 299  
 <211> 368  
 <212> DNA  
 <213> Homo sapiens

<400> 299  
 gtgcacgggtt tcgttggcat gcgcaatgac cgggagaact tgcgttttga tccgagactt  
 60  
 ccagcccaat ggacgtcgat caaacaccac atgctcattg gcgactctca catgctcggt  
 120  
 ttcttggaac gtgacgcat tacgttccag attctgtcgg gccatgaccg cgacgtgaca  
 180  
 gtgcgcgggtg agctctacca cattgggggtt gagccggtga ggggtgccgtt gtccgatcag  
 240  
 gggcggttgc gtctagcct gcgcgttacc catccgatct cgggggttgcg tcgagctgac  
 300  
 ggttctctta tcaactgcaga agttcccggc agcattgctg agacgattgg gtcttctccg  
 360  
 atctcgac  
 368

<210> 300  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 300  
 Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe  
 1 5 10 15  
 Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu  
 20 25 30  
 Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr  
 35 40 45  
 Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu  
 50 55 60  
 Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln  
 65 70 75 80  
 Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu  
 85 90 95  
 Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile  
 100 105 110  
 Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser  
 115 120

<210> 301  
 <211> 456  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 301

ggccgggtta ttgcccggcc gtttgtcggg gaaacccggc agaccttcga gcgcaccggc  
 60  
 aaccggcgcg actattccgt accgccggcc gaaccgacct tgctcgacag gcttacggac  
 120  
 gcggggccgga cggatgatcg aatcggcaag attggtgata tctacgcgca caaaggcgtg  
 180  
 tctcaggtgc gtaaggcaat ggcaatattg gccttgttcg atgaaacact cattgccatg  
 240  
 gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac  
 300  
 gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggctttcga ccggaggctg  
 360  
 ccggaagcca tggcgaaatt gcggacgggc gatcttctga tcctgacagc cgatcatggc  
 420  
 tgcgaccgca ccctcaaggg aaccgaccac acgcgt  
 456

&lt;210&gt; 302

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 302

Gly	Arg	Val	Ile	Ala	Arg	Pro	Phe	Val	Gly	Glu	Thr	Arg	Gln	Thr	Phe
1				5					10					15	
Glu	Arg	Thr	Gly	Asn	Arg	Arg	Asp	Tyr	Ser	Val	Pro	Pro	Pro	Glu	Pro
			20				25						30		
Thr	Leu	Leu	Asp	Arg	Leu	Thr	Asp	Ala	Gly	Arg	Thr	Val	Ile	Ala	Ile
		35				40					45				
Gly	Lys	Ile	Gly	Asp	Ile	Tyr	Ala	His	Lys	Gly	Val	Ser	Gln	Val	Arg
50					55					60					
Lys	Ala	Met	Ala	Ile	Leu	Ala	Leu	Phe	Asp	Glu	Thr	Leu	Ile	Ala	Met
65				70					75					80	
Asp	Asp	Ala	Gln	Asp	Gly	Asp	Leu	Val	Phe	Thr	Asn	Phe	Val	Asp	Phe
			85				90						95		
Asp	Met	Leu	Tyr	Gly	His	Arg	Arg	Asp	Val	Pro	Gly	Tyr	Ala	Ala	Ala
		100					105					110			
Leu	Glu	Ala	Phe	Asp	Arg	Arg	Leu	Pro	Glu	Ala	Met	Ala	Lys	Leu	Arg
		115				120					125				
Thr	Gly	Asp	Leu	Leu	Ile	Leu	Thr	Ala	Asp	His	Gly	Cys	Asp	Pro	Thr
130					135						140				
Leu	Lys	Gly	Thr	Asp	His	Thr	Arg								
145					150										

&lt;210&gt; 303

&lt;211&gt; 402

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 303

nncgtgggca tcgaggagtt cctcgacatg aagtatcacg cgacgccgat tcacgtcgc  
 60

tgacagcggg tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg  
 120  
 ggtgctcagc tggtcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtgagctc  
 180  
 atggaccgctc aggggtctgtc ggcgatcatc gtcaccgatac cggccaacat cttctatctg  
 240  
 atcggttaca acgcctggtc gttctacacc ccgcagatgc tgttcgtgcc gatcgacgga  
 300  
 gagatgggcc tctacgctcg cgagatggat cgcattggcg acatcngcac gacgtcggtg  
 360  
 cccgccgatac agatcgctcg ttaccggag agttatgtgc ac  
 402

<210> 304  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 304  
 Met Tyr Leu Gly Ala Gln Leu Phe Ser Asp Ser Glu Tyr Glu Gln Arg  
 1 5 10 15  
 Leu Arg Arg Val Arg Glu Leu Met Asp Arg Gln Gly Leu Ser Ala Ile  
 20 25 30  
 Ile Val Thr Asp Pro Ala Asn Ile Phe Tyr Leu Ile Gly Tyr Asn Ala  
 35 40 45  
 Trp Ser Phe Tyr Thr Pro Gln Met Leu Phe Val Pro Ile Asp Gly Glu  
 50 55 60  
 Met Val Leu Tyr Ala Arg Glu Met Asp Arg Met Ala His Ile Xaa Thr  
 65 70 75 80  
 Thr Ser Leu Pro Ala Asp Gln Ile Val Gly Tyr Pro Glu Ser Tyr Val  
 85 90 95  
 His

<210> 305  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

<400> 305  
 nnacgcgtcg gttccgcatac gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc  
 60  
 gtgtcgtcct ggccaatatg ggcgatcagc cggtagctt cgggacgctc gctcacctcg  
 120  
 gccgccattt cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc  
 180  
 gtcgccacca gcgcggcgcg atcttcacgc ggagtcagat cggcgcgggc gtcaggccccg  
 240  
 tcgccatgcg tcggaatcga catgcagcac cctcctgccg ggatcgatgg cgtaatacgt  
 300  
 gcgacgggtac acggcgcggtg ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat  
 360  
 acgtcacatc atatg  
 375

<210> 306  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 306  
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr  
 1 5 10 15  
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr  
 20 25 30  
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg  
 35 40 45  
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Ser Val Ala Thr Ser  
 50 55 60  
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro  
 65 70 75 80  
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp  
 85 90 95  
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln  
 100 105 110  
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met  
 115 120 125

<210> 307  
 <211> 685  
 <212> DNA  
 <213> Homo sapiens

<400> 307  
 actagttctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag  
 60  
 ggtaggaag gctattctct ttggccactc tcatacctaag acctatttgg agaacctctg  
 120  
 gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctgcgaca  
 180  
 tttgatgtct cttcttctca cccactcacc ccacctggg gggtggggca aaaaagtggc  
 240  
 tcaaagctgc gggtcagagt tccttgtaaa caaggctcct ccctcactgt cctcacctg  
 300  
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccattgcttg ttctaacca  
 360  
 gcagaactgg acataatggg aacaggggtct gaagacaatc aatccagggc tgcagtgggt  
 420  
 gctgagtctg gggaagctc cacctggagg ggcagctggg cagtggcagc tcccttgaa  
 480  
 tggtcagcc tctggacatc accccacca accagagccc tggtcttgc tggatgtcca  
 540  
 cagatgagtg cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagaggtgat  
 600  
 gaggagtg gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggctctgaaa  
 660  
 ttggtgctgc agcactggca cgcgt  
 685

<210> 308  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 308  
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser  
 1 5 10 15  
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala  
 20 25 30  
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu  
 35 40 45  
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly  
 50 55 60  
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly  
 65 70 75 80  
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro  
 85 90 95  
 Leu Ser Ser Ser  
 100

<210> 309  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

<400> 309  
 caggctcgta ctattcgat ccctgtgcat atgggtcgagg tcatcaataa gctggctcgc  
 60  
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac  
 120  
 gaactcgata tgaccgcaga gaaggctcatt gaggtgcaga aatacggtcg cgagccgac  
 180  
 tcgctgcata cccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat  
 240  
 tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttgcagga gcagctgcat  
 300  
 gatgtcctcg ataccttgtc cgagcgagag gccgggtgctg tgtcgatgcg attcggttg  
 360  
 accgacggac agcccaagac cctggatgag atcggcaaag tctacggtgt tactcgggag  
 420  
 cgcacccgcc ag  
 432

<210> 310  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 310  
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn  
 1 5 10 15  
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu

```

      20      25      30
Pro Thr Pro Glu Glu Leu Ala Asn Glu Leu Asp Met Thr Ala Glu Lys
      35      40      45
Val Ile Glu Val Gln Lys Tyr Gly Arg Glu Pro Ile Ser Leu His Thr
      50      55      60
Pro Leu Gly Glu Asp Gly Asp Ser Glu Phe Gly Asp Leu Ile Glu Asp
65      70      75      80
Ser Glu Ala Ile Val Pro Ala Asp Ala Val Asn Phe Thr Leu Leu Gln
      85      90      95
Glu Gln Leu His Asp Val Leu Asp Thr Leu Ser Glu Arg Glu Ala Gly
      100      105      110
Val Val Ser Met Arg Phe Gly Leu Thr Asp Gly Gln Pro Lys Thr Leu
      115      120      125
Asp Glu Ile Gly Lys Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln
      130      135      140

```

<210> 311  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

```

<400> 311
acgcgtatcg aaaatatccc tcccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtgggccg atgtggtggt cattggctct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccgcgag gccgcgcggc tgcttagctg cagcgtcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

```

<210> 312  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

```

<400> 312
Thr Arg Ile Glu Asn Ile Pro Pro Ile Ile Thr Ala Arg Pro Glu Leu
1      5      10      15
Met Ala His Glu Leu Thr Pro Glu Ser Leu Asp Ala Ser Leu Glu Trp
      20      25      30
Ala Asp Val Val Val Ile Gly Pro Gly Leu Gly Gln Gln Ala Trp Gly
      35      40      45
Lys Lys Ala Leu Gln Lys Val Glu Asn Cys Arg Lys Pro Met Leu Trp
      50      55      60
Asp Ala Asp Ala Leu Asn Leu Leu Ala Ile Asn Pro Asp Lys Arg His
65      70      75      80
Asn Arg Ile Leu Thr Pro His Pro Gly Glu Ala Ala Arg Leu Leu Ser
      85      90      95
Cys Ser Val Ala Glu Ile Glu Asn Asp Arg Leu Leu Xaa Cys Ala Arg

```



100 105 110  
 Leu Val Lys Arg  
 115  
 <210> 313  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens  
 <400> 313  
 ncaactgaaa gcattgagat gagcgacgtg ctgtccccct tccacccac caaggccaac  
 60  
 acccctgggtg gcgaaccgcg caccatccgc acctcgaacg cgcacatcat tgccgtcacc  
 120  
 agtggcaaag gcggcgtggg caagaccttt gtctccgcc aacctggcgc cgcgctgacc  
 180  
 cgccctgggac tgccgctgct ggtactggac gccgacctgg gcctggccaa cttggacgtg  
 240  
 gtgctgaacc tctaccccaa ggtgacgctg cagcatgtgt tcaccggcaa ggcctcgctg  
 300  
 caagacgcgg tggtcacggc ccccgcggc ttccatgtgc tgctagc  
 347

<210> 314  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 314  
 Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro  
 1 5 10 15  
 Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser  
 20 25 30  
 Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys  
 35 40 45  
 Thr Phe Val Ser Ala Asn Leu Ala Ala Leu Thr Arg Leu Gly Leu  
 50 55 60  
 Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val  
 65 70 75 80  
 Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly  
 85 90 95  
 Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His  
 100 105 110  
 Val Leu Leu  
 115

<210> 315  
 <211> 544  
 <212> DNA  
 <213> Homo sapiens

<400> 315  
 nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggagggaac catgcttgcc  
 60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggtcgtccc ggggccatcc  
 120  
 aacacacctgc tgctcagcgc ccgtttccat ttcggctcgc tgcgggcggc gcccttcac  
 180  
 ctgcttgagg cggtgggcta ctgctatcc atttcggcat ggggctgggt attggcgcgc  
 240  
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg  
 300  
 gcgcttctgg cggtgaagac ctggaatgcc ntcgatccgc agtgcggggc cggttaacttc  
 360  
 cgccatgggc ccctgccct gtctgtggca accctgtcga acccgaaggc gctgatcttc  
 420  
 gccagcgtga tctttcccg caaggcggtc ctcgacttct ggaacaacta cacgatctcg  
 480  
 ctgctggcct tcttggttgt gctggcgccc atcgggatgc tttgggtcgg gctggggggc  
 540  
 ggta  
 544

&lt;210&gt; 316

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 316

Ile	Tyr	Ala	Ile	Met	Leu	Phe	Ser	Ser	Leu	Ile	Leu	Val	Val	Pro	Gly
1				5					10					15	
Pro	Ser	Asn	Thr	Leu	Leu	Leu	Ser	Ala	Arg	Phe	His	Phe	Gly	Ser	Leu
			20					25					30		
Arg	Ala	Ala	Pro	Phe	Ile	Leu	Leu	Glu	Ala	Leu	Gly	Tyr	Ser	Leu	Ser
		35					40					45			
Ile	Ser	Ala	Trp	Gly	Trp	Val	Leu	Ala	Arg	Leu	Ser	Glu	Ser	Asn	Pro
		50				55					60				
Trp	Ile	Ile	Ser	Leu	Thr	Lys	Ala	Leu	Cys	Ala	Leu	Tyr	Val	Ala	Leu
65					70				75					80	
Leu	Ala	Val	Lys	Thr	Trp	Asn	Ala	Xaa	Asp	Pro	Gln	Cys	Gly	Ala	Gly
			85					90					95		
Asn	Phe	Arg	His	Gly	Pro	Leu	Pro	Leu	Phe	Val	Ala	Thr	Leu	Ser	Asn
			100					105					110		
Pro	Lys	Ala	Leu	Ile	Phe	Ala	Ser	Val	Ile	Phe	Pro	Gly	Lys	Ala	Phe
		115					120					125			
Leu	Asp	Phe	Trp	Asn	Asn	Tyr	Thr	Ile	Ser	Leu	Leu	Ala	Phe	Leu	Val
	130					135						140			
Val	Leu	Ala	Pro	Ile	Gly	Met	Leu	Trp	Val	Gly	Leu	Gly	Ala	Gly	
145					150					155					

&lt;210&gt; 317

&lt;211&gt; 343

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 317

nggtcagcct ctgccccagg caattctctt aagatacatg agctgctatg agtaccaaag  
 60

ccagaggttt gtcactgag agaagcacat tggaaagggg ggcgtgggccc tgggactgtg  
 120  
 tggcacttta tgcacggggg gggcctaagg gggnggtcc accaaccatg cactnggggt  
 180  
 ggggtgtggg taacatgccg tgcattttgg ggggtgtgcca tgagtggcac accatggggg  
 240  
 tggcatgtgg ggcattgatg catgtggtgt tggcgcagca aactcagctc ttacctggct  
 300  
 gggggccagcc tctaaaactt ctcacattgg gctcccttct gac  
 343

<210> 318

<211> 98

<212> PRT

<213> Homo sapiens

<400> 318

Met	Ser	Thr	Lys	Ala	Arg	Gly	Leu	Ser	Thr	Glu	Arg	Ser	Thr	Leu	Glu
1				5				10						15	
Arg	Gly	Ala	Trp	Ala	Trp	Asp	Cys	Val	Ala	Leu	Tyr	Ala	Arg	Gly	Gly
		20					25					30			
Pro	Lys	Gly	Gly	Gly	Pro	Pro	Thr	Met	His	Xaa	Gly	Trp	Gly	Val	Gly
		35					40					45			
Asn	Met	Pro	Cys	Ile	Leu	Gly	Val	Cys	His	Glu	Trp	His	Thr	Met	Gly
	50					55				60					
Val	Ala	Cys	Gly	Ala	Cys	Met	His	Val	Val	Leu	Ala	Gln	Gln	Thr	Gln
65					70					75				80	
Leu	Leu	Pro	Gly	Trp	Gly	Gln	Pro	Leu	Lys	Leu	Leu	Thr	Leu	Gly	Ser
			85					90						95	
Leu	Leu														

<210> 319

<211> 429

<212> DNA

<213> Homo sapiens

<400> 319

gaattctcga tgtaccccct cccggcagtc ctattctcga gctgagcggg cacagtggcc  
 60  
 ccgttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta  
 120  
 agggcatgat atgtacagga ggcgacgatg ctcagtgcct cgtatatgat ctgactagct  
 180  
 caactcttcg aacagcatct gctcaaggac ggcgctctcg aaacagtcca tataaacaaa  
 240  
 gccattcacc gggaatagac ggatggcgtg tcggcgcaga agtgccggtg ctcgcttata  
 300  
 cgccccgtc tatgggtcaac aatgctagct ggctcgcat gcctgcgcca tcaaacgca  
 360  
 catcgctaca gagcaaacac cgcagccttt accgcagctt actcagttag tggactgagt  
 420  
 atacgtccn  
 429

<210> 320  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 320  
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu  
 1 5 10 15  
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg  
 20 25 30  
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg  
 35 40 45  
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val  
 50 55 60  
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser  
 65 70 75 80  
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp  
 85 90 95  
 Thr Glu Tyr Thr Ser  
 100

<210> 321  
 <211> 530  
 <212> DNA  
 <213> Homo sapiens

<400> 321  
 ngtgcacgac gtgctcgcca agtccctcgg gtcctctaata gcatcaacg tggttcacgc  
 60  
 caccgtcgat gcgttgacgc agctcgagga gcccgaaagag gtcgcccgtc gccgcggcaa  
 120  
 gtccgttgag gagatcgccc cagcagccat gctgcgtgag cgcaaggagg ccgacgaggg  
 180  
 cgccgtgct gcccgcatgg agggaaaagg ggggggttaac tgatgagcaa gctgaagatc  
 240  
 acccagatca agtctggcat cgctaccaag ccaaatcatc gtgagaccct gcgcagcctc  
 300  
 ggactgaagc gtattggtga cacggtcatc aaggaggacc gcccgaggtt ccgcggcatg  
 360  
 gtcgggaccg ttcgtcacct cgtcaccatg gaagaggtgg actgacatgg ctattgagct  
 420  
 ccatgacctc aagcccgtc ctggtgcca caaggccaag acccggttg gtcgtggtga  
 480  
 gggttccaag ggtaagaccg ctggtcgagg taccaagggc accggtgcac  
 530

<210> 322  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 322  
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

```

      1             5             10             15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly
      20             25             30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg
      35             40             45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp
      50             55             60

```

<210> 323  
 <211> 468  
 <212> DNA  
 <213> Homo sapiens

```

<400> 323
ntccggaccc gctgtggcca cgtattctgc cgttcctgta ttgctaccag tctaaagaac
60
aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
120
gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctgggtt
180
tgcctcagtg aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
240
ccactacaag aacttgagga gacagcagca aggtgtgtat gtcccttttg tcagagggaa
300
ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggaggcct
360
gtgttctgtc cactttgcca tttaatacce gatgagaatc caagcagctt cagtggcagt
420
ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
468

```

<210> 324  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

```

<400> 324
Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr
 1             5             10             15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu
      20             25             30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser
      35             40             45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu
      50             55             60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly
65             70             75             80
Pro Leu Gln Glu Leu Glu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe
      85             90             95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr
      100            105            110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu
      115            120            125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His

```

130 135 140  
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe  
 145 150 155

<210> 325  
 <211> 374  
 <212> DNA  
 <213> Homo sapiens

<400> 325  
 acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc  
 60  
 actggagccc cctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc  
 120  
 aggtcgagcg caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt  
 180  
 ggagctctgc tcccaggga tccccactcc cgcagatgac ttgcccgaga gagttctgct  
 240  
 ggtggatttt gatggaaatt ctatttgatc gcaccactt ggttcactgt gtgcttcagg  
 300  
 gtccccaggt tttaggtgct tcatgccctg ctgggaacga gacacgctcc tgcctcagt  
 360  
 gaatcttcag tcta  
 374

<210> 326  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 326  
 Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser  
 1 5 10 15  
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu  
 20 25 30  
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser  
 35 40 45  
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr  
 50 55 60  
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val  
 65 70 75 80  
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu  
 85 90 95  
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg  
 100 105

<210> 327  
 <211> 538  
 <212> DNA  
 <213> Homo sapiens

<400> 327  
 cactataaaa tccagtttgg ggcccgtgtt ctttcctatt ggtctgtcag gtgaaaaact  
 60

ccggctgggg gaaaagcgtc cggtggtttg ttggtaaaga gggcgctga tgggctctgg  
 120  
 ggaatggagg atggcgacc ggctgtgggt ggactgtgga aacgggggt ggcagtgccg  
 180  
 gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag  
 240  
 agctcgggat gggctcagag cgaccacga aaataccagg ggccaagtaa aatgaaccca  
 300  
 ccctttaaca gtgcacaaag cgctggcaca cggccacgt ctggtgacgc aggctgcccg  
 360  
 aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc  
 420  
 cgcccctgtc ccactctggc cagccggagt ttttcaccta cagaccaata ggaaagaaca  
 480  
 cgggccccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgccc  
 538

&lt;210&gt; 328

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 328

Met	Val	Gly	Ala	Leu	Arg	Ala	Ala	Cys	Val	Thr	Arg	Arg	Gly	Pro	Cys
1				5					10					15	
Ala	Ser	Ala	Leu	Cys	Thr	Val	Lys	Gly	Trp	Val	His	Phe	Thr	Trp	Pro
			20					25					30		
Leu	Val	Phe	Ser	Trp	Val	Ala	Leu	Ser	Pro	Ser	Arg	Ala	Leu	Leu	Asp
	35					40						45			
Arg	Ile	Ser	Pro	Ala	Gln	Asp	Pro	Lys	Thr	Arg	Pro	Ala	Gly	Gln	Leu
	50				55					60					
Pro	Arg	His	Cys	His	Pro	Pro	Phe	Pro	Gln	Ser	Thr	His	Ser	Arg	Cys
65				70					75					80	
Ala	Ile	Leu	His	Ser	Pro	Glu	Pro	Ile	Thr	His	Pro	Leu	Tyr	Gln	Gln
			85					90						95	
Thr	Thr	Gly	Arg	Phe	Ser	Pro	Ser	Arg	Ser	Phe	Ser	Pro	Asp	Arg	Pro
		100					105						110		
Ile	Gly	Lys	Asn	Thr	Gly	Pro	Lys	Leu	Asp	Phe	Ile	Val			
	115					120						125			

&lt;210&gt; 329

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 329

tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa  
 60  
 gctcttcagt ctttctgctc cactgagcag tgttttcctg atacccttggt tatcctgcca  
 120  
 gcagcctcgt tatgactcct aactccattg ccctccatgg cccctgggag ctctctctct  
 180  
 ctttctctcc aggtagtaga gcactgcttc tggtctcttg tgcacagaag ggtttccac  
 240

agctgagagc tgggctccta ctgacatagt tatttccttt atatcctgcc ccaccttctt  
 300  
 ctggtagcac acagcaacct tgcatagtag ctggtatcat taccttccca atcaacaggc  
 360  
 cttgatttct tataggactt tttctctcag atttacattg cttcttt  
 407

<210> 330

<211> 113

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ile	Pro	Ala	Thr	Met	Gln	Gly	Cys	Cys	Val	Leu	Pro	Glu	Glu	Gly
1				5				10					15		
Gly	Ala	Gly	Tyr	Lys	Gly	Asn	Asn	Tyr	Val	Ser	Arg	Ser	Pro	Ala	Leu
		20					25					30			
Ser	Cys	Gly	Lys	Pro	Phe	Cys	Ala	Gln	Glu	Ala	Arg	Ser	Ser	Ala	Leu
	35					40					45				
Leu	Pro	Gly	Glu	Lys	Glu	Arg	Glu	Ser	Ala	Gln	Gly	Pro	Trp	Arg	Ala
	50				55					60					
Met	Glu	Leu	Gly	Val	Ile	Thr	Arg	Leu	Leu	Ala	Gly	Tyr	Gln	Gly	Tyr
65				70						75				80	
Gln	Glu	Asn	Thr	Ala	Gln	Trp	Ser	Arg	Lys	Thr	Glu	Glu	Leu	Gln	Ala
			85					90					95		
Leu	Phe	Pro	His	Gly	Phe	Leu	Glu	Gly	Ile	Pro	Gly	Glu	Gly	Thr	Leu
		100						105					110		

Arg

<210> 331

<211> 523

<212> DNA

<213> Homo sapiens

<400> 331

tgtaccgaac ctgctgggtct cgagggcctt gctggggtcg tcgtacgcac agctgacgaa  
 60  
 tccaccggcc cccatcccgg cgccactttc gctgaggcca tggagtcgat cggagccagc  
 120  
 tacgacggat cggccggggtt ggccggaagt cacgtcggcg tcgatgtgcc cgtgacaagg  
 180  
 ttcgacgcag cggctgaact cttcgtcgaa ttgtgaaca ccacgagcct ggttgaagag  
 240  
 gacatcgccc gtcagatcga cgcggcgcga gcctccctgg cccagaccag ccagcgcgga  
 300  
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtgggggc acggtcgtcc  
 360  
 ctgcccacga tcggtaccct ctcgtcggtg gaaaagctca acgccgcagc cgcacgagaa  
 420  
 ttctgggccc cgcactggac gatctccgat gccgtgctgg tggttgccgg agagggagtc  
 480  
 gaggacctcg acttgtcaat attcaaggag tggacgacca gct  
 523



<210> 332  
 <211> 174  
 <212> PRT  
 <213> Homo sapiens

<400> 332  
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg  
 1 5 10 15  
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu  
 20 25 30  
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala  
 35 40 45  
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala  
 50 55 60  
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu  
 65 70 75 80  
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr  
 85 90 95  
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Ala Arg Ala Leu  
 100 105 110  
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser  
 115 120 125  
 Ser Val Glu Lys Leu Asn Ala Ala Ala Arg Glu Phe Trp Ala Ala  
 130 135 140  
 His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val  
 145 150 155 160  
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser  
 165 170

<210> 333  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
 nntgttcgtc gtgtcgaccc ggaactcaag gcccgagcga tgacggtgaa ggtgccaacc  
 60  
 gatccccatc accgcccgagg agttccattg aagtctgcga aggaccgtat ggacatcatt  
 120  
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccacccac  
 180  
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccacccac cgggtggcaag  
 240  
 gaacggggccc gcaactacga tgcggtggcc cagctcgtcg cgcagcgagt cgcgcgggtca  
 300  
 caccggccgga tcaactgcaa acggctgcta ccggtagcgc gagcggcagg atatgagggg  
 360  
 tcggcgcgga at  
 372

<210> 334  
 <211> 88  
 <212> PRT

<213> Homo sapiens

<400> 334

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Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1           5           10           15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
           20           25           30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
           35           40           45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
           50           55           60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
65           70           75           80
Gly Tyr Glu Gly Ser Ala Arg Asn
           85

```

<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

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gtgcacgcct tgctgggcca gggcgatgag cctgcgcgca ccttcgtgga cggtaccttt
60
ggcaggggag ggcattcgag gctcatcctg cagcgggttg ggccgcaagg ccgcctggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accagggggt cagccatctc ggggaactgc ccgccgccag cgtgtccggt
240
gtgctgctgg acctgggcgt gagtccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

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<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

```

Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1           5           10           15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
           20           25           30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
           35           40           45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
           50           55           60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
65           70           75           80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
           85           90           95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

100 105 110  
 Thr Thr Pro Met His Gly  
 115  
 <210> 337  
 <211> 447  
 <212> DNA  
 <213> Homo sapiens  
 <400> 337  
 cagcctctct ccgaccgcgc cgggtgtgaag cacgggcatg ccggtgtgca agtggcacca  
 60  
 cagccaaaac agcgagctca cacttcaaac tccttcaaag accccaggcc tctgtaagaa  
 120  
 ccgctcatct ctgtgcccac agctcccccg cttccatgtg acccagaaat ggaaccacgc  
 180  
 agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc ttctgtgcaa  
 240  
 acaggcgcca tcatgtcagc cggtgagcag gagcaacgtg cgtgggtcag ggggtggcca  
 300  
 caggtccaac tttataagaa atgacagatt ccctgatggc catagggatc tgcaggggcca  
 360  
 gcagcaggca taggacttcc ggtggccctg cgtcttcac cacttgagt attgtcaggg  
 420  
 tttctgtact gtttttacag ccaattg  
 447

<210> 338  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 338  
 Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu  
 1 5 10 15  
 Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu  
 20 25 30  
 Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala  
 35 40 45  
 Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg  
 50 55 60  
 Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn  
 65 70 75 80  
 Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp  
 85 90 95  
 Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Ala  
 100 105 110

<210> 339  
 <211> 588  
 <212> DNA  
 <213> Homo sapiens

<400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aaggggcgtca  
60  
gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaaccca atggaagaca  
120  
ccgacctgca agcgctgatg gccagactcg aattgctaata tgatcgggtc gagcaactta  
180  
agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc  
240  
tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgcctgaagg  
300  
ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata  
360  
ttcgatcatc tgccccagg aagaacgcag cacctgggtga gtgctgcccg ctacctggaa  
420  
ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcacg ggtgccgacc gcatcgccgt  
480  
gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca  
540  
ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt  
588

<210> 340

<211> 123

<212> PRT

<213> Homo sapiens

<400> 340

Met	Glu	Asp	Thr	Asp	Leu	Gln	Ala	Leu	Met	Ala	Arg	Leu	Glu	Leu	Leu
1				5					10					15	
Ile	Asp	Arg	Val	Glu	Gln	Leu	Lys	Ser	Gln	Asn	Gly	Leu	Leu	Leu	Ala
			20					25					30		
Gln	Glu	Lys	Thr	Trp	Ala	Arg	Xaa	Arg	Ala	His	Leu	Ile	Glu	Lys	Asn
			35				40						45		
Glu	Ile	Ala	Arg	Arg	Lys	Val	Glu	Ser	Met	Ile	Ser	Arg	Leu	Lys	Ala
			50			55					60				
Leu	Glu	Gln	Asp	Tyr	Glu	Leu	Ser	Asn	Ser	Val	Thr	Cys	Arg	Ser	Ser
65					70					75				80	
Thr	Lys	Asn	Ile	Arg	Ser	Ser	Ala	Pro	Arg	Lys	Asn	Ala	Ala	Pro	Gly
			85					90						95	
Glu	Cys	Cys	Pro	Leu	Pro	Gly	Arg	Pro	Lys	Gly	Val	Lys	Ser	Ala	Ala
			100					105						110	
Ala	Ala	Lys	Ser	Ser	Val	Pro	Thr	Ala	Ser	Pro					
			115					120							

<210> 341

<211> 401

<212> DNA

<213> Homo sapiens

<400> 341

ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtgaccg ctcggccttt  
60  
gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggcttcttg  
120

ctgaacattc ttaaccccaa gctgacaatt ttcttctctgg ccttctctgcc tcaattcgta  
 180  
 acgccaggcg gcaccgcgcc ggccttgcag atgctggtac tgagcggcgt gttcatggcg  
 240  
 atgacgcttg cagtgtttgt gctgtatggc ctgttggcga atgtgtttcg tcgtgcagtg  
 300  
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg  
 360  
 ctgggggtga acctggcggt tgccgcagcg tgaggacgcg t  
 401

<210> 342

<211> 130

<212> PRT

<213> Homo sapiens

<400> 342

Xaa	Arg	Ala	Ala	Tyr	Leu	Leu	Tyr	Leu	Ala	Tyr	Ala	Thr	Trp	Arg	Asp
1				5					10					15	
Arg	Ser	Ala	Phe	Ala	Met	Asn	Asp	Thr	Pro	Thr	Val	Ala	Thr	Ala	Arg
		20						25					30		
Ser	Leu	Ile	Leu	Arg	Gly	Phe	Leu	Leu	Asn	Ile	Leu	Asn	Pro	Lys	Leu
		35					40					45			
Thr	Ile	Phe	Phe	Leu	Ala	Phe	Leu	Pro	Gln	Phe	Val	Thr	Pro	Gly	Gly
	50					55					60				
Thr	Ala	Pro	Ala	Leu	Gln	Met	Leu	Val	Leu	Ser	Gly	Val	Phe	Met	Ala
65				70						75				80	
Met	Thr	Leu	Ala	Val	Phe	Val	Leu	Tyr	Gly	Leu	Leu	Ala	Asn	Val	Phe
			85						90					95	
Arg	Arg	Ala	Val	Val	Glu	Ser	Pro	Arg	Val	Gln	Asn	Trp	Leu	Arg	Arg
		100						105					110		
Ser	Phe	Ala	Thr	Ala	Phe	Ala	Gly	Leu	Gly	Leu	Asn	Leu	Ala	Phe	Ala
		115					120						125		
Gln	Arg														
	130														

<210> 343

<211> 389

<212> DNA

<213> Homo sapiens

<400> 343

gtgttgcgca actacatggc gtccttgccg ttcagcgtgg tcgagtcggc gcgcatcgac  
 60  
 gggtgctcca acttccagat cttctggaag ctgatcgccc cgatggcgat gccggcgatg  
 120  
 gcggcggttcg cgaccctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc  
 180  
 ttcttcacca acgacaaccc cacggtgata gtcaagctcc aacagctttc cnggggcccc  
 240  
 aaggcccagg gtgcggagct gctgacggcg ggccgcttca tctccatcgt gctacccatg  
 300  
 atcgtcttct tcgtgctcca gaacttctg gtgcgcggtg tgacgtcggg tgccgtcaag  
 360

gggtgaccgc tcaactgcag tggcccggg  
389

<210> 344  
<211> 121  
<212> PRT  
<213> Homo sapiens

<400> 344  
Val Leu Arg Asn Tyr Met Ala Ser Leu Pro Phe Ser Val Val Glu Ser  
1 5 10 15  
Ala Arg Ile Asp Gly Cys Ser Asn Phe Gln Ile Phe Trp Lys Leu Ile  
20 25 30  
Ala Pro Met Ala Met Pro Ala Met Ala Ala Phe Ala Thr Leu Gln Phe  
35 40 45  
Leu Trp Val Trp Asn Asp Leu Leu Ile Ala Lys Leu Phe Leu Thr Asn  
50 55 60  
Asp Asn Pro Thr Val Ile Val Lys Leu Gln Gln Leu Ser Xaa Gly Pro  
65 70 75 80  
Lys Ala Gln Gly Ala Glu Leu Leu Thr Ala Gly Ala Phe Ile Ser Ile  
85 90 95  
Val Leu Pro Met Ile Val Phe Phe Val Leu Gln Asn Phe Leu Val Arg  
100 105 110  
Gly Met Thr Ser Gly Ala Val Lys Gly  
115 120

<210> 345  
<211> 360  
<212> DNA  
<213> Homo sapiens

<400> 345  
ctagtacttt atgctgatgg tgaacgtcgt tacatccttg cccctaaagg catggttgct  
60  
ggtgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg  
120  
cgtaatatc cagttggtac aacagtacac gctgtagaaa tgaaacctgc taaaggtgca  
180  
caaattgcac gttctgctgg ttcttacagc caaattatag ctctgatgg tgcttacggt  
240  
actctacggt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgtcg tgcaacaatc  
300  
ggtgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt  
360

<210> 346  
<211> 120  
<212> PRT  
<213> Homo sapiens

<400> 346  
Leu Val Leu Tyr Ala Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys  
1 5 10 15  
Gly Met Val Ala Gly Asp Val Ile Gln Ser Gly Glu Asp Ala Ser Ile

```

      20      25      30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
      35      40      45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
      50      55      60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
65      70      75      80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
      85      90      95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
      100      105      110
Leu Gly Lys Ala Gly Ala Thr Arg
      115      120

```

<210> 347  
 <211> 565  
 <212> DNA  
 <213> Homo sapiens

```

<400> 347
accggtgatg ccaaaggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgtc gggatcctca cggatgcctt cttggtgccc
180
atgaccctcg tccccgccgt gatggccctg ctaggtgaca aggcattggtg gttgcccggg
240
tggtctggatc gacgcctacc ccgcctcgac atcgagggag aagggatcac ccacgaggaa
300
aagctggccg cctggcccaac agcggatcac accgaggccc tgcacgccga ggggatccgg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctcgcccgtc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggatgaggtc gggaggattg ctgctaccgc agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

```

<210> 348  
 <211> 188  
 <212> PRT  
 <213> Homo sapiens

```

<400> 348
Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
1      5      10      15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
      20      25      30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
      35      40      45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val

```

```

      50              55              60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
65              70              75              80
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
      85              90              95
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
      100             105             110
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
      115             120             125
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
      130             135             140
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu
145             150             155             160
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
      165             170             175
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
      180             185

```

&lt;210&gt; 349

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 349

```

ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcggtt cggtaccgc tcatacgttt gcggacaatt tgccgttcct tcttaaactg
120
ctcgcggcag aagagccact atcgttgacg gctcatccca gtttggcgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg cccagaccg gaattaccac
240
gatcccaacc ataaaccgga gcttattgtt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

```

&lt;210&gt; 350

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 350

```

Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
1              5              10              15
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
      20              25              30
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
      35              40              45
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
      50              55              60
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
65              70              75              80
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His

```



85 90 95  
 Ala Leu Ala Gly Phe Arg Glu Pro Gln Arg Thr Leu Glu Leu Phe Asp  
 100 105 110  
 Ala

<210> 351  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 351  
 gcgcgccccca gtgccgagac ccggggcttc aggagccggc cccgggagag aagagtgcgg  
 60  
 cggcggacgg agaaaacaac tccaaagttg gcgaaaggca ccgcccctac tcccgggctg  
 120  
 ccgcgccttc cccgccccca gccctggcat ccagagtacg ggtcgagccc gnggccatgg  
 180  
 agcccccttg gggaggcggc accagggagc ctggggccccg gggctccgcc gcgaccccc  
 240  
 cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt  
 300  
 tggccaccn ntctctctcc tctctcttgg aggcgctctg gcccatccag accg  
 354

<210> 352  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
 Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu  
 1 5 10 15  
 Arg Arg Val Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys  
 20 25 30  
 Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Pro Arg Pro Gln Pro  
 35 40 45  
 Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly  
 50 55 60  
 Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His  
 65 70 75 80  
 Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser  
 85 90 95  
 Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Pro Trp Arg Arg  
 100 105 110  
 Ser Gly Pro Ser Arg Pro  
 115

<210> 353  
 <211> 1469  
 <212> DNA  
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt  
60  
attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgatcctt  
120  
gaaccattt cagctgttgt cagccacac ggcctcatgc tgttgctggg gaagcctcaa  
180  
tttgaggttg gttgcaaggc tttgggagcc catggcggtt tcacggaccc ggccctgcgc  
240  
ttgcaggcca tcgcgggtgt catggcagca gcggtagatt tgggttggcg tatgctgac  
300  
gagtgcgata gcccggttgc cgggcaggat ggaaacgttg agcacttcgt cttgctggaa  
360  
cgtaggggtc ggtgacagac gtccgggcat atcatgggcc gctactgtgg tcttgtgaac  
420  
gacacgagcc cttcgagata cgttgctcgc gtcacccatg ccacgcggga cgacgctttt  
480  
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattgggtt gcggttccg  
540  
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttggga  
600  
gagttcgccc acgaggcgga ggtggtcgtc gtctttggcg gcgacggcac gatcttgca  
660  
gctgctgaat ggtcattacc tcgcccggtt cccatgattg gcgtcaacct tggccatgtc  
720  
ggttttcttg ctgagctgga gcgtccgat atggcggtac tagtgaacaa ggtgtgttctg  
780  
cgcgactaca ccgttgagga tcgcctcgtg cttaaaacca ccgtcaccca gcattccgga  
840  
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agcccggcgg  
900  
cgcatgctcg acgttctggc gtctgtcgac gagttgccgg tgcaacgctg gagttgcgac  
960  
gggatccttg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcgggccc  
1020  
gtcatgtggc ccgatctcga cgccatgctc atggtgccgt tgagcgctca cgctctcttt  
1080  
gctcgaccgc tggatcatgag cccagctgct cgagtggacc ttgacatcca gccagacggt  
1140  
tcagaatcgg cggttctgtg gtgcgacggg cgccgatcgt gcaccgtacg accgggggaa  
1200  
agaatcacgg tcgtccgcca tcccagcgt ctgcgcattg ctcgtctggc cgcgcagccc  
1260  
ttcacatcgc gtctggtcaa gaagtttgag ctcccggtca gcgggtggcg tcagggtcgt  
1320  
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg  
1380  
tcacgatga gacggtcctc gaaccctcat ccgcgctgac ggagtcacc ggcgagaccg  
1440  
gcgccggaaa gaccatggtg gtcaccggt  
1469

&lt;210&gt; 354

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 354

```

Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1           5           10           15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
 20           25           30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
 35           40           45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
 50           55           60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
 65           70           75           80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
 85           90           95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
100           105           110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
115           120           125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
130           135           140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145           150           155           160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
165           170           175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
180           185           190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
195           200           205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
210           215           220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225           230           235           240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
245           250           255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
260           265           270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
275           280           285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
290           295           300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
305           310           315

```

&lt;210&gt; 355

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 355

```

nggatccac ctctggaat ggaaaccac ataccagttc tcttctcga tttgaatgcg
60
gatgacctca gtgcaatga gcagcttggt ggccccatg catcggcgt gaactccatc
120

```

ctgccaagg agcatggcag ccagtttttc tacctgcca tcataaagca cagtgatgat  
 180  
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg  
 240  
 gtcacaccac agaagtaaag gatttaccta attgtgaaaa ccacagttca actcagccac  
 300  
 cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaaacag  
 360  
 agtttcacgc agagtttgaa gaggagaata tccctgaaaa atatatttta ttctgtggt  
 420  
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa  
 480  
 acgctggctc tcttggcagc aaggagttaa aacgaaggca catcagatgg gaagacgtac  
 540  
 attgagaagt acactcga  
 558

&lt;210&gt; 356

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 356

Xaa	Ile	Pro	Pro	Gly	Met	Glu	Thr	His	Ile	Pro	Val	Leu	Phe	Leu
1			5				10					15		
Asp	Leu	Asn	Ala	Asp	Asp	Leu	Ser	Ala	Asn	Glu	Gln	Leu	Val	Gly
		20					25					30		Pro
His	Ala	Ser	Gly	Val	Asn	Ser	Ile	Leu	Pro	Lys	Glu	His	Gly	Ser
		35				40					45			Gln
Phe	Phe	Tyr	Leu	Pro	Ile	Ile	Lys	His	Ser	Asp	Asp	Glu	Val	Ser
	50					55				60				Ala
Thr	Ala	Ser	Trp	Asp	Ser	Ser	Val	His	Asp	Ser	Val	His	Leu	Asn
65					70				75					80
Val	Thr	Pro	Gln	Asn	Glu	Arg	Ile	Tyr	Leu	Ile	Val	Lys	Thr	Thr
			85				90						95	Val
Gln	Leu	Ser	His	Pro	Ala	Ala	Met	Glu	Leu	Val	Leu	Arg	Lys	Arg
		100					105					110		Ile
Ala	Ala	Asn	Ile	Tyr	Asn	Lys	Gln	Ser	Phe	Thr	Gln	Ser	Leu	Lys
		115				120					125			Arg
Arg	Ile	Ser	Leu	Lys	Asn	Ile	Phe	Tyr	Ser	Cys	Gly	Val	Thr	Tyr
	130					135				140				Glu
Ile	Val	Ser	Asn	Ile	Pro	Lys	Ala	Thr	Glu	Glu	Ile	Glu	Asp	Arg
145				150					155					160
Thr	Leu	Ala	Leu	Leu	Ala	Ala	Arg	Ser	Glu	Asn	Glu	Gly	Thr	Ser
			165				170						175	Asp
Gly	Lys	Thr	Tyr	Ile	Glu	Lys	Tyr	Thr	Arg					
		180					185							

&lt;210&gt; 357

&lt;211&gt; 323

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

acgcgtgcgt gtgttggtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg  
60  
gtacgatcag gctgaaggct gatcaggcac aaggctctgg gggagagccc tggttccagg  
120  
cctgggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg  
180  
cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggttga cagagtggat  
240  
ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg  
300  
gtcaccatgg gtcagcgagg atn  
323

<210> 358

<211> 102

<212> PRT

<213> Homo sapiens

<400> 358

Met	Val	Thr	Leu	Thr	His	Ala	Ser	Leu	Ile	Leu	Leu	Thr	Gly	Pro	Arg
1				5				10					15		
Arg	Cys	Phe	Arg	Arg	His	Pro	Ser	Thr	Leu	Ser	Ser	Pro	Ser	Arg	Gly
			20					25					30		
Leu	His	Ala	Leu	Pro	Ser	Val	Ala	Leu	Pro	Cys	Pro	Ala	Gly	Ala	Val
			35				40					45			
Leu	Thr	Pro	Ala	Val	Phe	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Pro	Gly	Leu
			50			55					60				
Glu	Pro	Gly	Leu	Ser	Pro	Arg	Ala	Leu	Cys	Leu	Ile	Ser	Leu	Gln	Pro
65					70				75					80	
Asp	Arg	Thr	Pro	Pro	Ala	Ala	His	Pro	His	Ala	Cys	Thr	His	Pro	Thr
				85					90					95	
His	Thr	Thr	His	Ala	Arg										
															100

<210> 359

<211> 265

<212> DNA

<213> Homo sapiens

<400> 359

acgcgtaccg acaagcgccc ggtgatggcc gaccttcgcg aatcgggcgc aatcgagcag  
60  
gatgcggaca tgategtctt catctaccgc gacgattact acaacaagga aaattcgccg  
120  
gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggctcgtgc  
180  
aagctgaagt tcttcggcga gtacaccctg ttcgacaacc tggcccacaa ctcggttggt  
240  
tcgttcgaat aacggatgat tccgg  
265

<210> 360

<211> 83

<212> PRT

<213> Homo sapiens

<400> 360

```

Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1             5             10             15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
      20             25             30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
      35             40             45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
      50             55             60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65             70             75             80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

```

gctttgcagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagcctca cccacccgac catccccctc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gcctcttcag gaagtggttc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aagggtgttg ggctttcaga agcctttggt tccgtggggt atgaatatga atcctgccca
300
gatctaattc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaaacat catgccctca acattcaaag tggcatcctg
420
cacaaaggga atggnagaga ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1             5             10             15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
      20             25             30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
      35             40             45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
      50             55             60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```

```

65          70          75          80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
          85          90          95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
          100          105          110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
          115          120          125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
          130          135          140
Gly Glu Asn Gln Phe Val Ser
145          150

```

<210> 363  
 <211> 502  
 <212> DNA  
 <213> Homo sapiens

```

<400> 363
ggtagcaaaa aagtttgcca cagtattcac actccaggtc tccataaacc ttccagatcc
60
gctcacacaa gctggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaag
120
cggtagatgc tgaccggtgc tcaggggagc ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgagga ctcagctggg ttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc cttcccccta
300
gggggctctg ggcgccatgg ctttctgat ctgaccagc actctggggc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgcggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

<210> 364  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

```

<400> 364
Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1          5          10          15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
          20          25          30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
          35          40          45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
          50          55          60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65          70          75          80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```

[illegible]

```
<210> 365
<211> 333
<212> DNA
<213> Homo sapiens
```

```
<400> 365
atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca
60
ccactgatcg ttgggattct atttgggggt gagaccctct ctggagtcct tgctggtgcc
120
cttgtctctg gtgttcagat tgccatttct gcatccaaca ctggtggtgc ctgggacaac
180
gccaagaagt acattgaggc tggagtttca gagcatgcc a ggacccttg cccaaaaggt
240
tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
300
tctggccctt cctcaacat cctcatcaag ctt
333
```

```
<210> 366
<211> 111
<212> PRT
<213> Homo sapiens
```

```

<400> 366
Ile Ser Thr Asp Ala Ser Ile Lys Glu Met Ile Pro Pro Gly Ala Leu
 1          5          10          15
Val Met Leu Thr Pro Leu Ile Val Gly Ile Leu Phe Gly Val Glu Thr
          20          25          30
Leu Ser Gly Val Leu Ala Gly Ala Leu Val Ser Gly Val Gln Ile Ala
          35          40          45
Ile Ser Ala Ser Asn Thr Gly Gly Ala Trp Asp Asn Ala Lys Lys Tyr
          50          55          60
Ile Glu Ala Gly Val Ser Glu His Ala Arg Thr Leu Gly Pro Lys Gly
65          70          75          80
Ser Asp Pro His Lys Ala Ala Val Ile Gly Asp Thr Ile Gly Asp Pro
          85          90          95
Leu Lys Asp Thr Ser Gly Pro Ser Leu Asn Ile Leu Ile Lys Leu
          100          105          110

```

```
<210> 367
<211> 381
<212> DNA
<213> Homo sapiens
```

<400> 367



gcgttcgctcg cactaccggg cggcggcgga acccttgacg agctactcga agcatggaca  
60  
tggcagcagc tcggtgtaca cagcaaaccg gtngccttg tacgactcga cnncttctgg  
120  
gcaccgctga ccgcgctact caaccacatg accatcgaaa gcttcattcg ccctgaggac  
180  
cgcgcctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg  
240  
accccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca  
300  
ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct  
360  
cngttcaggt ggcccgaat g  
381

&lt;210&gt; 368

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 368

Ala	Phe	Val	Ala	Leu	Pro	Gly	Gly	Gly	Gly	Thr	Leu	Asp	Glu	Leu	Leu
1			5					10					15		
Glu	Ala	Trp	Thr	Trp	Gln	Gln	Leu	Gly	Val	His	Ser	Lys	Pro	Val	Xaa
		20					25					30			
Leu	Val	Arg	Leu	Asp	Xaa	Phe	Trp	Ala	Pro	Leu	Thr	Ala	Leu	Leu	Asn
		35				40						45			
His	Met	Thr	Ile	Glu	Ser	Phe	Ile	Arg	Pro	Glu	Asp	Arg	Ala	Ser	Leu
	50					55					60				
Val	Ile	Ala	Asp	Thr	Ile	His	Gln	Leu	Met	Ala	Asp	Leu	Glu	Gly	Trp
65					70				75					80	
Thr	Pro	Pro	Pro	Pro	Lys	Trp	Arg	Ser							
					85										

&lt;210&gt; 369

&lt;211&gt; 313

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 369

gatacatgat cctctcatac cgcacacaca ccgctcccct ctgccgcaat tcgcagacaa  
60  
acttgcgag gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc  
120  
gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac  
180  
acattctacg agcagcaagc gaccagtctt cttcgccagc tgaacgacct cccaccgaa  
240  
gagcttcccg acgtcatcga ggacttcttc cgctgtcca ctgatgtcct tctttaccat  
300  
ttccagcaag ctt  
313

&lt;210&gt; 370

<211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 370  
 Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg  
 1 5 10 15  
 Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp  
 20 25 30  
 Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val  
 35 40 45  
 Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala  
 50 55 60  
 Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro  
 65 70 75 80  
 Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr  
 85 90 95  
 His Phe Gln Gln Ala  
 100

<210> 371  
 <211> 380  
 <212> DNA  
 <213> Homo sapiens

<400> 371  
 atgacggggtc acgtcatcct ggcgattcca caggtgggtga cgtcatggat cggcctcatc  
 60  
 tgcacgcgcca ttggcacggg ctttatcaag ccgaacctct ccacggtggt aggaggtctt  
 120  
 tacgatgacg gtgacccccg ccgcgatcag ggtttctgt acttctacat gtcgatcagt  
 180  
 attggatctc tcttcgcgcc gatcgtcacc ggctcctca aggaccatta cggctaccac  
 240  
 gtaggtttca ttgccgtgc tatcggtatg gctctgggtc tgatcgctt cttccacggg  
 300  
 cgttccaaac tgcgtgagct cgccttcgac atccccaatc cgctggcccc cggcgagggt  
 360  
 cgccggatgg tgctccgcgg  
 380

<210> 372  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 372  
 Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp  
 1 5 10 15  
 Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn  
 20 25 30  
 Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg  
 35 40 45  
 Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

```

      50              55              60
Phe Ala Pro Ile Val Thr Gly Leu Leu Lys Asp His Tyr Gly Tyr His
65              70              75              80
Val Gly Phe Ile Ala Ala Ala Ile Gly Met Ala Leu Gly Leu Ile Ala
      85              90              95
Phe Phe His Gly Arg Ser Lys Leu Arg Glu Leu Ala Phe Asp Ile Pro
      100              105              110
Asn Pro Leu Ala Pro Gly Glu Gly Arg Arg Met Val Leu Arg
      115              120              125

```

<210> 373  
 <211> 475  
 <212> DNA  
 <213> Homo sapiens

```

<400> 373
acatgttgga aaaattgcct ccactctgg tgctacaggt atgaatctca gccacagtga
60
tgactgtggc agctacaggc ctgatgaaca cccaccaag aaaaggagca tcatgtgcct
120
gcttctctct ggttcctaaa tcctttggcc aaacattttc ccacaaccc tccactccag
180
ttgctggtc actgcctctc agaaagaagt cccagggtccc tgtcagcccc agagcgctg
240
catggactct gccactgtc cctttccaac acggaggccc ccaattctgg ggaccctac
300
accctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
360
agtgggacca aagcagttct taaagggtcca atccactcag ttcttaaagt aaaaacagtt
420
gcccatgagt ccccccaaaa gacgtccgca catatgccaa acattcggtg tgcac
475

```

<210> 374  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

```

<400> 374
Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
1      5      10      15
Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
      20      25      30
Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
      35      40      45
Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
      50      55      60
Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
65      70      75      80
Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
      85      90      95
Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
      100      105

```

<210> 375  
 <211> 332  
 <212> DNA  
 <213> Homo sapiens

<400> 375  
 nnacgcgtcg cctccacctc gaaacccgcc ggcggtcggt ttttcacccat ggccgaccgc  
 60  
 aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga  
 120  
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg  
 180  
 gcggcatgct ccttcatagc ggcagtgggt gcgaagctgg gctgcccgcg gcgcactatg  
 240  
 ggacggcgcg agctgctgta ccagcgtttc catctatttc atgcgcccgc tgagttttcg  
 300  
 ttacatgagg tggctttgac gtgtctcttc ac  
 332

<210> 376  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 376  
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr  
 1 5 10 15  
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr  
 20 25 30  
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp  
 35 40 45  
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser  
 50 55 60  
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met  
 65 70 75 80  
 Gly Thr Ala Gln Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro  
 85 90 95  
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe  
 100 105 110

<210> 377  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

<400> 377  
 cgcggtgccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg  
 60  
 aggctggaac gagtgggtgct gtgttcggtg tggactcagg gaactgccgc agacgccgag  
 120  
 aacgctatgg cggagctgaa agcccttctg gaaacggcgg gatctcaggt actcgaagct  
 180  
 gtcattgcaac gtcggactac cccggatccg gcgacgtaca ttggttcggg caaggtggct  
 240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cgggtgaactc  
 300  
 gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccggctcg  
 360  
 gtctgattc  
 369

<210> 378  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 378  
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu  
 1 5 10 15  
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr  
 20 25 30  
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala  
 35 40 45  
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg  
 50 55 60  
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala  
 65 70 75 80  
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys  
 85 90 95  
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val  
 100 105 110  
 Lys Xaa Lys Val Val Asp Arg Ser Val  
 115 120

<210> 379  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

<400> 379  
 acgcgttact taaacttatc tgtaaataat aaattcatta tttctagttg gtttaggtact  
 60  
 atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca  
 120  
 gtagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctgtt  
 180  
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcatta  
 240  
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat  
 300  
 gctaaatttg ctgaagctgc tggtggtaaa ggctatgttg tgagagatgt aagtcgtctt  
 360  
 gacgacatcg ttgaagaggc aatgggtcaa gatgttccaa caatcggt  
 408

<210> 380  
 <211> 136  
 <212> PRT

<213> Homo sapiens

<400> 380

```

Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10           15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
      65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100          105          110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115          120          125
Ala Gln Asp Val Pro Thr Ile Val
      130          135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

```

nacgcgtcat aggcggggccc agtgggaagac cacgccaaca cagttggttg agatccgcgt
60
tgagggcaag gtccctgcgcg tcccgcgaaa tctgggtcaag gcctaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcgggtccag catgactgct caggctcatt
180
accaaaacgc gtcgatcccg taggggtgtc gtcatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcgttgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgcactac gtcggcggtgg ccttaagcaa tggctcgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccaggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggctg gtggacgacg caaactcgtc
480
atccccacc accttgctta cggtcgcgaa ggaatctccg gtgtgatcgc tggcggtag
540
acgctgggtc tegtctgcga ccttgtcaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

```

<210> 382

<211> 137

<212> PRT

<213> Homo sapiens

<400> 382

```

Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
 20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
 35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
 50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
 65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
 85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
 100          105          110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
 115          120          125
Phe Val Cys Asp Leu Val Asn Ile Ile
 130          135

```

<210> 383

<211> 352

<212> DNA

<213> Homo sapiens

<400> 383

```

nggagcaaca cctggtcctt gggaatgaag tgtaggagtt gcatttgctg aggttggtgt
60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctcccccggt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgttttagaa cctaggattc tgtttttccc aaacaggatc an
352

```

<210> 384

<211> 93

<212> PRT

<213> Homo sapiens

<400> 384

```

Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
 20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
 35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```

50                      55                      60  
 Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser  
 65                      70                      75                      80  
 Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile  
                     85                      90

<210> 385.

<211> 342

<212> DNA

<213> Homo sapiens

<400> 385

gccggcgcca cgaaatgcaa aatgcgccct tcaccggacg ccaggttgat cgagccgcca  
 60  
 gcacctcggg caatgtcctg ggcctgactg gcacacgcaa tcaaagcgag caacaacaca  
 120  
 caaaaacgca tcatgaggca gacgccaggg aagtgcagaga agccgcagca ggcgcgcggc  
 180  
 gattggaaat atcggtgagg ctaatggtca ccagcgcttg caggttgat tccgtggcca  
 240  
 attcgcggaa cgacagcacc gccagttcca gtcgcccgcg cagcaccagg cgacgcaagc  
 300  
 tgcggcgcaa ctccgggtgc accaacaaca ccgcactgtt ca  
 342

<210> 386

<211> 109

<212> PRT

<213> Homo sapiens

<400> 386

Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser  
 1                      5                      10                      15  
 Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu  
                     20                      25                      30  
 Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr  
                     35                      40                      45  
 Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met  
                     50                      55                      60  
 Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp  
 65                      70                      75                      80  
 Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu  
                     85                      90                      95  
 Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe  
                     100                      105

<210> 387

<211> 379

<212> DNA

<213> Homo sapiens

<400> 387

acgcgtgacg cgccggcatc ggaagcggtg actgcagaga agaccgcgca cgtggctgtg  
 60



ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc  
 120  
 atgcaagagg agcttgacaa tgtgctgat ctgcgccatg cgcggcagca agcgctcgat  
 180  
 gctgttcggt ccgagctgct cgaagcgcag caagcatgtg cctcgtgcca gctgcagctg  
 240  
 cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac  
 300  
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct  
 360  
 gagaatgcga gcctgcgcg  
 379

<210> 388

<211> 114

<212> PRT

<213> Homo sapiens

<400> 388

Met	Arg	Leu	Val	Arg	Asp	Gln	Val	Leu	Ala	Ala	Cys	Lys	Gln	Arg	Pro
1				5				10						15	
His	Gly	Ala	Pro	Gly	Ile	Trp	Asp	Ala	Leu	Ala	His	Asp	His	Leu	Ala
		20					25					30			
His	Ala	Ala	Ala	Ala	Ala	Gly	Thr	Arg	His	Met	Leu	Ala	Ala	Leu	Arg
	35					40					45				
Ala	Ala	Arg	Asn	Glu	Gln	His	Arg	Ala	Leu	Ala	Ala	Ala	His	Gly	Arg
	50				55				60						
Asp	His	Ala	His	Cys	Gln	Ala	Pro	Leu	Ala	Trp	His	Ala	Gln	Ala	Lys
65				70				75					80		
Arg	Arg	Arg	Val	His	Ala	Pro	Cys	Gln	Thr	Cys	Gln	His	Val	Pro	Gln
			85					90					95		
Pro	Arg	Ala	Arg	Ser	Ser	Leu	Gln	Ser	Thr	Leu	Pro	Met	Pro	Ala	Arg
		100						105					110		
His	Ala														

<210> 389

<211> 382

<212> DNA

<213> Homo sapiens

<400> 389

ngatggccga ctgtccact gtcagtacgc gaagctcgcc gtcgagtcgg tccacgtccg  
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 ggctccac gtgtccgca accctccgaa gcgatgacct ggcccggggg cggcaacgag  
 120  
 gtattgcgtt tggagacgct tggggtaaat tacggccagg tgcgcgccgt cgatgccctg  
 180  
 acgaccaccg tagagcgcgg caccatcacc tgcctcatgg gtcgaaatgg atcagggaag  
 240  
 tcgtctctga tgtgggcat ccaaggggca acaaagtctt cagggagggt actggtcaac  
 300  
 cacgagggtt cttgggctga cccccgaaa gccgacgccg cgaccgctcg acgaatggtg  
 360

agcttagtcc cgcagtcagc cn  
382

<210> 390  
<211> 127  
<212> PRT  
<213> Homo sapiens

<400> 390  
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val  
1 5 10 15  
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met  
20 25 30  
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly  
35 40 45  
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val  
50 55 60  
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys  
65 70 75 80  
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg  
85 90 95  
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp  
100 105 110  
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala  
115 120 125

<210> 391  
<211> 456  
<212> DNA  
<213> Homo sapiens

<400> 391  
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60  
tgcgacccta tcggtggcat gcacgccttg ttcagcgact ctattcccca gcagatcttc  
120  
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga  
180  
ggccgatgaa tcctggacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc  
240  
ttgcaaggag cgggagggcat gtggccgtgg tctcgtcct gtctgaagca cctgcgcgtg  
300  
cgtgctgatg aacttgacct agttcttate gccgacgagg tcgctactgg atttgggcgg  
360  
actggcaaac ttttcgcatg cgagtgggcc gatatcgttc ctgacatcat ggtggttggg  
420  
aatccatga ctggcggata cctgaccag tcggcc  
456

<210> 392  
<211> 55  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 392

Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro  
 1 5 10 15  
 Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Ile  
 20 25 30  
 Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Gly Arg Arg Gly  
 35 40 45  
 Asp Val Val Gln Arg Gly Arg  
 50 55

&lt;210&gt; 393

&lt;211&gt; 371

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 393

nacgcgttgc tcgtcattgg tggctactcg gcctacgaag gtatctacac catgatgact  
 60  
 gagcgggacc ggtacccggc ttcccgatt cgcacgggtg gcacccggc ttctatcgac  
 120  
 aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc  
 180  
 gaggcgatgg acaagattaa ggagtcgggt atcgcgcca gacgctgctt cgtcgctgag  
 240  
 acgatgggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgcagc tggcgctgag  
 300  
 cggatctata ccaacgagga cggtatctcc ctggacgac tagccaacga cgtccattgg  
 360  
 ttgcgggagt c  
 371

&lt;210&gt; 394

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 394

Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr  
 1 5 10 15  
 Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr  
 20 25 30  
 Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu  
 35 40 45  
 Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp  
 50 55 60  
 Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu  
 65 70 75 80  
 Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala  
 85 90 95  
 Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp  
 100 105 110  
 Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu  
 115 120

<210> 395  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 395  
 gaattctagt tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta  
 60  
 gcgacaggtg gtcttgtgca tggtagaaag gcagtcgaag cctatgtctc tgaaacctgc  
 120  
 tctcatttct gttttctact ttacgattta tgttatctca tactcccat gttgcctgtt  
 180  
 ctccagtttt ttacttgtg ttatttccat tcttctatc ctgctcaatt tctgcctcag  
 240  
 ggcagaattg tgtccaacag ctcttaaatg cagcgcagaa actgtgatgt taaaaacatc  
 300  
 ttgttatccg gccccaaaac atgttgtcct tggtaactct tactggtttg t  
 351

<210> 396  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 396  
 Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile  
 1 5 10 15  
 Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys  
 20 25 30  
 Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu  
 35 40 45  
 Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys  
 50 55 60  
 Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys  
 65 70 75 80  
 His Val Val Leu Gly Asn Ser Tyr Trp Phe  
 85 90

<210> 397  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<400> 397  
 gccgtcatta aagagatcac ccctctctc caacctggtg atgtcctcgt cgacgggtggt  
 60  
 aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtccac cggcattcac  
 120  
 tatgttggtg ctggcatctc cgggtggggga gtcggggccc tgagggtccc atcaattatg  
 180  
 cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgcc  
 240  
 cacgtcgacg gtgaaccctg ctgcgcatgg atgggtactg acggcgccgg acacttcgtc  
 300

aagatgggtcc ataatggcat cgagtacgcc gatatgcagt tcattggcga ggcgcccttc  
 360  
 ctttttgcn tgcccgccgg ttgaccaat gctgaggccg ccgatgcctt cgagtcgtgg  
 420  
 aaccatggcg acctcaattc ctacctcgtc gaaatcactt ctcgggtact gcgtgccaag  
 480  
 gat  
 483

<210> 398

<211> 161

<212> PRT

<213> Homo sapiens

<400> 398

Ala	Val	Ile	Lys	Glu	Ile	Thr	Pro	Leu	Leu	Gln	Pro	Gly	Asp	Val	Leu
1				5					10					15	
Val	Asp	Gly	Gly	Asn	Ala	Tyr	Phe	Gly	Asp	Thr	Arg	Arg	Arg	Glu	Glu
		20						25					30		
Glu	Ile	Arg	Pro	Thr	Gly	Ile	His	Tyr	Val	Gly	Thr	Gly	Ile	Ser	Gly
		35					40					45			
Gly	Gly	Val	Gly	Ala	Leu	Arg	Val	Pro	Ser	Ile	Met	Pro	Gly	Gly	Val
	50					55					60				
Lys	Glu	Ser	Tyr	Glu	Ile	Ile	Gly	Pro	Val	Leu	Glu	Lys	Ile	Ser	Ala
65				70						75				80	
His	Val	Asp	Gly	Glu	Pro	Cys	Cys	Ala	Trp	Met	Gly	Thr	Asp	Gly	Ala
			85						90					95	
Gly	His	Phe	Val	Lys	Met	Val	His	Asn	Gly	Ile	Glu	Tyr	Ala	Asp	Met
			100					105						110	
Gln	Phe	Ile	Gly	Glu	Ala	Pro	Phe	Leu	Phe	Ala	Xaa	Pro	Ala	Gly	Leu
		115					120						125		
Thr	Asn	Ala	Glu	Ala	Ala	Asp	Ala	Phe	Glu	Ser	Trp	Asn	His	Gly	Asp
	130					135						140			
Leu	Asn	Ser	Tyr	Leu	Val	Glu	Ile	Thr	Ser	Arg	Val	Leu	Arg	Ala	Lys
145					150					155					160
Asp															

<210> 399

<211> 314

<212> DNA

<213> Homo sapiens

<400> 399

nngggaatga agaccaccca gcccttcctt tcctcaaate ttctccaggc ttctgtgcat  
 60  
 ggctcatcca cccatccact cattcaccca tctatccate cactcatcca cccatccagt  
 120  
 cattcactca tttgtccate cactcatgta cccatccact cattcgcca tttatccate  
 180  
 cactcaacca tccactcate caccatcca nctcatcate cgtccagtca cccatctate  
 240  
 caccatgta tccatccact catccaccca tccactcate tgtccatcca cttatccacc  
 300

catctactca ccca  
314

<210> 400  
<211> 104  
<212> PRT  
<213> Homo sapiens

<400> 400  
Xaa Gly Met Lys Thr Thr Gln Pro Phe Leu Ser Ser Asn Leu Leu Gln  
1 5 10 15  
Ala Ser Val His Gly Ser Ser Thr His Pro Leu Ile His Pro Ser Ile  
20 25 30  
His Pro Leu Ile His Pro Ser Ser His Ser Leu Ile Cys Pro Ser Thr  
35 40 45  
His Val Pro Ile His Ser Phe Ala His Leu Ser Ile His Ser Thr Ile  
50 55 60  
His Ser Ser Thr His Pro Xaa His His Pro Ser Ser His Pro Ser Ile  
65 70 75 80  
His Pro Cys Ile His Pro Leu Ile His Pro Ser Thr His Leu Ser Ile  
85 90 95  
His Leu Ser Thr His Leu Leu Thr  
100

<210> 401  
<211> 2165  
<212> DNA  
<213> Homo sapiens

<400> 401  
gagaaaatgg aactacctgt atataaatta ggtgagcaaa cagtgatata ggtagtttta  
60  
agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatgggtg  
120  
caaaatgaaa gatctattga agtttcacta tacattgcat tgattgaacc ttggagagtt  
180  
ttatgaaaaa gaggggcac ccttgccac tgtttgccag tcttccttgc cccttccttt  
240  
gaaatgcctg cctctttttt gccagattg tttcctgacc atccgaactc agatgggggc  
300  
ctctaagttc ttcttggaà ttcacaaatc ccttcacaag gccacgtgc gaagtgaatg  
360  
atctggaggt gcctgggcat ctgtgttga agggagtcaa gactcaccag ccagtcagtt  
420  
tgtgggctac agttgtccca caaaatcag gcatgttcac ctcctctctg ggccctaca  
480  
gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag  
540  
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc  
600  
tgagcctaca gttttgtact ggggtgcacg gatgacagct gggaagatgg aaaggcagct  
660  
tgaggattta tagcagctaa agggtaaatg ctgttatgca aaaggtcccc atatgaactt  
720

cctacagggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatga  
780  
aaaattcctc tttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaagc  
840  
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagtgg  
900  
aggcccaggt tacacaggct cccggaatac agacctggga agatagggga ggagagggga  
960  
agcttgtggc cttttgatcc gcccccgaa tgcccaccgt gcgctgcttt gctgccttca  
1020  
tctcctgctc agaggecttc tccttcccag agacctcctt ggatgggtct aaggagaca  
1080  
ctgcccgggc ctttttcctt gcaatcaca ggtccaaatc ctccaggctg cgcttgatcg  
1140  
gccgcgccgc cccaatgttc tacgggtca tttccgggtg caggattggg tggaccatgc  
1200  
cttccatctt cctgaaatc tccagtctca catggtgagg ttttctgat cttgaaagcg  
1260  
attcagggtg ttttttaggg cctgacatgg tcatgggtga taccgacag gctttggggg  
1320  
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg  
1380  
gccctgtggt ggaatgagcc agggccagga ccttgccggg aggtttgtgc gggttcttgg  
1440  
gaaggctcag atctgtaggc tgatcatccg taggggcttc tgctgccgc gactttttgt  
1500  
cttgacagggt caggacgtg agataattta catggagctt ttcttgggtg ctgtgggaag  
1560  
gaaaagaact gttttccgat tcctgtaca tgctccctgga agggatattg gatgtctgtt  
1620  
cattatgaag atggtgctcg gtgtgtctgt agaggctatg gagatgaggg gacgagtaga  
1680  
agtcagccag gaagctaggc atgtgggaat gggggagggc cttttctct aagagtttat  
1740  
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaagggg ttaaggtgat  
1800  
gcttgagaa gctgcagcg tggggatctg atcgactcag tttctcatgc ttaaagatgt  
1860  
cattgatggt ctttctctct tccgagggct tgcttctgaa actctggacg tgctgaatca  
1920  
ctgatggcg gctgaccgcc atatggtcag tgctttggcc atggtgggtc tgggacaaac  
1980  
tggaacacaa gtcatcccta gcaatcagtt tctttttgct gatcaaagg ggtggggagc  
2040  
cataagggta gctgctggag aggctggccc cactcacttg ggacaaaagc ttttcttgg  
2100  
ccagtgggga catcatgcct ggggtgcccc tagagtagag caggggcgtg taattaagtc  
2160  
catgg  
2165

&lt;210&gt; 402

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 402

Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu  
 1 5 10 15  
 Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp  
 20 25 30  
 Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro  
 35 40 45  
 Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met  
 50 55 60  
 Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly  
 65 70 75 80  
 Pro Asn Pro Pro Gly Cys Ala  
 85

&lt;210&gt; 403

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 403

cccatgggtg tgtcccagga cggcgtcatg aagcgtcagg taaatgacaa ggaaacggtc  
 60  
 gcgcacttgt tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgtccag  
 120  
 ccttcgcccc cgtcgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag  
 180  
 cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta  
 240  
 cagccccgaca tggtcgtctt ggtggacgtc ggcacgaagc ccggccacct cgccctatac  
 300  
 catctatggc aggcattcta tcaccgacct accttgggcg gtgcttgcg cgaaattcat  
 360  
 gctatgatc  
 369

&lt;210&gt; 404

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 404

Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp  
 1 5 10 15  
 Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val  
 20 25 30  
 Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn  
 35 40 45  
 Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys  
 50 55 60  
 Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu  
 65 70 75 80  
 Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His



```

      85              90              95
Leu Ala Leu Tyr His Leu Trp Gln Ala Phe Tyr His Arg Pro Thr Leu
      100              105              110
Gly Gly Ala Cys Gly Glu Ile His Ala Met Ile
      115              120

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<210> 405  
 <211> 840  
 <212> DNA  
 <213> Homo sapiens

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<400> 405
gaattcccg gcaccagctc gaagctggag cactttgtgt ctatcctgct gaagtgtctc
60
gactcgccct ggaccacgag ggcctgtcgc gagacagtgg tggaggagag cgacccaag
120
ccggccttca gcaagatgaa tgggtccatg gacaaaaagt catcgaccgt cagtgaggac
180
gtggaggcca ccgtgcccat gctgcagcgg accaagtcac ggatcgagca gggatcgtg
240
gaccgctcag agacgggctg gctggacaag aaggaggggg agcaagccaa ggcgctgttt
300
gagaaggtga agaagttccg gacccatgtg gaggaggggg acattgtgta ccgcctctac
360
atgcggcaga ccatcatcaa ggtgatcaag ttcacctca tcactgcta caccgtctac
420
tacgtgcaca acatcaagtt cgacgtggac tgcaccgtgg acattgagag cctgacgggc
480
taccgcacct accgctgtgc ccacccctg gccacactct tcaagatcct ggcgtccttc
540
tacatcagcc tagtcatctt ctacggcctc atctgcatgt atacactgtg gtggatgcta
600
cggcgctccc tcaagaagta ctgcttgag tcgatccgtg aggagagcag ctacagcgac
660
atccccgacg tcaagaacga cttcgcttc atgtgcacc tcattgacca atacgacccg
720
ctctactcca agcgcttcgc cgtcttctcg tcggaggtga gtgagaacaa gctgcggcag
780
ctgaacctca acaacgagtg gacgctggac aagctccggt acggagagaa gacaacgcgt
840

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<210> 406  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

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<400> 406
Leu Ile Cys Met Tyr Thr Leu Trp Trp Met Leu Arg Arg Ser Leu Lys
 1          5          10          15
Lys Tyr Ser Phe Glu Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile
      20          25          30
Pro Asp Val Lys Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln
      35          40          45
Tyr Asp Pro Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val

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50                      55                      60  
 Ser Glu Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu  
 65                      70                      75                      80  
 Asp Lys Leu Arg Tyr Gly Glu Lys Thr Thr Arg  
                     85                      90

<210> 407  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 407  
 gcctattgta ccagctctcc agggctgggg acttgctaga gcagggttcc cagtgtcccc  
 60  
 aggtcttact ttgctctgcc tggcttcagg gtgtagggga tggagagctg gacttccagg  
 120  
 ctgtctcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca  
 180  
 caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgccaagg  
 240  
 agatgctcgc tcggagtggg tgctctggct ctgggattcc aaaccaagct gccttctctg  
 300  
 atgtggcctt agtgctctgg gcggatgtac cttggctctg cctggaccct ctctctcttc  
 360  
 caggcctctg tcccaccagg atgatgccta tccagagctc attgtcctct ccacttctct  
 420  
 ccccagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtgtt  
 480  
 gcactgagga ccacagcagc cctcgcattc ccacgggcaa aggggtatgt gtagg  
 535

<210> 408  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 408  
 Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala  
 1                      5                      10                      15  
 Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu  
                     20                      25                      30  
 Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met  
                     35                      40                      45  
 Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro  
                     50                      55                      60  
 Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys  
 65                      70                      75                      80  
 Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys  
                     85                      90                      95  
 Val

<210> 409  
 <211> 375

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 409

ngtgtcatgg gtgtctatac cagcgatgag gccaaagactg ccaagacttt tggatttggg  
 60  
 ggacttccga ttacgactaa tatttctctt gccacaact tcaatatgga tgaaatttct  
 120  
 gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct  
 180  
 agaaaattga ccgaaattgc tggctctcag caaggggagt atcaggtgtc agatgcgact  
 240  
 gcagccttcc aagaagtgc acaattgttc ggctttataa ctacgattat tagtgccatt  
 300  
 gcagggaattt ccctttttgt tggagggact ggtgttatga acatcatgct ggtttcgggtg  
 360  
 acggagcgta cgcgt  
 375

&lt;210&gt; 410

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 410

Xaa	Val	Met	Gly	Val	Tyr	Thr	Ser	Asp	Glu	Ala	Lys	Thr	Ala	Lys	Thr
1				5					10					15	
Phe	Gly	Ile	Gly	Gly	Leu	Pro	Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Asn
			20					25					30		
Asn	Phe	Asn	Met	Asp	Glu	Ile	Ser	Asp	Ile	Val	Phe	Arg	Val	Asn	Asp
		35					40				45				
Thr	Ser	Leu	Thr	Pro	Thr	Val	Gly	Pro	Glu	Leu	Ala	Arg	Lys	Leu	Thr
	50					55					60				
Glu	Ile	Ala	Gly	Leu	Gln	Gly	Glu	Tyr	Gln	Val	Ser	Asp	Ala	Thr	
65					70				75					80	
Ala	Ala	Phe	Gln	Glu	Val	Gln	Gln	Leu	Phe	Gly	Phe	Ile	Thr	Thr	Ile
			85					90					95		
Ile	Ser	Ala	Ile	Ala	Gly	Ile	Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val
		100						105					110		
Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg	Thr	Arg			
		115					120					125			

&lt;210&gt; 411

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 411

ccacatactt caccctcctc accccctcca cctactccac cacctggcag tcgccatcga  
 60  
 ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca  
 120  
 gcacgcggtc ggggcccctt gagctcgaag gcgcggcgca tcgggcagtg ctcgccggcc  
 180

tggtcgcagg gcacgtcgta ctggtgcgag acgcggaagc acttgaggcc gatgtaggcg  
 240  
 cgatcggctg tcccgaactg gcgctgatag gccgtgtaca caacacaaac tgttgactc  
 300  
 ccggtccacc acgatcatgg gctgggactc gtgttccagg tggggggcca gggcttgggc  
 360  
 ctgcggtgag cgcgtggggg ggatggggca tagcgtcggg gaggaggtg  
 409

<210> 412  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 412  
 Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro  
 1 5 10 15  
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val  
 20 25 30  
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln  
 35 40 45  
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser  
 50 55 60  
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala  
 65 70 75 80  
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr  
 85 90 95  
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp  
 100 105 110  
 Gly Asp Cys Gln Val Val Glu  
 115

<210> 413  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 413  
 ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggg agggactcca  
 60  
 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag  
 120  
 gcaccacctc catatcccgg cccacatcca gctggacccc ctgtcataca gcagccaaca  
 180  
 acacccatgt ttgtagctcc cccccaaaag acccagcggc ttcttcactc agaggcctac  
 240  
 ctgaaataca ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca  
 300  
 ctggcagctc ggagacgga cgtccatttg tcgaaagaac aggagagccg cctaccc  
 357

<210> 414  
 <211> 119  
 <212> PRT

<213> Homo sapiens

<400> 414

```

Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1           5           10           15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
      20           25           30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
      35           40           45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
      50           55           60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
65           70           75           80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
      85           90           95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Asp Val His Leu Ser Lys
      100          105          110
Glu Gln Glu Ser Arg Leu Pro
      115

```

<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

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tctagagcca acttggttat cgtaatgaat agagagacta catctatatc aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg gcgacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

```

<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

```

Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1           5           10           15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
      20           25           30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
      35           40           45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
      50           55           60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```

65                                      70                                      75                                      80  
 Gln Ala Pro Asn Leu Ala Ile Arg Leu Ile Val Ser Asn Pro Pro Glu  
    85                                      90                                      95  
 Gly Gln Pro Ile Ser Arg  
    100

<210> 417  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<400> 417  
 gaattcctcg cgcgtctctga ggtgggagag gacacctttg tgcgctccac cgaggagagac  
 60  
 tacgcggcca acgtcgaggc cgtggtgacc ccagcaccgg cggagaaaga tattgagggc  
 120  
 cagccagaag cacaggaaca tgacaccccg ggtacagaga ccattgagaa gctggtcgaa  
 180  
 tgggcccagg ggcgaggcat tactgtaaac cccgcgcttg tttgttatta taccctcaag  
 240  
 tgcattgatga tcaagctcca ccacccggcc gcggagagcg aagagcgcgga gtccgagttg  
 300  
 gcggcggttc tcattccttg cgatcgagag ctggatgaaa agcgccttga ggccgcactc  
 360  
 gagccggttg agtttgagtt ggcaggggat aaggactttg cagacaatga cttcctagtc  
 420  
 aagggtatg ttggcccgcg cgctttgaac gccaatggca tcaaggtctt ggccgatcca  
 480  
 cgc  
 483

<210> 418  
 <211> 161  
 <212> PRT  
 <213> Homo sapiens

<400> 418  
 Glu Phe Leu Ala Val Ser Glu Val Gly Glu Asp Thr Phe Val Arg Ser  
 1                                      5                                      10                                      15  
 Thr Glu Gly Asp Tyr Ala Ala Asn Val Glu Ala Val Val Thr Pro Ala  
    20                                      25                                      30  
 Pro Ala Glu Lys Asp Ile Glu Gly Gln Pro Glu Ala Gln Glu His Asp  
    35                                      40                                      45  
 Thr Pro Gly Thr Glu Thr Ile Glu Lys Leu Val Glu Trp Ala Gln Gly  
    50                                      55                                      60  
 Ala Gly Ile Thr Val Asn Pro Arg Val Val Cys Tyr Tyr Thr Leu Lys  
 65                                      70                                      75                                      80  
 Cys Met Met Ile Lys Leu His His Pro Ala Ala Glu Ser Glu Glu Arg  
    85                                      90                                      95  
 Glu Ser Glu Leu Ala Ala Val Leu Ile Pro Gly Asp Arg Glu Leu Asp  
    100                                      105                                      110  
 Glu Lys Arg Leu Glu Ala Ala Leu Glu Pro Val Glu Phe Glu Leu Ala  
    115                                      120                                      125  
 Gly Asp Lys Asp Phe Ala Asp Asn Asp Phe Leu Val Lys Gly Tyr Val

130                      135                      140  
 Gly Pro Arg Ala Leu Asn Ala Asn Gly Ile Lys Val Leu Ala Asp Pro  
 145                      150                      155                      160  
 Arg

<210> 419  
 <211> 797  
 <212> DNA  
 <213> Homo sapiens

<400> 419  
 atttcacccc aggaaaacca gtaaggacca atgattaagc ccaagggttg gtaccgagtt  
 60  
 cggatccata agtaccggcc gccaggggtg ctggaatttg ggctcccccc ggtgaaaata  
 120  
 tccatgcagc cgcgttgtct taggtagaaa agggagactg ggggtgggtg ggctgagctc  
 180  
 aagccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc  
 240  
 gaacttctag taagcgcgcc ccgctgcaag cgaaagcact ccctgccaa gaaacagatc  
 300  
 tttccactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta  
 360  
 catgatctga agggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg  
 420  
 aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa  
 480  
 tttcagtgtg gcagtgcacg cagattcttc attgggtgta gtgtatttcc atacggtatg  
 540  
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt  
 600  
 tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat  
 660  
 aatttacaga gcaatcacag ctttctttga aacggagaaa ttagattcta tgaaattttg  
 720  
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaa agatgaggct  
 780  
 tgaatgatgg ctggcca  
 797

<210> 420  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 420  
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu  
 1                      5                      10                      15  
 Arg Cys Leu Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys  
 20                      25                      30  
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn  
 35                      40                      45  
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg

```

      50              55              60
Thr Leu Ser His Thr Asn Val Leu Ser Pro Glu Asn Val Lys Asp Phe
65              70              75              80
His Gln Pro Leu Pro Asp Ser Pro Asn Leu Glu Asn Val Met Ser Thr
      85              90              95
Leu Gln Ile Met Tyr Thr Leu Phe Val Gln
      100              105

```

<210> 421  
 <211> 406  
 <212> DNA  
 <213> Homo sapiens

```

<400> 421
ggatccacca tgatggagcc caccaccca tctcagtc acctgctgca gcttctccat
60
aaccacacac aggtcaatct tgtctcccta aacacacat gtgctctcat gctgcatgg
120
tttgctggg gccctctcta cctcctctgc tttctggaga acccttgac tctcccaag
180
ccttcaagtt ggaaagtga cagtcagcat atgtctctag ctcagccctt actgctgga
240
ttcatgaaga ttggttact gtcagccct gaccagaacg tgtgttttag gaaagcagga
300
accaagtctt accaatgtct gtagtccag cctccaccct ggcatacagt aggtgctcat
360
tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
406

```

<210> 422  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

```

<400> 422
Met Met Glu Pro Thr His Pro Ser Ser Val His Leu Leu Gln Leu Leu
1      5      10      15
His Asn Pro Thr Gln Val Asn Leu Val Ser Leu Asn Thr Pro Cys Ala
      20      25      30
Leu Met Leu Pro Trp Phe Ala Trp Gly Pro Leu Tyr Leu Leu Cys Phe
      35      40      45
Leu Glu Asn Pro Cys Thr Pro Pro Lys Pro Ser Ser Trp Lys Val Asn
      50      55      60
Ser Gln His Met Ser Leu Ala Gln Pro Leu Leu Arg Gly Phe Met Lys
65      70      75      80
Ile Gly Ser Leu Ser Ala Pro Asp Gln Asn Val Cys Phe Arg Lys Ala
      85      90      95
Gly Thr Lys Ser Tyr Gln Cys Leu
      100

```

<210> 423  
 <211> 628  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 423

ngccacccta cgctcgcct gcaatggcaa cttcagatcc ccggtggcac cgtagtctta  
 60  
 gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cgaggaagg agagggagaa  
 120  
 ggagatgggg atttgctgac gcagacccaa gcccaaacgc cgactccagc acccgcttgg  
 180  
 ccggcgcccc cagccacacc gcgcttcttg gccctcgcaa atggctccct gttggtgccc  
 240  
 ctctgagtg ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcgcc  
 300  
 aactctacgt caatacgct ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc  
 360  
 gccgggggag aaccgcacgg acaggccccg acctctgagc gcaagtcac agccaagggc  
 420  
 cggggcaaca gcgtcctgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc  
 480  
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgaggagag  
 540  
 gaggccgaag accagatcct cgcggaccgc gcggaggagc agcgctgtgg caacggggac  
 600  
 ccctctcggt acgtttctaa ccacgcgt  
 628

&lt;210&gt; 424

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 424

Xaa His Pro Thr Pro Arg Leu Gln Trp Gln Leu Gln Ile Pro Gly Gly  
 1 5 10 15  
 Thr Val Val Leu Glu Pro Pro Val Leu Ser Gly Glu Asp Asp Gly Val  
 20 25 30  
 Gly Ala Glu Glu Gly Glu Gly Glu Gly Asp Gly Asp Leu Leu Thr Gln  
 35 40 45  
 Thr Gln Ala Gln Thr Pro Thr Pro Ala Pro Ala Trp Pro Ala Pro Pro  
 50 55 60  
 Ala Thr Pro Arg Phe Leu Ala Leu Ala Asn Gly Ser Leu Leu Val Pro  
 65 70 75 80  
 Leu Leu Ser Ala Lys Glu Ala Gly Val Tyr Thr Cys Arg Ala His Asn  
 85 90 95  
 Glu Leu Gly Ala Asn Ser Thr Ser Ile Arg Val Ala Val Ala Ala Thr  
 100 105 110  
 Gly Pro Pro Lys His Ala Pro Gly Ala Gly Gly Glu Pro Asp Gly Gln  
 115 120 125  
 Ala Pro Thr Ser Glu Arg Lys Ser Thr Ala Lys Gly Arg Gly Asn Ser  
 130 135 140  
 Val Leu Pro Ser Lys Pro Glu Gly Lys Ile Lys Gly Gln Gly Leu Ala  
 145 150 155 160  
 Lys Val Ser Ile Leu Gly Glu Thr Glu Thr Glu Pro Glu Glu Asp Thr  
 165 170 175  
 Ser Glu Gly Glu Glu Ala Glu Asp Gln Ile Leu Ala Asp Pro Ala Glu

180 185 190  
 Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser Asn His  
 195 200 205  
 Ala

<210> 425  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 425  
 ccggccgctcg aagactttga ggacgatgta gctcgacgag cagcggttacg agccctggag  
 60  
 tacgtggatt tgaccccagg cactnaagtg cgcgcatcgc ccattgacac cgtgttccta  
 120  
 ggatcgtgca cgaatggccg tgaggactta cggctggctg ctgaggttcc caaaggacga  
 180  
 catatcgag cgggcacccg gatgctcgtc gccctggat ctgctcgtgt ccgtctgcag  
 240  
 gctatggagg aaggcctcga cgagatcggg tcccggtttg ctgacatctt tcgcaataac  
 300  
 tctgcgaaca atggcttggt actggctcag gttgaccccg aggtcgtcga agagttgtgg  
 360  
 gactttgccg agcagcatcc tggtagcag ctcaccgtct ccctcgagaa tcggacgatc  
 420  
 aaccttccgg gtcgcacgac ctaccggttc catattgatg acgtcacgag t  
 471

<210> 426  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 426  
 Pro Ala Val Glu Asp Phe Glu Asp Asp Val Ala Arg Ser Ala Ala Leu  
 1 5 10 15  
 Arg Ala Leu Glu Tyr Val Asp Leu Thr Pro Gly Thr Xaa Val Arg Val  
 20 25 30  
 Ile Ala Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Glu  
 35 40 45  
 Asp Leu Arg Leu Ala Ala Glu Val Pro Lys Gly Arg His Ile Ala Ala  
 50 55 60  
 Gly Thr Arg Met Leu Val Ala Pro Gly Ser Ala Arg Val Arg Leu Gln  
 65 70 75 80  
 Ala Met Glu Glu Gly Leu Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile  
 85 90 95  
 Phe Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp  
 100 105 110  
 Pro Glu Val Val Glu Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly  
 115 120 125  
 Glu Gln Leu Thr Val Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly  
 130 135 140  
 Arg Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg

145

150

155

&lt;210&gt; 427

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 427

ctagcggtag tagaaggtat gcagtttgat cgcggctact tgtctccgta tttcatcaac  
 60  
 aatcaagaaa caatgaatgc agagctagaa aaccatttta ttcttcttgt tgataagaaa  
 120  
 atttctaata tccgtgactt gctaccaatt ttggaagggt ttgctaaagc atcgcgcccc  
 180  
 ttgttgatca ttgcggaaga cgttgaaggc gaagcgttgg caaccttggg tgtaaacact  
 240  
 atgcgcggca tcgtaaaaagt agcggcagcg aaagcgccag gttttggtga tcgccgtaaa  
 300  
 gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc  
 360  
 attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgcgt tacattgaca  
 420  
 aaagaaagta caacgattgt tgatggtgcg ggtgttgag ctaatattac tggtcgtgtt  
 480  
 gagcaaatc gtgcagaaat tgctaactct tcttctggct acgataaaga gaaattgcaa  
 540  
 gaacgc  
 546

&lt;210&gt; 428

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 428

Leu Ala Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro  
 1 5 10 15  
 Tyr Phe Ile Asn Asn Gln Glu Thr Met Asn Ala Glu Leu Glu Asn Pro  
 20 25 30  
 Phe Ile Leu Leu Val Asp Lys Lys Ile Ser Asn Ile Arg Asp Leu Leu  
 35 40 45  
 Pro Ile Leu Glu Gly Val Ala Lys Ala Ser Arg Pro Leu Leu Ile Ile  
 50 55 60  
 Ala Glu Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr  
 65 70 75 80  
 Met Arg Gly Ile Val Lys Val Ala Ala Lys Ala Pro Gly Phe Gly  
 85 90 95  
 Asp Arg Arg Lys Ala Met Leu Gln Asp Ile Ala Val Leu Thr Gly Ser  
 100 105 110  
 Thr Val Ile Ser Glu Glu Ile Gly Ile Lys Leu Glu Glu Ala Thr Ile  
 115 120 125  
 Glu Gln Leu Gly Thr Ala Lys Arg Val Thr Leu Thr Lys Glu Ser Thr  
 130 135 140  
 Thr Ile Val Asp Gly Ala Gly Val Ala Ala Asn Ile Thr Gly Arg Val

145                      150                      155                      160  
 Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys  
                          165                      170                      175  
 Glu Lys Leu Gln Glu Arg  
                          180

<210> 429

<211> 425

<212> DNA

<213> Homo sapiens

<400> 429

gctagcagcc cttacaggag acgggctaata aataatgcag cagtggctcc gacaacttgc  
 60  
 ccgttgacgc cggtcacgga tccatttgct tttagtagac aggcgctcca aagtacacca  
 120  
 ctgggcagtt cgtccaaaag cagtcacact gtcttgcaag gccagcccc cgcagggttt  
 180  
 tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcagggacc  
 240  
 ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg  
 300  
 tgcattgaca ccttcagcac ctctggggcc tgagatgaac aggagtgcag aggtcggctc  
 360  
 cagttcagag cctgaagttc agactctgcc atatcttcct cactacattc caggagtgga  
 420  
 tcctg  
 425

<210> 430

<211> 130

<212> PRT

<213> Homo sapiens

<400> 430

Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile  
 1                      5                      10                      15  
 His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val  
                          20                      25                      30  
 Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly  
                          35                      40                      45  
 Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn  
                          50                      55                      60  
 Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro  
 65                      70                      75                      80  
 Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro  
                          85                      90                      95  
 Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu  
                          100                      105                      110  
 Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val  
                          115                      120                      125  
 Asp Pro  
 130

<210> 431  
 <211> 192  
 <212> DNA  
 <213> Homo sapiens

<400> 431  
 ctaggcatcc accagcgtag acacacggga gagaggccct aactggcct cgggtgcaac  
 60  
 cgccgcttcc gccagcgac gccctcgtc atccaccagc gcattcacac gggcgagaag  
 120  
 cctnaccgt gcccgactg cgagcggcgc ttctctcct cctctcgct ggtcagtcac  
 180  
 cgcggtgtgc ac  
 192

<210> 432  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<400> 432  
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly  
 1 5 10 15  
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His  
 20 25 30  
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu  
 35 40 45  
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His  
 50 55 60

<210> 433  
 <211> 635  
 <212> DNA  
 <213> Homo sapiens

<400> 433  
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tctttggtac  
 60  
 ctcatggagg agcgtggcgc gtagcggag gccgccgcgc tcatgccgct gctgctccgg  
 120  
 accgaccgag gcgcgtggga cacgtttgtg tgctgtacc tcgagcggca ccaaagggat  
 180  
 gcgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc  
 240  
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg  
 300  
 ccgagtcaca tctactcgaa gcaggcgggtg gctgcggcga tcggcgatca cgcacgaacc  
 360  
 agccgcacgc tgctcgagt cctcgcacag ctgtacatgg ccgcacatca gcccggaag  
 420  
 gctctgacat actacatgag cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtac  
 480  
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc  
 540

gccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccac  
 600  
 tcgattccca tccagcgcg catggcgag ctcga  
 635

<210> 434  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 434  
 Xaa Pro Ala Ala Ala Leu Gly Tyr Asp Val Ala Ala Ile Gly Arg Glu  
 1 5 10 15  
 Tyr Leu Trp Tyr Leu Met Glu Glu Arg Gly Ala Tyr Ala Glu Ala Ala  
 20 25 30  
 Ala Leu Met Pro Leu Leu Leu Arg Thr Asp Arg Gly Ala Trp Asp Thr  
 35 40 45  
 Phe Val Cys Cys Tyr Leu Glu Arg His Gln Arg Asp Ala Ile Leu Pro  
 50 55 60  
 His Ile Pro Thr Gln Asp Pro Gln Leu Ser Glu Met Val Tyr Asp Leu  
 65 70 75 80  
 Val Leu Val His Leu Leu Gln His Asp Pro Thr Gln Leu Leu Ala Thr  
 85 90 95  
 Leu Arg Ala Trp Pro Ser His Ile Tyr Ser Lys Gln Ala Val Ala Ala  
 100 105 110  
 Ala Ile Gly Asp His Ala Arg Thr Ser Arg Thr Leu Leu Glu Cys Leu  
 115 120 125  
 Ala Gln Leu Tyr Met Ala Ala His Gln Pro Gly Lys Ala Leu Thr Tyr  
 130 135 140  
 Tyr Met Arg Leu Arg Asp Pro Cys Val Phe Asp Leu Ile Arg Glu Tyr  
 145 150 155 160  
 Asp Leu Leu Ile Asp Val Gln His His Ile Gly Thr Leu Val Glu Leu  
 165 170 175  
 Asp Gln Glu Cys Ala Gly Ser Thr Glu Pro Arg Ser Ser Ala Leu Met  
 180 185 190  
 Pro Leu Leu Val Pro Tyr Thr His Ser Ile Pro Ile Gln Arg Ala Met  
 195 200 205  
 Ala Gln Leu  
 210

<210> 435  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 435  
 nncgtacgtt cgcgtatttt ccgcgcccgg gaagctatcg ataataaagt tcaaccgctg  
 60  
 atccagcggt agcaatggcg ggcacaggaa gggtagcttag gcatgcagaa agaaaagctt  
 120  
 tccgctctga tggatgggtga atcgttcgac agcgagctgt tgagttctct gtcgcaagat  
 180  
 cgaacgcttc aacaaagctg gcagggctat cacctgatac gtgacacact gcgaggtgat  
 240

gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa  
 300  
 cccgcccggc tgggtgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag  
 360  
 aaaatgccgt tctgggacaa agtgcgtccc tgggcgagcc agattacgca aatcggtatg  
 420  
 gcggcctgcg tgtcgtggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcg  
 480  
 ccatcgaacg cgt  
 493

<210> 436

<211> 130

<212> PRT

<213> Homo sapiens

<400> 436

Met	Gln	Lys	Glu	Lys	Leu	Ser	Ala	Leu	Met	Asp	Gly	Glu	Ser	Phe	Asp
1				5					10					15	
Ser	Glu	Leu	Leu	Ser	Ser	Leu	Ser	Gln	Asp	Arg	Thr	Leu	Gln	Gln	Ser
		20						25					30		
Trp	Gln	Gly	Tyr	His	Leu	Ile	Arg	Asp	Thr	Leu	Arg	Gly	Asp	Val	Gly
		35					40					45			
Gln	Val	Met	His	Leu	Asp	Ile	Ala	Asp	Arg	Val	Ala	Ala	Ala	Leu	Glu
	50					55				60					
Lys	Glu	Pro	Ala	Arg	Leu	Val	Pro	Ser	Ala	Val	Gln	Glu	Ser	Gln	Pro
65				70					75					80	
Gln	Pro	His	Thr	Trp	Gln	Lys	Met	Pro	Phe	Trp	Asp	Lys	Val	Arg	Pro
		85						90					95		
Trp	Ala	Ser	Gln	Ile	Thr	Gln	Ile	Gly	Met	Ala	Ala	Cys	Val	Ser	Leu
		100						105					110		
Ala	Val	Ile	Val	Gly	Val	Gln	Gln	Tyr	Asn	Gln	Pro	Ser	Ala	Pro	Ser
		115					120						125		
Asn	Ala														
	130														

<210> 437

<211> 447

<212> DNA

<213> Homo sapiens

<400> 437

ntggtaaccg gtgtccctga tatggaccct gctgtgttag agcgtaaatt atttatttta  
 60  
 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttac  
 120  
 attaatacat tctcatacaa aacaatcggt tataaagggtc agttaaccac tgaacaagtg  
 180  
 ccacaatatt tcttagattt acaaaatcca agtatggtaa cggcattagc gcttgttcat  
 240  
 tcacgtttct caacaaatac atttctctgt tggcgtttag cacaaccatt ccgttacatc  
 300  
 gctcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa  
 360

gcgttacttg aagctgaatt ttccactcgc tcagaattag atatgttaat gccaatctgt  
 420  
 acggatggta tgtctgactc ggcaagg  
 447

<210> 438

<211> 149

<212> PRT

<213> Homo sapiens

<400> 438

Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys  
 1 5 10 15  
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val  
 20 25 30  
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr  
 35 40 45  
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe  
 50 55 60  
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His  
 65 70 75 80  
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro  
 85 90 95  
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn  
 100 105 110  
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe  
 115 120 125  
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met  
 130 135 140  
 Ser Asp Ser Ala Arg  
 145

<210> 439

<211> 395

<212> DNA

<213> Homo sapiens

<400> 439

nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tcctgcagca gctgcaccag  
 60  
 cttcccaggg gccggctgga cctggccacg caaagcctga cggtggagac ctgcagggcc  
 120  
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggtcctgag tgactgcatg  
 180  
 ctcagcgagg aaggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc  
 240  
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc  
 300  
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg  
 360  
 gacgatgcct tcgccacctt ctgcgggggc ctggc  
 395

<210> 440



<211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 440  
 Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His  
 1 5 10 15  
 Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val  
 20 25 30  
 Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys  
 35 40 45  
 Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr  
 50 55 60  
 Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp  
 65 70 75 80  
 Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys  
 85 90 95  
 Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn  
 100 105 110  
 Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu  
 115 120 125

<210> 441  
 <211> 364  
 <212> DNA  
 <213> Homo sapiens

<400> 441  
 gccagtgact acgtgaacat gttcgatgcc gagcagggt tcttcgacag gcgcagcccg  
 60  
 ggcggcgagt tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc  
 120  
 gacgggttga acttcgcctt ccacgtcca caggacggcc gggggctggc cgcgctctac  
 180  
 ggcgggtccga aaggcttga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcy  
 240  
 gacaagccgg cgtacggcgg aatccacgaa atggtcgagg ccagagcggt ccggatgggc  
 300  
 caattgggca tgtccaacga gccctcgac catattccct acatctacaa ctatgccggc  
 360  
 gcgc  
 364

<210> 442  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 442  
 Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp  
 1 5 10 15  
 Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser  
 20 25 30  
 Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

```

      35              40              45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys
      50              55              60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala
65              70              75              80
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala
      85              90              95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile
      100              105              110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala
      115              120

```

&lt;210&gt; 443

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 443

```

accgggttacg gctcagtgc acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
60
ctcatggtgc tggcaatccc cttcgccaag atcctctcga cgaccctgtc catcggatcg
120
ggcgggtccgg cggcgctctt cggccctggc atggtcatcg gcggagccac tggcgcgga
180
ctgtggcgcc tctcagagg gctgccaggt atcccatcct caccgatgag ttctgctatt
240
gtcggcatga tcgcctgctt cgggtcggtt gcccatgccc cactcggcgt gctgctcatg
300
gttggcgaga tgaccggaaa cctgtcgctg ctcgctcctg gcatgatcgc cgtegccgctc
360
gctggccgag ttgtcgggga cacttcgatc tacacctctc agtcaagga tcgcctggag
420
ggcgacgcgt
430

```

&lt;210&gt; 444

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 444

```

Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
1      5      10      15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
20     25     30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
35     40     45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
50     55     60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
65     70     75     80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
85     90     95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala

```

100 105 110  
 Pro Gly Met Ile Ala Val Ala Val Ala Gly Arg Val Val Gly Asp Thr  
 115 120 125  
 Ser Ile Tyr Thr Ser Gln Leu Lys Asp Arg Leu Glu Gly Asp Ala  
 130 135 140

<210> 445  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 445  
 ccatgggggt gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt  
 60  
 tcttgcttta ttgctcacc tgtccagggt tccctctgtt tgtgaggag ctgctgccac  
 120  
 cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtgggagg acttttcctt  
 180  
 agttttcttt gctcttctgc tctgagtcca gccctggctg gacctttgat cccttctctc  
 240  
 tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc  
 300  
 caagtgggaa caagccatga aggagctgca ccccgaaag tctgagggtg ggacacgcgt  
 360

<210> 446  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 446  
 Met Ala Cys Ser His Leu Glu Met Ala Ser Gln Ile Leu Lys Arg Gln  
 1 5 10 15  
 Lys Lys Lys Val Arg Lys Phe Pro Asp Lys Glu Arg Arg Asp Gln Arg  
 20 25 30  
 Ser Ser Gln Gly Trp Thr Gln Ser Arg Arg Ala Lys Lys Thr Lys Glu  
 35 40 45  
 Lys Ser Ser His Gln Glu Ala Asp Leu Arg Ser Phe Met Leu Pro Gly  
 50 55 60  
 Pro Lys Val Ala Ala Ala Pro Ser Gln Thr Glu Gly Thr Leu Asp Arg  
 65 70 75 80  
 Val Ser Asn Lys Ala Arg Asn Leu Pro Cys Trp Cys His Gln Leu Arg  
 85 90 95  
 Gly Leu Pro Arg Gly  
 100

<210> 447  
 <211> 487  
 <212> DNA  
 <213> Homo sapiens

<400> 447  
 acgcgtgaag ggggaaattg ctcgtgccac ctgaggatta atcattaccc tggaaccctt  
 60

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc  
 120  
 gagtgaggct gaggtcatgg agaaggggaat ggggggcccc catggccagc tggacctgat  
 180  
 cactgcctcc ccaactcagcc acagccctca gggccctgtg ccagtccaga agccccattca  
 240  
 gggacacctt tggccaatgt tctgtttcat ctgcgaggca accttcccca gtgccccaac  
 300  
 catagcgttt tccccaaac accctcagga aggagggacc actacctgtg cagggggggc  
 360  
 caggagcctc ctgagagcct catatgggga ggaagtggta ccattctacc cccattgcct  
 420  
 ttctctccta cttccacctg gccagcttcc ctcaagtccc ctctgcctc agtgccccct  
 480  
 cacgcgt  
 487

<210> 448

<211> 117

<212> PRT

<213> Homo sapiens

<400> 448

Met	Glu	Lys	Gly	Met	Gly	Gly	Pro	His	Gly	Gln	Leu	Asp	Leu	Ile	Thr
1				5					10					15	
Ala	Ser	Pro	Leu	Ser	His	Ser	Pro	Gln	Gly	Pro	Val	Pro	Val	Gln	Lys
			20					25					30		
Pro	Ile	Gln	Gly	His	Leu	Trp	Pro	Met	Phe	Cys	Phe	Ile	Cys	Glu	Ala
		35					40					45			
Thr	Phe	Pro	Ser	Ala	Pro	Thr	Ile	Ala	Phe	Ser	Pro	Lys	His	Pro	Gln
	50					55					60				
Glu	Gly	Gly	Thr	Thr	Thr	Cys	Ala	Gly	Gly	Ala	Arg	Ser	Leu	Leu	Arg
65					70					75				80	
Ala	Ser	Tyr	Gly	Glu	Glu	Val	Val	Pro	Ser	His	Pro	His	Cys	Leu	Ser
			85					90					95		
Leu	Leu	Leu	Pro	Pro	Gly	Gln	Leu	Pro	Ser	Val	Pro	Leu	Leu	Pro	Gln
			100					105					110		
Cys	Pro	Phe	Thr	Arg											
			115												

<210> 449

<211> 353

<212> DNA

<213> Homo sapiens

<400> 449

gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag  
 60  
 gagaaggggg agcgggcaga gaaactggag agggagctac agcgactcca ggaggagaac  
 120  
 gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaaagt cgaggccctg  
 180  
 gagcatgaga gccagggcct gcagctggag aaccggactc tgaggaagtc tctggacacc  
 240

ttgcagaacg tgtccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca  
300  
gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt  
353

<210> 450

<211> 117

<212> PRT

<213> Homo sapiens

<400> 450

Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His Arg Asp Leu  
1 5 10 15  
Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu  
20 25 30  
Leu Gln Arg Leu Gln Glu Glu Asn Gly Arg Leu Ala Arg Lys Val Thr  
35 40 45  
Ser Leu Glu Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser  
50 55 60  
Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr  
65 70 75 80  
Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys  
85 90 95  
Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met  
100 105 110  
Arg Arg Arg Gln Arg  
115

<210> 451

<211> 444

<212> DNA

<213> Homo sapiens

<400> 451

gtgatgcggc tgactaagcc tactttattc accaatatcc cagtaacatg tgaagagaaa  
60  
gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cgттаатггт  
120  
gcagaagttt таатгттггг agaaatgctg actttaccac agaattttgg gaatatattt  
180  
ttgggagaga ctttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa  
240  
gacatattag taaaagctga tcttcagaca agttctcagc gtttaaactt ttcagcctcc  
300  
aatgctgcag tggctgaact taaaccggat tgttgtattg atgatgtcat acatcatgaa  
360  
gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga  
420  
gaaaaaatgt atttcagaaa attt  
444

<210> 452

<211> 148

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 452

```

Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
 1           5           10           15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
 20           25           30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
 35           40           45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
 50           55           60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
 65           70           75           80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
 85           90           95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
100           105           110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
115           120           125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
130           135           140
Phe Arg Lys Phe
145

```

&lt;210&gt; 453

&lt;211&gt; 373

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 453

```

gctagctctg accccacctt tgccaagtgg cactagggtg gccaatgggg actagggttg
60
tataattgga aaatacagtc tcccctgttg tccaagaaaag gcccagatg acctggggct
120
tgaaaggcac tcccgtggg tgcttctgagg gaggcagtg ggggcagcgg ggcgggggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag cccactggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagacctg
300
ccacaggagg agtgggagga gaagctgttg atgttcctgc gagacaccct ggccatcatt
360
tctgacaacg cgt
373

```

&lt;210&gt; 454

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 454

```

Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
 1           5           10           15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```

```

      20      25      30
Gln Ala Ser Pro Ser Gln Asn Ala Pro Val Gly Leu Arg Ala Gln His
      35      40      45
Leu Pro Trp Ser Trp Gly Cys Ser Ala Gln Thr Gly Pro Ala Ala Pro
      50      55      60
Leu Pro Pro Thr Cys Ser Gln Glu Ala Pro Ser Gly Ser Ala Phe Gln
      65      70      75      80
Ala Pro Gly His Leu Gly Pro Phe Leu Asp Asn Arg Gly Asp Cys Ile
      85      90      95
Phe Gln Leu Tyr Asn Pro Ser Pro His Trp Pro Pro
      100      105

```

<210> 455  
 <211> 602  
 <212> DNA  
 <213> Homo sapiens

```

<400> 455
cctaggcaaa gcatgccac cctacctccc cttacctta ccttcattt tcccctaagc
60
acccatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccaccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagctttgta ggggtgttggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtcct ttttctctcg cccctctca ctgacctggt tttgatgcca
360
gacagcacag atgggctagg gaggcagggtg gggaagcaga gatctgcgtc tcttgagct
420
ggagctgggtg ggtggggctc cttcctggtg ctgcggaggc tcattgggga ggtggcagcg
480
acccctcag gagcctctgt cgctgcact cagatctgtg cctttccaca gcgcccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
600
gt
602

```

<210> 456  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

```

<400> 456
Met Pro Thr Leu Pro Pro Leu Thr Leu Thr Leu His Phe Pro Leu Ser
1      5      10      15
Thr His His His Arg Cys Tyr Cys Met Cys Leu Leu Thr Leu Thr Ala
20      25      30
His His Pro His Trp Asn Val Arg Thr Thr Lys Ala Gly Leu Leu Ala
35      40      45
Ala Leu Ala Thr Ala Gly Ser Pro Glu Leu Cys Arg Val Leu Gly Thr

```

```

      50              55              60
Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
65              70              75              80
Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
      85              90              95
Leu Ala Thr Tyr
      100

```

<210> 457  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

```

<400> 457
acgcgtcatg tggatattcc tgggaggttc ccaggaacgt ttctggacgg gccccgacc
60
agaggtcagg gaacttttct tattattctg cacgtgccca gggatagtca aaccaggtct
120
tccccttctg ctggccgcaa caccgagcc gccgccacga ccgcacgctg aattcatgac
180
ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga
240
tcgttttctg tccactggcc agcgccacta tgatcaggtg gggatatccgc ccggcgggcgg
300
gagcaccggg acgcccggggc gccg
324

```

<210> 458  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

```

<400> 458
Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
1              5              10              15
Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly
      20              25              30
Ile Val Lys Pro Gly Leu Pro Leu Leu Ala Ala Thr Arg Gln Pro
      35              40              45
Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
      50              55              60
Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
65              70              75              80
Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
      85              90              95
Gly Gly Ser Thr Gly Thr Pro Gly Arg
      100              105

```

<210> 459  
 <211> 415  
 <212> DNA  
 <213> Homo sapiens

<400> 459



acgcgttcat tcggcatctg cttccatgga tttcctgcgg ggaggcgcgg ccgagagtgc  
60  
gggtgtcgaa caccgacctt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg  
120  
ctgggcttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccggtggtt  
180  
tatgctgccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg  
240  
agaggcctca cccgacagct gggcatcgga tttacgaagc ccacgacgaa tcttcctcgc  
300  
ctcctcaaag ccgatcatcg gcatgccagg tttgtggttg aatgcttcga tcaacacact  
360  
aggatcggtg gggccacca catacacga gcggcaatcg agcggatacg acctc  
415

<210> 460  
<211> 105  
<212> PRT  
<213> Homo sapiens

<400> 460  
Met Pro Met Ile Gly Phe Glu Glu Ala Arg Lys Ile Arg Arg Gly Leu  
1 5 10 15  
Arg Lys Ser Asp Ala Gln Leu Ser Gly Glu Ala Ser Pro Phe Lys His  
20 25 30  
Val Gln Ile Pro Arg Glu Gly Arg Ala Gln Ser Ser Ala Gly Ser Ile  
35 40 45  
Asn His Arg Asn Arg Ala Ala Arg Asp Gln Glu Arg Glu Arg Lys Arg  
50 55 60  
Leu Glu Ala Gln Arg Gln Asp Pro Ser Arg Pro Val Val Glu Thr Ile  
65 70 75 80  
Thr Glu Val Ser Cys Ser Thr Pro Ala Leu Ser Ala Ala Pro Pro Arg  
85 90 95  
Arg Lys Ser Met Glu Ala Asp Ala Glu  
100 105

<210> 461  
<211> 357  
<212> DNA  
<213> Homo sapiens

<400> 461  
acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt ggctcacaac  
60  
cgggtcacat gcatgatgac aaaaactggc agaataagatg tgatgtcatc ccgtctacca  
120  
gtccttagaa ccagctcaga gagtcccggg gtcggtaccg tcgagactca gtacacaact  
180  
gtcgcgatac cggacgaccc tcttcactctg gttgcagatg ggcgtotcaa tcacgtcact  
240  
gtcgtttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggg ctatacctgt  
300  
catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg  
357

<210> 462  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 462  
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val  
 1 5 10 15  
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile  
 20 25 30  
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser  
 35 40 45  
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro  
 50 55 60  
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr  
 65 70 75 80  
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala  
 85 90 95  
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe  
 100 105 110  
 His Pro Gly Val Val Arg Pro  
 115

<210> 463  
 <211> 434  
 <212> DNA  
 <213> Homo sapiens

<400> 463  
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac  
 60  
 gaggcagctg gtgacgatga agtgggtgcga tgcgaggaat gcgatcgat cctgggtgcgt  
 120  
 accggagagt ccatctgagc ccttcttctg gcggtgatgc cgggatatcc gtagaattag  
 180  
 cggtcggacg agccatccgg gtgatcgcg cagcgggtgag ttgtcgagga aagtccgggc  
 240  
 tccatagagc aggggtggtg gtaacgccc cccgggggtga cccgcgggaa agtgccacag  
 300  
 agaacagact gccggtttcg agccgggtgag ggtgaaacgg tggagtaagt gcccaccgcg  
 360  
 tcacgggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga  
 420  
 ggtcgaggac gcgt  
 434

<210> 464  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

      1           5           10           15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
      20           25           30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
      35           40           45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
      50           55           60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
      65           70           75           80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
      85           90           95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
      100          105          110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
      115          120          125

```

<210> 465  
 <211> 438  
 <212> DNA  
 <213> Homo sapiens

```

<400> 465
gatcatttag aatttatgga agaagctgat gtgaaagcta tgggtcaaadc tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttcgacgg atgctaatacc agggacgtcg
180
ccagcgttat cattacggtt aatgatgaat atggcatgta ccttggttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaaag cggtggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattggtt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

```

<210> 466  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

```

<400> 466
Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
1           5           10           15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
      20           25           30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
      35           40           45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
      50           55           60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro

```

```

65          70          75          80
Glu Thr Ala Leu Ala Gly Val Thr Ile His Ala Ala Lys Ala Leu Gly
            85          90          95
Ile Ser Asp Ser His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe
            100          105          110
Val Cys Trp Asp Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly
            115          120          125
Glu Gln Leu Val Lys Gln Arg Ile Gln His Gly Val Ser His Glu
            130          135          140

```

&lt;210&gt; 467

&lt;211&gt; 460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 467

```

ntttccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaga gcggttaagc
60
tgcattccctg caccttcttc tcccaccgct tcaaagccac agtgaggaac ttcggagctt
120
ctcgcagtga agatggcggt ggaggaatgg atgccctggc tagaagaggc ggaatatctg
180
ttgattgtgt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
240
tccaggcaag caagaagggc ccagctgttt acctggttcc acttttccct ctcctaccgg
300
ccgggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catgggcccc
360
ttctccagg cttgcctgtc acccgggctc ccgtcaaacc ctggccttcg tgcgacaaca
420
ctcttggtgc cttctatggt tctgtatggt gccgcaattg
460

```

&lt;210&gt; 468

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 468

```

Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
1          5          10          15
Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
20          25          30
Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
35          40          45
Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
50          55          60
Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
65          70          75          80
Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
85          90          95
Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
100          105          110
Leu Tyr Val Ala Ala Ile

```

115

<210> 469  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
 cttgtgcaca cggtattttt ccaatacaaa tagtttaaaa agtaaaactcc aaatacctat  
 60  
 aagccccctc aaagcacctt ccaaataatga accttgtaa tgcccaagggt ccagaggggt  
 120  
 cccccagaaa ggcccaggag cctggggcat gggaaagctg tcgggggtccc catgctgact  
 180  
 ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct  
 240  
 tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag  
 300  
 ccctgagttc ctggctagct gtgggtaacc acaaaaaatg cgggggggtga tgattttcga  
 360  
 agtccatcgg caaagaaaga c  
 381

<210> 470  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 470  
 Met Asp Phe Glu Asn His His Pro Pro His Phe Leu Trp Leu Thr Thr  
 1 5 10 15  
 Ala Ser Gln Glu Leu Arg Ala Ser His Gln Gln Arg Pro Leu Pro Leu  
 20 25 30  
 Gln Tyr Pro Gly Pro Asn Gly Phe Trp Val Lys Ala Ser Leu Pro Gln  
 35 40 45  
 Pro Gly Gly Pro Gly Phe Met Glu Tyr Arg Leu Glu Ser Arg Glu Ser  
 50 55 60  
 Ala Trp Gly Pro Arg Gln Leu Ser His Ala Pro Gly Ser Trp Ala Phe  
 65 70 75 80  
 Leu Gly Asp Pro Ser Gly Pro Trp Ala Leu Thr Arg Phe Ile Phe Gly  
 85 90 95  
 Arg Cys Phe Glu Gly Ala Tyr Arg Tyr Leu Glu Phe Thr Phe  
 100 105 110

<210> 471  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<400> 471  
 accggtgact acctgcagca ctggattgac atgggtaaaa agggcggcga ccgcatgccca  
 60  
 gaggtcttcc tgggtaactg gtcccgccgc ggcgacgatg gccgcttcct gtggccgngg  
 120

cttggcgaaa acttccccgt cctanagtgg atcatcgacc gcattgaagg caacgtagag  
 180  
 gccgaggaca cgggtggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt  
 240  
 gacttcgatg tcgacgacgt tcgcgccgca ctcgccgttg acccgaagga atgggaaggc  
 300  
 gatatgcaag acaacgccga gtacctgaac ttcttgggct cccgcgtgcc cgaggaagtg  
 360  
 tggaaccagt tccgcgcc  
 378

<210> 472

<211> 126

<212> PRT

<213> Homo sapiens

<400> 472

Thr	Gly	Asp	Tyr	Leu	Gln	His	Trp	Ile	Asp	Met	Gly	Lys	Lys	Gly	Gly
1				5				10						15	
Asp	Arg	Met	Pro	Glu	Val	Phe	Leu	Val	Asn	Trp	Phe	Arg	Arg	Gly	Asp
			20					25					30		
Asp	Gly	Arg	Phe	Leu	Trp	Pro	Xaa	Leu	Gly	Glu	Asn	Phe	Pro	Val	Leu
			35				40					45			
Xaa	Trp	Ile	Ile	Asp	Arg	Ile	Glu	Gly	Asn	Val	Glu	Ala	Glu	Asp	Thr
	50				55					60					
Val	Val	Gly	Arg	Thr	Ala	Arg	Ala	Glu	Asp	Ile	Asp	Leu	Gln	Gly	Leu
65				70					75					80	
Asp	Phe	Asp	Val	Asp	Asp	Val	Arg	Ala	Ala	Leu	Ala	Val	Asp	Pro	Lys
				85					90					95	
Glu	Trp	Glu	Gly	Asp	Met	Gln	Asp	Asn	Ala	Glu	Tyr	Leu	Asn	Phe	Leu
			100				105						110		
Gly	Ser	Arg	Val	Pro	Glu	Glu	Val	Trp	Asn	Gln	Phe	Arg	Ala		
			115				120						125		

<210> 473

<211> 339

<212> DNA

<213> Homo sapiens

<400> 473

accggttggt gggggaaggg acccatccca tgccacctgt cctagaaaat gtttcccctt  
 60  
 gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa  
 120  
 aggcaccaag taaaagaagg gggaagctgc caaaaccccc cctgccaaaa ctctcccacc  
 180  
 ctgcttccat ttccctctcc agggaacagg tgtacctccc ctctccctg tcctcctcag  
 240  
 atgccccagg ggctctctac ttcattcctg ccgacctgc caggagtggc ctcaggggta  
 300  
 gaggtccta gttggagaat ttgcttcgag gaaggtgaa  
 339

<210> 474

<211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 474  
 Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu  
 1 5 10 15  
 Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly  
 20 25 30  
 Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe  
 35 40 45  
 Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln  
 50 55 60  
 Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val  
 65 70 75 80  
 Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly  
 85 90 95  
 Glu

<210> 475  
 <211> 345  
 <212> DNA  
 <213> Homo sapiens

<400> 475  
 acgcgtgaag ggtccctcc aaactctgag cctccttcca agccttgctg ggagctcccc  
 60  
 agcgctgccc ggagaggcct ctctccagg cgggcttccc gcgccgatgt gaaggagagg  
 120  
 ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtccacagc cataatcccc  
 180  
 aatgctggga ctcttcagta aaggaagaga tggctttttc gttcatctgc ctttctgaaa  
 240  
 ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc  
 300  
 ctttgatgga tcttggttaga agtgggttgt tcattctggg gtttt  
 345

<210> 476  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 476  
 Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro  
 1 5 10 15  
 His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu  
 20 25 30  
 Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu  
 35 40 45  
 Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr  
 50 55 60  
 Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys

<400> 478																
Thr	Arg	Gly	Arg	Ala	Ser	Val	Leu	Lys	Glu	Met	Val	Asn	Gly	Thr	Leu	
1				5					10					15		
Ile	Asn	Gly	Trp	Asp	Ser	Pro	Glu	Val	Glu	Arg	Ala	Leu	Asp	Leu	Cys	
			20					25					30			
Met	Ala	Cys	Lys	Gly	Cys	Ala	Arg	Asp	Cys	Pro	Thr	Gly	Ile	Asp	Met	
		35					40					45				
Ala	Ser	Tyr	Arg	Ser	Thr	Val	Leu	Asp	Glu	Lys	Tyr	Arg	His	Arg	Leu	
	50					55					60					
Arg	Pro	Arg	Ser	His	Leu	Thr	Met	Gly	Leu	Leu	Pro	Met	Trp	Glu	Arg	
65					70					75					80	
Leu	Leu	Asn	Arg	Thr	Pro	Gly	Ala	Pro	Ser	Leu	Ala	Asn	Ala	Val	Leu	
				85					90					95		
Ser	Met	Pro	Val	Phe	Ala	Arg	Leu	Ala	Arg	Trp	Thr	Ala	Gly	Val	Asp	
		100						105					110			
Gln	Arg	Arg	Pro	Leu	Pro	Arg	Phe	Gln	Pro	Ser	Ala	Arg	Leu	Ala	Ser	
		115					120					125				
Pro	Gln	Ala	Ala	Pro	Val	Lys	Glu	Ile	Val	Ala	Asp					
	130					135					140					



<210> 479  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<400> 479  
 cgcgtggcca ttggccgggc gctggtgcgg caccgcgac tggtgattgc cgatgagccg  
 60  
 atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga gcgcctgcag  
 120  
 gcgcagtacg gctttgcctg cctgttcac tcccacgacc tggcagcggg ggaacgcac  
 180  
 gcccaccggg tggcggatgat gagcgagggc aggggtggtg aaatgggtgc ccgcgacgag  
 240  
 atcttcgacc gcccgacga cccctacacc cgcaagctgc tggccgccgc cagccccttg  
 300  
 gagaaacttg aaaacgggtg ctaccgcac cgccagggcc ccgtaccg  
 348

<210> 480  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 480  
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile  
 1 5 10 15  
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile  
 20 25 30  
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu  
 35 40 45  
 Phe Ile Ser His Asp Leu Ala Val Glu Arg Ile Ala His Arg Val  
 50 55 60  
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu  
 65 70 75 80  
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala  
 85 90 95  
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln  
 100 105 110  
 Gly Pro Val Pro  
 115

<210> 481  
 <211> 441  
 <212> DNA  
 <213> Homo sapiens

<400> 481  
 aagcttctga ctgtggcatt ctccctgctt aatatgtcct caatatcccc tacttactgg  
 60  
 gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tgggtgccttc  
 120  
 cctgccctgc cggcttgccg tggcttcctc agtgtagga ttaccatcac attgcatcat  
 180

gagagcagaa gaccatctcc atgtgactgc tgcccctgct cccagcaggg cccacaanca  
 240  
 cccagtccag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct  
 300  
 gcctcttctc ctgcaggacc aggaaaccgc tgccctgtcc ctgccccagg aaaccctcag  
 360  
 taaatcccca gtcatttgag tttccctca gcgccagaga ccaataacac atctccacca  
 420  
 acctgaaaaa ccttcacgcg t  
 441

<210> 482

<211> 120

<212> PRT

<213> Homo sapiens

<400> 482

Lys	Leu	Leu	Thr	Val	Ala	Phe	Ser	Leu	Leu	Asn	Met	Ser	Ser	Ile	Ser
1				5					10					15	
Pro	Thr	Tyr	Trp	Ala	Lys	Ser	Cys	Leu	Cys	Phe	Gly	Thr	Ser	Ser	Lys
			20					25					30		
Thr	Thr	Pro	Leu	Asp	Gly	Ala	Phe	Pro	Ala	Leu	Pro	Ala	Cys	Ala	Gly
			35				40					45			
Phe	Leu	Ser	Val	Arg	Ile	Thr	Ile	Thr	Leu	His	His	Glu	Ser	Arg	Arg
	50					55				60					
Pro	Ser	Pro	Cys	Asp	Cys	Cys	Pro	Cys	Ser	Gln	Gln	Gly	Pro	Gln	Xaa
65				70					75					80	
Pro	Ser	Pro	Gly	Pro	Gly	Ser	Arg	Trp	Val	Ala	Asp	Ala	Gln	Glu	Trp
			85					90					95		
Gly	Ser	Gly	Ser	Ala	Ser	Ser	Pro	Ala	Gly	Pro	Gly	Asn	Arg	Cys	Pro
			100					105					110		
Val	Pro	Ala	Pro	Gly	Asn	Pro	Gln								
			115				120								

<210> 483

<211> 330

<212> DNA

<213> Homo sapiens

<400> 483

acgcgttcat tccctgatgg ccacgcacga gctaacggag ggatggggcg aagggaaggc  
 60  
 caagggtgcc tcgaagacca aggagtgtgc agggcaggac ctcgttttta aggaatatcc  
 120  
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg  
 180  
 agcgtctgcc cagcccagca tccctgtccc cagccaggaa tatgtcttcg tggcatagag  
 240  
 ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggaggggctc  
 300  
 tcccgggacc ctgcagcgtg ggctggggccc  
 330

<210> 484

<211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 484  
 Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys  
 1 5 10 15  
 Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala  
 20 25 30  
 Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val  
 35 40 45  
 Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly  
 50 55 60  
 Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro  
 65 70 75 80  
 His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro  
 85 90 95

<210> 485  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<400> 485  
 acgcgtgctc gcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtagcc  
 60  
 gcccgattcg gcgacgccc cattcggccg gccggaatcg agaaggaatg cgtggacgta  
 120  
 cgggggatac caaaggaatc ttgtcgaggg cttcgcgccc ctgcagtggtg atcacctgta  
 180  
 cccgacggac gtggggaagc cgtcccgcga gctcacggga ctccgcgaca tcgatgtgcg  
 240  
 atacgatttg caccgtcgtc ggctgctgct gcgacacatg ctccgcgatc gcctcagcgg  
 300  
 tggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg  
 360  
 cattcccatt cctcggg  
 377

<210> 486  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 486  
 Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro  
 1 5 10 15  
 Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu  
 20 25 30  
 Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp  
 35 40 45  
 Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg  
 50 55 60  
 Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

65					70					75				80	
Pro	Arg	Ser	Pro	Gln	Arg	Trp	Phe	Pro	Thr	Ser	Ala	Gly	Thr	Trp	Arg
				85					90					95	
Arg	Val	Ala	Trp	Arg	Ser	Pro	Leu	Cys	Arg	His	Ser	His	Ser	Ser	
			100					105					110		

&lt;210&gt; 487

&lt;211&gt; 459

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 487

```

nnacgcgtaa gatcgattgt ggatcagcac cgatgctggt ccccccgcg ttgttggtgg
60
cgggtggttg tgtaaggagt gtgtgtgatg cgtgttggtg ttcctactga ggtaagaat
120
agtgaagttc gtgtggctgt gacgccggcg ggtgttcattg cgttggttg tctgggtcat
180
gagggtggtg ttcaggctgg tgctggtgtg ggttcgggta ttccggattc ggattttgtg
240
gggtgctggtg cgccgggttg ggggtgatgt gagtcggtgt ggggtgatgc tgatttggtg
300
ttgaagggtga aggagcctgt tgcggaggag tatgggcggt tgcattgaggg tttggttctt
360
tttacgtatc ttcatttggtc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
420
gtgacgtcga ttgcgtatga gacggtggag ttggccgat
459

```

&lt;210&gt; 488

&lt;211&gt; 124

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 488

Met	Arg	Val	Gly	Val	Pro	Thr	Glu	Val	Lys	Asn	Ser	Glu	Phe	Arg	Val
1				5					10					15	
Ala	Val	Thr	Pro	Ala	Gly	Val	His	Ala	Leu	Val	Gly	Arg	Gly	His	Glu
			20					25					30		
Val	Leu	Val	Gln	Ala	Gly	Ala	Gly	Val	Gly	Ser	Gly	Ile	Pro	Asp	Ser
			35				40					45			
Asp	Phe	Val	Gly	Ala	Gly	Ala	Arg	Val	Val	Gly	Asp	Val	Glu	Ser	Val
			50			55				60					
Trp	Gly	Asp	Ala	Asp	Leu	Val	Leu	Lys	Val	Lys	Glu	Pro	Val	Ala	Glu
65					70					75				80	
Glu	Tyr	Gly	Arg	Leu	His	Glu	Gly	Leu	Val	Leu	Phe	Thr	Tyr	Leu	His
			85					90					95		
Leu	Ala	Ala	Asp	Glu	Ala	Leu	Thr	Arg	Glu	Leu	Leu	Gly	Arg	Gly	Val
			100					105					110		
Thr	Ser	Ile	Ala	Tyr	Glu	Thr	Val	Glu	Leu	Ala	Asp				
			115				120								

&lt;210&gt; 489

&lt;211&gt; 542

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 489

nacgcgtttg gcgtactgag tgcggtggtg gatggcgacg acagtggcaa gccgctgctc  
 60  
 aaccagcacg gttgctacaa agtgcgcttt ccatttacct gcgatcaaaa gccagcact  
 120  
 cgggggttcgg catggctgcg caggggtgctg ttgtctgccg gttccagcca tggcatgcac  
 180  
 ttcccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tggggggcga ccccgaccgg  
 240  
 ccgattatcg ttggctgcgt accaaactcg gaaaccccg gcatggctcg tgagcgtaac  
 300  
 gccaccacga gcggcttctc caccggccga gggcacttcc tggcgatgga agaccacccc  
 360  
 ggggctgccc atctgaagct ggggtgcgct ggcggaaca gcgtcttcac actgggcaat  
 420  
 ggcaaagtcg ccggcgcgca actgcgaccc aacgccccac atgcaattga catcgtcttc  
 480  
 gctcaaacac gaagtgcccg gcgtgtactc attgtcgatg ggcaccgggg acccgggcggc  
 540  
 cg  
 542

&lt;210&gt; 490

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 490

Xaa	Ala	Phe	Gly	Val	Leu	Ser	Ala	Val	Val	Asp	Gly	Asp	Asp	Ser	Gly	1	5	10	15
Lys	Pro	Leu	Leu	Asn	Gln	His	Gly	Cys	Tyr	Lys	Val	Arg	Phe	Pro	Phe	20	25	30	
Thr	Arg	Asp	Gln	Lys	Pro	Ser	Thr	Arg	Gly	Ser	Ala	Trp	Leu	Arg	Arg	35	40	45	
Val	Ser	Leu	Ser	Ala	Gly	Ser	Ser	His	Gly	Met	His	Phe	Pro	Leu	Leu	50	55	60	
Lys	Gly	Ser	Glu	Val	Leu	Val	Ser	Phe	Leu	Gly	Gly	Asp	Pro	Asp	Arg	65	70	75	80
Pro	Ile	Ile	Val	Gly	Cys	Val	Pro	Asn	Ser	Glu	Thr	Pro	Ser	Met	Val	85	90	95	
Val	Glu	Arg	Asn	Ala	Thr	Gln	Ser	Gly	Phe	Ser	Thr	Ala	Gly	Gly	His	100	105	110	
Phe	Leu	Ala	Met	Glu	Asp	His	Pro	Gly	Ala	Ala	His	Leu	Lys	Leu	Gly	115	120	125	
Ala	Pro	Gly	Gly	Asn	Ser	Val	Phe	Thr	Leu	Gly	Asn	Gly	Lys	Val	Ala	130	135	140	
Gly	Ala	Gln	Leu	Arg	Thr	Asn	Ala	Pro	His	Ala	Ile	Asp	Ile	Val	Phe	145	150	155	160
Ala	Gln	Thr	Arg	Ser	Ala	Arg	Arg	Val	Leu	Ile	Val	Asp	Gly	His	Arg	165	170	175	
Gly	Pro	Gly	Gly																

180

<210> 491  
 <211> 825  
 <212> DNA  
 <213> Homo sapiens

<400> 491  
 nacgcgtcga ggcgacggtc ggcgccgtca tggcgactgt tctcgagggc acatgggaac  
 60  
 gcatcggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg  
 120  
 tgggcggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg  
 180  
 aactcatcgg cgggcccgtc ggcgcgggtg ccgcgatgca cggaggggtca atcgaattgg  
 240  
 tcgacgtgtc ggtcgggtgac gaagagcgca gagtcgacgt caccatgaag ggagcatgcc  
 300  
 gaggttgccc ggcagccatc agaccctaca tcagcgcctg gaacatcaac tgagtctgcg  
 360  
 nattgcgcga gccgggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg  
 420  
 acgagcacct ccacgacgag gccaagccac tcgtagacgc attcctcctc ggcatccaat  
 480  
 tcctccccggg ccgcccgagc gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg  
 540  
 gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgcgt catcacaggg  
 600  
 ttcatggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg  
 660  
 tcttcccagc gcgccgcgac atcctcggcg tcatggtcga catggaattg cgcgtcagct  
 720  
 gagtcgtcgt cacgataggc gctgggcagg atcaatcgac gcacctcgtc gtcctcctgg  
 780  
 agtcacagaaa actggctctc ccaaaaagcg aacgggtccc cctcc  
 825

<210> 492  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<400> 492  
 Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg  
 1 5 10 15  
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg  
 20 25 30  
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser  
 35 40 45  
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro  
 50 55

<210> 493  
 <211> 863

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 493

nacgcgttcc aacctcgtca aaacggctat cgcaggaaat gaccccaact ggggtcgcac  
 60  
 cctcgcggcg atcggatgtg ttctgagaa tatagtctcc ttcgatcccg accaggtgga  
 120  
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct  
 180  
 cgtcgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga  
 240  
 agctgcggta tggactaatg atctgaccca ccaatacgtc gaagagaata gcgcgtatac  
 300  
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa  
 360  
 tctgaggtcc tggtagaagc gctgccttgg atcaggcggt ttcaggggcg cactgtcgtc  
 420  
 gtgaaatatg gcggcaacgc gatggttgat cccggtctgc agcaggcctt cgccgacgac  
 480  
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacgggtg tggccctcag  
 540  
 atcaatgcca tgcttgctga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg  
 600  
 acatctccgg aggtcatgga ggttgtccgg atggtgctcg tcgggcagggt gggccgtcag  
 660  
 ctcgtaacc gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt  
 720  
 ggcctttttt cggcccggaa gtcgcgggta attgttgatg gcgagcaa at agacatgggt  
 780  
 ttagtgggag acatcgttga cgtcaacatc gatctcgta tctctatgct tgatcgcggt  
 840  
 cagattccgg tcattgcacc ggt  
 863

&lt;210&gt; 494

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 494

Met Thr Leu Ala Leu Asp Ile Pro Leu Asn Asp Ser Gln Phe Ser Ala  
 1 5 10 15  
 Gln Arg Lys Ser Glu Val Leu Val Glu Ala Leu Pro Trp Ile Arg Arg  
 20 25 30  
 Phe Gln Gly Arg Thr Val Val Val Lys Tyr Gly Gly Asn Ala Met Val  
 35 40 45  
 Asp Pro Gly Leu Gln Gln Ala Phe Ala Asp Asp Ile Val Phe Met Ala  
 50 55 60  
 Ser Val Gly Ile Arg Pro Ile Val Val His Gly Gly Gly Pro Gln Ile  
 65 70 75 80  
 Asn Ala Met Leu Ala Glu Ser Ala Thr Pro Val Glu Phe Arg Asn Gly  
 85 90 95  
 Leu Arg Val Thr Ser Pro Glu Val Met Glu Val Val Arg Met Val Leu

```

      100              105              110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala
      115              120              125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala
      130              135              140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu
145              150              155              160
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu
      165              170              175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro
      180              185

```

<210> 495  
 <211> 514  
 <212> DNA  
 <213> Homo sapiens

```

<400> 495
ggcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
60
tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
120
cgttggccga tccaccggga tcccccgcc ttcgatgacc ttgagcccga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
240
ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcgggtt ttcgccggtg tcggtgagcg taccgcgag
360
ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcgccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggccaactg ctgtgggacc ttgg
514

```

<210> 496  
 <211> 171  
 <212> PRT  
 <213> Homo sapiens

```

<400> 496
Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr
1      5      10      15
Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser
      20      25      30
Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro
      35      40      45
Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly
      50      55      60
Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
65      70      75      80
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu

```



```

      85              90              95
Met Ile Tyr Arg Ile Ala His Asn Phe Gly Gly Thr Ser Val Phe Ala
      100              105              110
Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Leu Ile Asn Glu Met
      115              120              125
Asp Glu Ala Gly Val Leu Lys Asp Thr Ala Leu Val Phe Gly Gln Met
      130              135              140
Asp Glu Pro Pro Gly Thr Arg Tyr Glu Leu Ser Arg Trp Gln Pro Cys
      145              150              155              160
Gly Pro Cys Leu Val Asn Cys Cys Gly Thr Leu
      165              170

```

<210> 497  
 <211> 662  
 <212> DNA  
 <213> Homo sapiens

```

<400> 497
acgcgtcctg ggatctcaac cccagcagtc tggcttggtt ctcattccca caatttcctg
60
ggttcaccca agcagcgaaa actgccagga tgaatgagga aaaaaccag cccacaaaac
120
gagacacacg ctggcgggga gagacgcagc agagctcctt cctgtctgtg gactcggagc
180
aaagacgtgg ggccccatct tttgtgtttt cctcaagcgg ggaaagaatg gactgtttgc
240
atgcttcgtg ccacacgccc gcggtgatcc cagccagggc cccgagcgca gaggcggagc
300
tgtgtcagc acaggcctg gacctcccc ggcaggcacc tgtggggggt gcagcccccg
360
ggaaggaggc aactgcctca cttaacatcc tccgctgcaa ggtggtggcg ccgagaggcg
420
tgtctgtgaa gacaggtacc aggatggcag gaccgcacg cctcttccca cacctgtcag
480
cttcggaagc atctctcgag gactctggtc ccaggatgtc tcccaggaca agccagtctg
540
cctcttcctc ctacttctgc tgtagcctgg gaccagacct ggccaaggtc agccagcggg
600
gagggccgag gtctgagctc tcgtcctgcc gtggcccccg cgatggcttg ggtgcaagc
660
tt
662

```

<210> 498  
 <211> 191  
 <212> PRT  
 <213> Homo sapiens

```

<400> 498
Met Asn Glu Glu Lys Thr Gln Pro His Lys Arg Asp Thr Arg Trp Arg
1      5      10      15
Gly Glu Thr Gln Ser Ser Phe Leu Ser Val Asp Ser Glu Gln Arg
20     25     30
Arg Gly Ala Pro Ser Phe Val Phe Ser Ser Ser Gly Glu Arg Met Asp

```

```

      35          40          45
Cys Leu His Ala Ser Cys His Thr Pro Ala Val Ile Pro Ala Arg Ala
      50          55          60
Pro Ser Ala Glu Ala Glu Leu Cys Ser Ala Gln Ala Trp Asp Leu Pro
65      70      75      80
Arg Gln Ala Pro Val Gly Gly Ala Ala Pro Gly Lys Glu Ala Thr Ala
      85          90          95
Ser Leu Asn Ile Leu Arg Cys Lys Val Val Ala Pro Arg Gly Val Ser
      100      105      110
Val Lys Thr Gly Thr Arg Met Ala Gly Pro Ala Arg Leu Phe Pro His
      115      120      125
Leu Ser Ala Ser Glu Ala Ser Leu Glu Asp Ser Gly Pro Arg Met Ser
      130      135      140
Pro Arg Thr Ser Gln Ser Ala Ser Ser Ser Tyr Phe Cys Cys Ser Leu
145      150      155      160
Gly Pro Asp Leu Ala Lys Val Ser Gln Arg Gly Gly Pro Arg Ser Glu
      165      170      175
Leu Ser Ser Cys Arg Gly Pro Arg Asp Gly Leu Gly Cys Lys Leu
      180      185      190

```

&lt;210&gt; 499

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 499

```

acgcgtgaag ggtgggcagt gttgagctga gtgagccctc ctccttgcaa tgctggagcc
60
ctgccttctg cctgaccctc tggcttccta agcagtctat acgtgagaag ccctttcttc
120
aagtgaagc ttctgagctc actacgagag cactggagct ggaacctctc tgggttcaaa
180
tcttcaactg gggggttgga ggaggttact tcacttctca aaacctcaat ttccttatct
240
gcaaaatggg gtaataggag cccctcttca tcaatgcttg gagggaaatgc ctggcacagt
300
agggcagtta ccgtcatgga gaacagaaaag gccccgagct atcctggatg tggtgagaat
360
gggtcctgga tctgcctgc tcggcctttt cattctcttc ttcacctaca ggctcccaca
420
aagggcctct gaaaacacag ggtg
444

```

&lt;210&gt; 500

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 500

```

Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
  1          5          10          15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
      20      25      30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn

```

```

      35              40              45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe
      50              55              60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu
65              70              75              80
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr
      85              90              95
Gln Leu Asn Thr Ala His Pro Ser Arg
      100              105

<210> 501
<211> 800
<212> DNA
<213> Homo sapiens

<400> 501
agatctgatc cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
60
ggtactcctt attcaatgag aggcttgagg tgagaccgcg catgcggcgc gtggatcgca
120
tggtgttagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
180
gaccttgtag tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
240
gaagtttatt ctcccatgga tgatgtggc ttcccggtca aagctgagga gtttgtggtg
300
ctttctcagg aaccttctgt cacggaaacc attgcacca aaattgcaag acctttcata
360
gaggccctca agagtattga gtatctggag gaggatgccc agaagtccgc acaggagggg
420
gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
480
gaaccatccc aattagagga gctagctgac ttcattggagc agcttacacc aattgaaaaa
540
tatgctttaa attacctgga atcttgaggc agggcctgag agagcacgct gcgcctgact
600
tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
660
tgcagttcga ctcaggtatg cggcagttgg gggcgtggcc cgtgcgggag ctgcactggc
720
cctggatgat gaggcgctct tgatgtgatt cgtttcccag ggaagttgga agctttagct
780
atcttgcttc agaaactgaa
800

<210> 502
<211> 103
<212> PRT
<213> Homo sapiens

<400> 502
Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
1              5              10              15
Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

```

      20      25      30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
      35      40      45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
      50      55      60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
65      70      75      80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
      85      90      95
Ala Leu Asn Tyr Leu Glu Ser
      100

```

<210> 503  
 <211> 538  
 <212> DNA  
 <213> Homo sapiens

```

<400> 503
nnacgcgttg tcgtctctcc gatcattgat tttgttgat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcataaggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttgcagct attggaaggg gaagggtccc
180
cgtcagggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga
240
agggaagcga aactgggtcat ccggtgggta gacatcactc agcttgagaa gaatgcccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacggtcca gtgagcattt cttctctgta
360
ttcctcaaca tcaacgagac cttcaagta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggccct tcacgcgt
538

```

<210> 504  
 <211> 179  
 <212> PRT  
 <213> Homo sapiens

```

<400> 504
Xaa Arg Val Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
1      5      10      15
Asp Val Lys Glu Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
20      25      30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
35      40      45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
50      55      60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
65      70      75      80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```

```

      85              90              95
Lys Asn Ala Pro Leu Leu Leu Pro Asp Val Ile Lys Val Ser Thr Arg
      100              105              110
Ser Ser Glu His Phe Phe Ser Val Phe Leu Asn Ile Asn Glu Thr Phe
      115              120              125
Lys Leu Met Glu Gln Leu Ala Asn Ile Ala Met Arg Gln Leu Leu Asp
      130              135              140
Asn Glu Gly Phe Glu Gln Asp Arg Ser Leu Pro Lys Leu Lys Arg Lys
      145              150              155              160
Ser Pro Lys Lys Val Ser Ala Leu Lys Arg Asp Leu Asp Ala Trp Ala
      165              170              175
Leu His Ala

```

<210> 505  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

```

<400> 505
gtgcacgaca ccgaacggta cgaacgtatc tcccaggcac gtcgcgagga acagcaggcc
60
atgctcggct acgacngctc aagaacctgt cgcacgacct tgctcaccgg gcagctggac
120
gacccctcca cgactccttg cggacgctgc gacgtctgtg ctggcccgtg gtactcagtc
180
gaggtcgatc agtcagccgc tgtgagagcc gtccaatccc tcaaccgggt gggagttccg
240
gtggaaccac gcgccgcctg gcccgagggt atggacgccc tccaggttgc gctcaagggt
300
cgcatcagtg ccgaggagat cgctgcagag ggccgcgtca tcgccagact ctccgatctg
360
ggttggggag gggcgctgcg c
381

```

<210> 506  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

```

<400> 506
Val His Asp Thr Glu Arg Tyr Glu Arg Ile Ser Gln Ala Arg Arg Glu
1      5      10      15
Glu Gln Gln Ala Met Leu Gly Tyr Asp Xaa Ser Arg Thr Cys Arg Met
20     25     30
Thr Leu Leu Thr Gly Gln Leu Asp Asp Pro Ser Thr Thr Pro Cys Gly
35     40     45
Arg Cys Asp Val Cys Ala Gly Pro Trp Tyr Ser Val Glu Val Asp Gln
50     55     60
Ser Ala Ala Val Arg Ala Val Gln Ser Leu Asn Arg Val Gly Val Pro
65     70     75     80
Val Glu Pro Arg Ala Ala Trp Pro Ala Gly Met Asp Ala Leu Gln Val
85     90     95
Ala Leu Lys Gly Arg Ile Ser Ala Glu Glu Ile Ala Ala Glu Gly Arg

```

100                      105                      110  
 Val Ile Ala Arg Leu Ser Asp Leu Gly Trp Gly Gly Ala Leu Arg  
 115                      120                      125

<210> 507

<211> 499

<212> DNA

<213> Homo sapiens

<400> 507

gccggcgtgt tcaacctcat ggtgtgggcc ttcattaccg acgtcatcga tgcccaggag  
 60  
 gtcattgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgc aaa  
 120  
 cttgcccagg ccattgccgg tggaatcggc ggagccatgc tgacgatgat cggctaccag  
 180  
 tcctcctccc aagggtggtgc cgttcagtcg gagtcgctcg tcaatcacct gtacacgctc  
 240  
 gccaccgcca tcccgcagat ctgctgcctc ggcgctgccc tgctcatgct gggctaccgc  
 300  
 ctcacccgcg acaaggtggt cgccaacgcc gacgagttgg ctgctcgcca cgcagtacag  
 360  
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgctca tgcggatcac  
 420  
 cgaccatttg acaacctcgc cgggtatcca attgaaaatt gacaagcgat ggggtgcctc  
 480  
 cgtcacattt gtgacgcgt  
 499

<210> 508

<211> 125

<212> PRT

<213> Homo sapiens

<400> 508

Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile  
 1                      5                      10                      15  
 Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr  
 20                      25                      30  
 Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly  
 35                      40                      45  
 Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln  
 50                      55                      60  
 Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu  
 65                      70                      75                      80  
 Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met  
 85                      90                      95  
 Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu  
 100                      105                      110  
 Leu Ala Arg Arg His Ala Val Gln Ala Glu Gln Asn Ser  
 115                      120                      125

<210> 509

<211> 360

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 509

ttggccatgg atttggtctg caagttcagt cccaaagatg tcacgctcta tctaattggac  
 60  
 ttcgggacca atggtgtggc accactaggc caattaccac aggtggccga caccttgctt  
 120  
 ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg  
 180  
 cgtaagaagc tcttggtccga ctacggtggt ggtacactag agctctaccg tcaggctagg  
 240  
 ggtcagcaag agccggccat cgtcatcctg ctggacagtt atgagtccat gaaggaagag  
 300  
 gcctatgaag cggagctctt cacgctcttg gtgcggatct cccgggaagg tctcagcatc  
 360

&lt;210&gt; 510

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 510

Leu Ala Met Asp Leu Ala Arg Lys Phe Ser Pro Lys Asp Val Thr Leu  
 1 5 10 15  
 Tyr Leu Met Asp Phe Gly Thr Asn Gly Val Ala Pro Leu Gly Gln Leu  
 20 25 30  
 Pro Gln Val Ala Asp Thr Leu Leu Leu Asp His Thr Glu Lys Ile Ala  
 35 40 45  
 Lys Phe Val Arg Ile Met Glu Arg Glu Leu Asn Arg Arg Lys Lys Leu  
 50 55 60  
 Leu Ser Asp Tyr Gly Val Gly Thr Leu Glu Leu Tyr Arg Gln Ala Ser  
 65 70 75 80  
 Gly Gln Gln Glu Pro Ala Ile Val Ile Leu Leu Asp Ser Tyr Glu Ser  
 85 90 95  
 Met Lys Glu Glu Ala Tyr Glu Ala Glu Leu Phe Thr Leu Leu Val Arg  
 100 105 110  
 Ile Ser Arg Glu Gly Leu Ser Ile  
 115 120

&lt;210&gt; 511

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 511

ntcgcaacc gcggctatgc ggtgctccag cccaatttcc gcggatcggg cggttatggc  
 60  
 actgcgttcg gcgatgccgg catcggccag atcgggcgca agatgcagga cgatctcgac  
 120  
 gacgggatgg actggctggt caaggagggc atcgtcgaca agggccgggt gtgcatcgtc  
 180  
 ggggcctcct atggcggcta tgccgcgatg tggggcgcca tccgcaatcc cgaacgctat  
 240

cgctgcgcgg cgagcctggc gggggttgcc gattaaggcc atgctcaaataa acccggcg  
 300  
 ctatctcgac aaggaggcgg gcaagcgctg gccgccccgn tcaaccggcg aaccgaatt  
 360  
 c  
 361

<210> 512  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 512  
 Xaa Ala Asn Arg Gly Tyr Ala Val Leu Gln Pro Asn Phe Arg Gly Ser  
 1 5 10 15  
 Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly  
 20 25 30  
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys  
 35 40 45  
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr  
 50 55 60  
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr  
 65 70 75 80  
 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp  
 85 90

<210> 513  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

<400> 513  
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 ccagaaaatc tgattcaaga gatcaaacga cgccagactt gtgatttgac catagtgtca  
 120  
 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc  
 180  
 aaaatggtgt cttcttatgt gggtgaaaat gcactgtttg agaagcaatt attacaaggt  
 240  
 gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcggc  
 300  
 gcgggaattc ctgccttttt cacagcaacg ggtgtaggta cacctattgg tgagggtaaa  
 360  
 gacacgcgt  
 369

<210> 514  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 514  
 Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly



```

1           5           10           15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
20           25           30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
35           40           45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
50           55           60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
65           70           75           80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
85           90           95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
100          105          110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
115          120

```

&lt;210&gt; 515

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 515

```

gcgtgggacg agaaggccgc cggcaactgc gcgatcgact acgggttcca ccagatcctc
60
tccgacgtgc aggactcgtc gctgaccgcg atggacgagc tgatcaccga gggcgtgaca
120
tccttcaagc tcttcgtggc ctacaagggc gtcttctctc cggacgacgg gcagatcctg
180
cgggcggttc agaagggcgc cgacaacggc gcgatgatga tgatgcacgc cgagaacggc
240
gcatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
300
cacggcatca gccggccgtg gcaggccgag gaggaggcca cccaccgcgc gatcatgatc
360
gccgacctga ccggtgcgcc gttgtac
387

```

&lt;210&gt; 516

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 516

```

Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
1           5           10           15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
20           25           30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
35           40           45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
50           55           60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
65           70           75           80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

```

```

      85          90          95
Thr Pro Tyr Tyr His Gly Ile Ser Arg Pro Trp Gln Ala Glu Glu Glu
      100          105          110
Ala Thr His Arg Ala Ile Met Ile Ala Asp Leu Thr Gly Ala Pro Leu
      115          120          125
Tyr

```

<210> 517  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

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<400> 517
acgcgtgaag ggctggtggg caggccttgc gccccctctg gggacagctc tcctccaccc
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agacccttc gggccaacag tggggagggg ctgccgtctg agccactgtt cgcacagggg
120
attcgcgagt tccgggggag ctggggactg agctgcgggc ctctggggct ggggctcttc
180
tccgaggttg gaggcagctt tagaaacttg agacccttag ctggagaggg cagaaggggt
240
ccctgagctt cccaggaga aggggggcca atttggagct tgcttttcac ctgagatgag
300
gaatgggggt ggccaggccg agagcccagt ggggcatccc cagcacccat gaacatgcta
360
aggaagggga ggggccc
377

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<210> 518  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

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<400> 518
Met Phe Met Gly Ala Gly Asp Ala Pro Leu Gly Ser Arg Pro Gly His
1      5      10      15
Pro His Ser Ser Ser Gln Val Lys Ser Lys Leu Gln Ile Gly Pro Pro
20     25     30
Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly
35     40     45
Leu Lys Phe Leu Lys Leu Pro Pro Thr Ser Glu Lys Ser Pro Ser Pro
50     55     60
Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro
65     70     75     80
Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg
85     90     95
Arg Gly Leu Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu
100    105    110
Pro Thr Ser Pro Ser Arg
115

```

<210> 519  
 <211> 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 519

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60  
agaatttaaa ttattataaa ggaacctttt ctgcaactct gaaaaatgtt agaatatcca  
120  
aagaaattga taattttcta ggaaaacatg acttaccaaa attaactcta gaaaagaatc  
180  
gatacacatc agtaacaaca gaagttgaga aagtagttaa catattgcca aacctggaat  
240  
tcattgattga attctttgag atctactgtg agtacatact ctgcctctgt tcagctgttc  
300  
cagaacttaa g  
311

&lt;210&gt; 520

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 520

Met	Arg	Gly	Lys	Tyr	Gln	Ile	Leu	Lys	Asn	Leu	Asn	Tyr	Tyr	Lys	Gly
1				5					10					15	
Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
			20					25					30		
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
		35					40					45			
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50					55					60				
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65					70				75					80	
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85						90						

&lt;210&gt; 521

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 521

nnngatgcca cgccggtcta cggaatctcc accggcttcg gcgcgcttgc ccgcccgcac  
60  
attccagaag agatgcgcgc gcagctgcag ctgtccctgg tgcgctccca cgcggccggc  
120  
accggccctg aggtggaaga agaagtaatt cgcgcgctca tgctgctgcg cctatccacc  
180  
ctgtgtaccg gccgtaccgg cgtgcgcccc gtggtggtag aaacttatgc caaggcgctc  
240  
aacgccggca tcgtgccggg ggtgcgcgaa tacgggtcgc tgggctgctc cggcgacttg  
300  
gccccgctgg ctactgcgc cctagcgctg ttgggtgagg gtgaggtacg cn  
352

<210> 522  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 522  
 Xaa Asp Ala Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly Ala Leu  
 1 5 10 15  
 Ala Arg Arg His Ile Pro Glu Glu Met Arg Ala Gln Leu Gln Leu Ser  
 20 25 30  
 Leu Val Arg Ser His Ala Ala Gly Thr Gly Pro Glu Val Glu Glu Glu  
 35 40 45  
 Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly  
 50 55 60  
 Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu  
 65 70 75 80  
 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys  
 85 90 95  
 Ser Gly Asp Leu Ala Pro Leu Ala His Cys Ala Leu Ala Leu Leu Gly  
 100 105 110  
 Glu Gly Glu Val Arg  
 115

<210> 523  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 523  
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 60  
 tcagagccac caagctgcgg caccatctaa ggagaacatg tcccctggag gtcctgttag  
 120  
 aagctcctgg ttgagaaggc cctgaagctg ggtggcatca atgtccagcc tctgctgagc  
 180  
 atatctgttg aaaatgcttt gttgggagcc atgttctgaa gggcttccct tcattctgag  
 240  
 gttgaaatgg ctgctcaggt gcctgtcact gtctggcatt ttcaggaaga ttcggagcaa  
 300  
 gaactccgct gattttctcc gtgtctgtgc aaccacaaca tagttcccag ggctcagatg  
 360  
 gtaagtcagtg gtgaagttgc ggcggaattt attatttgag ctttggacag tgtttctgaa  
 420  
 cgaggaaaaa aacacgggtg gaaatttctc ccggaaccgc tgtgagccag ccagaatcac  
 480  
 ttggaaatcg agtggaatt ttgcattctc tgctttcaaa tttgatgggtg tgacagcaac  
 540  
 tgtgacgcac acgacaacat tggcgcttct cattggctct tgcacagaga agttgaattg  
 600  
 agcatcatctt ccgggtcctc ctggcggtgtt tcctagaatc attgcttctt aaacattatt  
 660  
 tgggaccatc cttcgtggag tgtgtttcca tgg  
 693

<210> 524  
 <211> 193  
 <212> PRT  
 <213> Homo sapiens

<400> 524  
 Met Ile Leu Gly Asn Thr Pro Gly Gly Pro Gly Asn Asp Ala Gln Phe  
 1 5 10 15  
 Asn Phe Ser Val Gln Glu Pro Met Glu Gly Thr Asn Val Val Val Cys  
 20 25 30  
 Val Thr Val Ala Val Thr Pro Ser Asn Leu Lys Ala Glu Asp Ala Lys  
 35 40 45  
 Phe Pro Leu Asp Phe Gln Val Ile Leu Ala Gly Ser Gln Arg Phe Arg  
 50 55 60  
 Glu Lys Phe Pro Pro Val Phe Phe Ser Ser Phe Arg Asn Thr Val Gln  
 65 70 75 80  
 Ser Ser Asn Asn Lys Phe Arg Arg Asn Phe Thr Met Thr Tyr His Leu  
 85 90 95  
 Ser Pro Gly Asn Tyr Val Val Val Ala Gln Thr Arg Arg Lys Ser Ala  
 100 105 110  
 Glu Phe Leu Leu Arg Ile Phe Leu Lys Met Pro Asp Ser Asp Arg His  
 115 120 125  
 Leu Ser Ser His Phe Asn Leu Arg Met Lys Gly Ser Pro Ser Glu His  
 130 135 140  
 Gly Ser Gln Gln Ser Ile Phe Asn Arg Tyr Ala Gln Gln Arg Leu Asp  
 145 150 155 160  
 Ile Asp Ala Thr Gln Leu Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr  
 165 170 175  
 Gly Pro Pro Gly Asp Met Phe Ser Leu Asp Gly Ala Ala Ala Trp Trp  
 180 185 190  
 Leu

<210> 525  
 <211> 1101  
 <212> DNA  
 <213> Homo sapiens

<400> 525  
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 120  
 gtccctaccga gaccgatccg cagcggtttg cccgggtcgc cctattgcat cgggagcccc  
 180  
 cgagcaccgg cgaaggactg gcgggtgggg tagggaggtg gcggcggcgg catggcgagg  
 240  
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 300  
 cagtttcagt tcgccgatgg gaaacccgga gaccaaattc ttgattggca gtatggagtt  
 360  
 actcaggcct tccctcacac agaggaggag gtggaagttg attcacacgc gtacagccac  
 420

aggtggaaaa gaaacttggg ctttctcaag gcggtagaca cgaaccgagc aagcgtcggc  
 480  
 caagactctc ttgagcccag aagcttcaca gacctgctgc tggatgatgg gcaggacaat  
 540  
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 660  
 aagattcatg gaattattgtc caatactcat cggcaagctg caagagtga tctgtccttc  
 720  
 gattttccat tttatggcca cttcctacgt gaaatcactg tggcaaccgg gggtttcata  
 780  
 tacactggag aagtcgtaca tcgaatgcta acagccacac agtacatagc acctttaatg  
 840  
 gcaaatttcg atcccagtgt atccagaaat tcaactgtca gatattttga taatggcaca  
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 1020  
 gtcttggtca cacagataag ttcaaccaat catccagtga aagtcggact gtccgatgca  
 1080  
 tttgtcgttg tccacaggat c  
 1101

&lt;210&gt; 526

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 526

Met	Ala	Arg	Phe	Pro	Lys	Ala	Asp	Leu	Ala	Ala	Gly	Val	Met	Leu
1				5				10					15	
Leu	Cys	His	Phe	Thr	Asp	Gln	Phe	Gln	Phe	Ala	Asp	Gly	Lys	Pro
		20				25						30		
Gly	Asp	Gln	Ile	Leu	Asp	Trp	Gln	Tyr	Gly	Val	Thr	Gln	Ala	Phe
		35				40						45		
His	Thr	Glu	Glu	Glu	Val	Glu	Val	Asp	Ser	His	Ala	Tyr	Ser	His
		50				55						60		
Trp	Lys	Arg	Asn	Leu	Asp	Phe	Leu	Lys	Ala	Val	Asp	Thr	Asn	Arg
				70						75				80
Ser	Val	Gly	Gln	Asp	Ser	Leu	Glu	Pro	Arg	Ser	Phe	Thr	Asp	Leu
			85					90					95	
Leu	Asp	Asp	Gly	Gln	Asp	Asn	Asn	Thr	Gln	Ile	Glu	Glu	Asp	Thr
			100					105					110	
His	Asn	Tyr	Tyr	Ile	Ser	Arg	Ile	Tyr	Gly	Pro	Ser	Asp	Ser	Ala
		115				120						125		
Arg	Asp	Leu	Trp	Val	Asn	Ile	Asp	Gln	Met	Glu	Lys	Asp	Lys	Val
		130				135						140		
Ile	His	Gly	Ile	Leu	Ser	Asn	Thr	His	Arg	Gln	Ala	Ala	Arg	Val
				150						155				160
Leu	Ser	Phe	Asp	Phe	Pro	Phe	Tyr	Gly	His	Phe	Leu	Arg	Glu	Ile
				165					170				175	
Val	Ala	Thr	Gly	Gly	Phe	Ile	Tyr	Thr	Gly	Glu	Val	Val	His	Arg
														Met

180	185	190
Leu Thr Ala Thr Gln Tyr Ile	Ala Pro Leu Met Ala Asn Phe Asp Pro	
195	200	205
Ser Val Ser Arg Asn Ser Thr	Val Arg Tyr Phe Asp Asn Gly Thr Ala	
210	215	220
Leu Val Val Gln Trp Asp His	Val His Leu Gln Asp Asn Tyr Asn Leu	
225	230	235
Gly Ser Phe Thr Phe Gln Ala Thr	Leu Leu Met Asp Gly Arg Ile Ile	
245	250	255
Phe Gly Tyr Lys Glu Ile Pro Val	Leu Val Thr Gln Ile Ser Ser Thr	
260	265	270
Asn His Pro Val Lys Val Gly Leu	Ser Asp Ala Phe Val Val Val His	
275	280	285
Arg Ile		
290		

&lt;210&gt; 527

&lt;211&gt; 5343

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 527

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nngtgccgtg tgctcctcac attcacgcag actgagactg agctgcccga ggaagagtgt
60
gaaggcccca agctgcccac cgaacggccc tgcttctctgg aagcatgcga tgagagcccc
120
gcctcccag agctagacat ccctctccct gaggacagtg agacggctta cgactgggag
180
tacgctgggt tcaccccttg cacagcaaca tgcttgggag gccatcaaga agccatagca
240
gtgtgcttac atatccagac ccagcagaca gtcaatgaca gcttgtgtga tatggtccac
300
cgctctccag ccattgagcca ggctgttaac acagagccct gtccccccag gtggcatgtg
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480
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540
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780
gcagccaaag gtcggcgcat cccctcagt gagatgatgt gcagggatct accagggtc
840
cctcttgtaa gatcttgcca gatgcctgag tgcagtaaaa tcaaatcaga gatgaagaca
900
aaacttgggtg agcaggggtc gcagatctc agtgtccaga gagtctacat tcagacaagg
960

```

gaagagaagc gtattaacct gaccattggc agcagagcct atttgctgcc caacacatcc  
1020  
gtgattatta agtgccccgt gcgacgattc cagaaatctc tgatccagtg ggagaaggat  
1080  
ggccgttgcc tgcagaactc caaacggctt ggcacacca agtcaggctc actaaaaatc  
1140  
cacggtcttg ctgccccga catcggcgtg taccgggtgca ttgcaggctc tgcacaggaa  
1200  
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1260  
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1320  
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1440  
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<212> PRT

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&lt;210&gt; 530

&lt;211&gt; 802

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 530

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Asp Leu Gln Leu Gly Ile Pro Pro Ser Phe Met Arg Phe Gln Pro Arg
      355          360          365
Gln Arg Glu Glu Ile Leu Glu Trp Glu Phe Leu Thr Gly Lys Tyr Leu
      370          375          380
Tyr Ser Ala Val Asp Gly Gln Pro Pro Arg Arg Gly Met Asp Ser Ala
385          390          395          400
Gln Arg Glu Ala Leu Asp Asp Ile Val Met Gln Val Met Glu Met Ile

```



405 410 415  
 Asn Ala Asn Ala Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile  
 420 425 430  
 Gln Tyr Gly Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile  
 435 440 445  
 Leu Asp Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr  
 450 455 460  
 Val Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile  
 465 470 475 480  
 Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys Arg  
 485 490 495  
 Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser Leu Lys  
 500 505 510  
 Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu His Lys Glu  
 515 520 525  
 Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu Ser Gly Arg Phe  
 530 535 540  
 Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu Lys Thr Cys Leu Ile  
 545 550 555 560  
 Pro Asn Gln Asn Val Lys Leu Val Val Leu Leu Phe Asn Ser Asp Ser  
 565 570 575  
 Asn Pro Asp Lys Ala Lys Gln Val Glu Leu Met Thr Asp Tyr Arg Ile  
 580 585 590  
 Lys Tyr Pro Lys Ala Asp Met Gln Ile Leu Pro Val Ser Gly Glu Phe  
 595 600 605  
 Ser Arg Ala Leu Ala Leu Glu Val Gly Ser Ser Gln Phe Asn Asn Glu  
 610 615 620  
 Ser Leu Leu Phe Phe Cys Asp Val Asp Leu Val Phe Thr Thr Glu Phe  
 625 630 635 640  
 Leu Gln Arg Cys Arg Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe  
 645 650 655  
 Pro Ile Ile Phe Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys  
 660 665 670  
 Val Pro Ser Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp  
 675 680 685  
 Arg Asn Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val  
 690 695 700  
 Arg Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp  
 705 710 715 720  
 Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe Arg  
 725 730 735  
 Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe Cys Asp  
 740 745 750  
 Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly Ser Lys Ala  
 755 760 765  
 Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met Trp Leu Glu Lys  
 770 775 780  
 Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn Asn Gly Ser Val Arg  
 785 790 795 800  
 Thr Ala

&lt;210&gt; 531

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 531

```

ngatgatgaa tccccccgca gcctcgtaa tatggggggc ttcctacccc agcaaaaggc
60
acggcaatac gtctcgaaca aaggctcttt gtttcgaaat aacaaggggt tagagctaag
120
aggaagaagc gtgaaacgct gtaggaccag cgtttcgaac gcccccgagg tgaaccctcg
180
ggggcgctcg aatcaggcca gttgggcctg ggacgacagc ggttcagcgc gcagcaatgg
240
cgcgtagcga tcagccttga tcgattcacg ccaggcgccg agccactcgg cgtggccttc
300
gttccacacc tgctgggtgca g
321

```

&lt;210&gt; 532

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 532

```

Met Gly Gly Phe Leu Pro Gln Gln Lys Ala Arg Gln Tyr Val Ser Asn
1      5      10      15
Lys Gly Leu Leu Phe Arg Asn Asn Lys Gly Leu Glu Leu Arg Gly Arg
20     25     30
Ser Val Lys Arg Cys Arg Thr Ser Val Ser Asn Ala Pro Glu Val Asn
35     40     45
Pro Arg Gly Arg Leu Asn Gln Ala Ser Trp Ala Trp Asp Asp Ser Gly
50     55     60
Cys Ser Gly Ser Asn Gly Ala Cys Gly Ser Ala Leu Ile Asp Ser Arg
65     70     75     80
Gln Ala Pro Ser His Ser Ala Trp Pro Ser Phe His Thr Cys Trp Cys
85     90     95

```

&lt;210&gt; 533

&lt;211&gt; 335

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 533

```

nagtttccgg tgaaccgctc cgcaatgcct cgtgacatcg acttcagcga agccaacagg
60
agcatcatcg acaacatggc aactgcctca atcccgttt tccgaacca caaaaactgg
120
gagacgtggc cgagtcaggc ccggcatttc attagccttt tacacccaaa agtcaccctc
180
accaacattg acaacgtcct caacaaagat cacctgcgtt ggctacactt tcttttggag
240
ggtcgcctgg agccaaacgt gcgcctgatt gtccagggtt actgttcgcc tggcaagctg
300
taccgcaagc ttgaggagct atatgcccct tctgc
335

```

<210> 534  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 534  
 Met Pro Arg Asp Ile Asp Phe Ser Glu Ala Asn Arg Ser Ile Ile Asp  
 1 5 10 15  
 Asn Met Ala Thr Ala Ser Ile Pro Leu Phe Arg Thr His Lys Asn Trp  
 20 25 30  
 Glu Thr Trp Ser Ser Gln Val Arg His Phe Ile Ser Leu Leu His Pro  
 35 40 45  
 Lys Val Thr Leu Thr Asn Ile Asp Asn Val Leu Asn Lys Asp His Leu  
 50 55 60  
 Arg Trp Leu His Phe Leu Leu Glu Gly Arg Leu Glu Pro Asn Val Arg  
 65 70 75 80  
 Leu Ile Val Gln Gly Tyr Cys Ser Pro Gly Lys Leu Tyr Arg Lys Leu  
 85 90 95  
 Glu Glu Leu Tyr Ala Pro Ser  
 100

<210> 535  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<400> 535  
 acgcgtctct acagccggac taagcacagg ctcagccccg gtcgccatgc gcccaggctc  
 60  
 ggttatcagc cgaggaatcc acggcgaaat gaccagtagc ggccctaata caactatgct  
 120  
 gccgagcagc agacgtcgag gtcgggtcat gaggatgccg acggccaccg cgaccgggta  
 180  
 taccacaaat gcaggaacaa ggctgatagc tagggctgac cacagagcca ggccgctgct  
 240  
 cgaggaaacg cccccacct ggtgactgcc agtatcagca ccgcgcagct caacgacgtc  
 300  
 aacagtctcg ggattgacca accgccacgt atgcagggcc atgtggggga gaatcacccc  
 360  
 caacgccaat gctgtcaccg agcctcgggc taggcgcgcg gc  
 402

<210> 536  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 536  
 Met Ala Leu His Thr Trp Arg Leu Val Asn Pro Glu Thr Val Asp Val  
 1 5 10 15  
 Val Glu Leu Arg Gly Ala Asp Thr Gly Ser His Gln Val Gly Gly Val  
 20 25 30  
 Ser Ser Ala Gly Gly Leu Ala Leu Trp Ser Ala Leu Ala Ile Ser Leu

```

      35              40              45
Val Pro Ala Leu Trp Val Tyr Pro Val Ala Val Ala Val Gly Ile Leu
      50              55              60
Met Thr Arg Pro Arg Arg Leu Leu Leu Gly Ser Ile Val Val Leu Gly
65              70              75              80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
      85              90              95
Gly Arg Met Ala Thr Gly Ala Glu Pro Val Leu Ser Pro Ala Val Glu
      100             105             110
Thr Arg

```

<210> 537  
 <211> 404  
 <212> DNA  
 <213> Homo sapiens

```

<400> 537
gtgcacatcg gcggcaccga cttcgacaaa caactctcgc tggctggcat gatgccgctg
60
ttcggctacg gcagccgcat gaagagcggc gcctacatgc ccaccagcca ccacatgaac
120
ctggcgacct ggcacacccat caactcgggtg tactcgcaaa aatcccagct ggccctgggc
180
agcatgcgct acgacatcga agacaccggc ggcacgcacc gcctgttcaa gctgatcgaa
240
cagcgtgctg ggcactggct tgccatggaa gtggaagaaa ccaagatcca gctcacccat
300
caagacagcc gccacgtgcc gctggaccgc atcgaagcgg gcctgagcgt agacctgagc
360
cgggcgctgt tcgaatcgtc catcgacaac ctgctcgaac gcgt
404

```

<210> 538  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

```

<400> 538
Met Met Pro Leu Phe Gly Tyr Gly Ser Arg Met Lys Ser Gly Ala Tyr
1              5              10              15
Met Pro Thr Ser His His Met Asn Leu Ala Thr Trp His Thr Ile Asn
      20              25              30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
      35              40              45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
      50              55              60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
65              70              75              80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
      85              90              95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
      100             105             110
Asp Asn Leu Leu Glu Arg

```

115

<210> 539  
 <211> 534  
 <212> DNA  
 <213> Homo sapiens

<400> 539  
 nnacgcgtga aaaagaagaa aatgaaggaa agcgaggctg acagcgaggt gaagcatcaa  
 60  
 ccaattttca taaaagaaag attgaagctt tttgaaatac tgaagaaaga ccatcagctc  
 120  
 ttacttgcca tttatggaaa aaagggggat acaagcaaca tcatcacagt aagagtggct  
 180  
 gatgggcaaa cagtgaagg ggaagtctgg aaaacaacgc cttaccaagt ggctgctgaa  
 240  
 attagtcagg aactggctga aagcacggta atagccaaag tcaatgggtga actgtgggac  
 300  
 ctggaccgcc cattggaagg ggactcttct ctagagctgc ttacatttga taatgaggaa  
 360  
 gctcaagctg tgagtatttt aaaaccagac agccaaactt tgggtagtta tgttgtaaac  
 420  
 tacattatat aagaggccac atattgaatt cacgaatggt gagttttttg ggggtttcta  
 480  
 agatttaaaa tttgattatt gatgtttaat aaatatttgc ctcatgaatg ttaa  
 534

<210> 540  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 540  
 Xaa Arg Val Lys Lys Lys Lys Met Lys Glu Ser Glu Ala Asp Ser Glu  
 1 5 10 15  
 Val Lys His Gln Pro Ile Phe Ile Lys Glu Arg Leu Lys Leu Phe Glu  
 20 25 30  
 Ile Leu Lys Lys Asp His Gln Leu Leu Leu Ala Ile Tyr Gly Lys Lys  
 35 40 45  
 Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr  
 50 55 60  
 Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu  
 65 70 75 80  
 Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly  
 85 90 95  
 Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu  
 100 105 110  
 Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys  
 115 120 125  
 Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile  
 130 135 140

<210> 541  
 <211> 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 541

```

ggtagcgagc tgcgcgtgtg gtatgcccgc ttctatgcca agaagatgga caagcccatg
60
ctgaagcagg ccggctcttg cgtccacgct gcaggcaccc cagaaaacag cgccccctg
120
gagtcggagc ccagccagtg ggcgtgtaaa gtgtgttctg ccaccttctt ggagctgcag
180
ctcctcaatg gtaaggagga cgtgtgggga gccccagttg taaaactcct gtgtcgattt
240
ctctctgact tacgctgtca cctgtctgcg gctgtcgggg gtgtcccaga ctttctctt
300
tctgccccat tgccccacaa tgtagtcgcc agaaccaagg ctttctcagg gtttaaagct
360
tctgggcagt cccgcttccc acccccagacc cctgcaggcc tcaactctca ctcctcttg
420
ttgggaagtt gcatttcagc tgggcgcctt gactctggag cactggcagg ggccaggggc
480
caggagccag ccgtggcatg tgttgtgcac tcttgccctt gttgtctcta cttgacagcc
540
ccctcacgcg t
551

```

&lt;210&gt; 542

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 542

```

Met Asp Lys Pro Met Leu Lys Gln Ala Gly Ser Gly Val His Ala Ala
1      5      10      15
Gly Thr Pro Glu Asn Ser Ala Pro Val Glu Ser Glu Pro Ser Gln Trp
20     25     30
Ala Cys Lys Val Cys Ser Ala Thr Phe Leu Glu Leu Gln Leu Leu Asn
35     40     45
Gly Lys Glu Asp Val Trp Gly Ala Pro Val Val Lys Leu Leu Cys Arg
50     55     60
Phe Leu Ser Asp Leu Arg Cys His Leu Ser Ala Ala Val Gly Gly Val
65     70     75     80
Pro Asp Phe Val Leu Ser Ala Pro Leu Pro His Asn Val Val Ala Arg
85     90     95
Thr Lys Ala Phe Ser Gly Phe Lys Ala Ser Gly Gln Ser Arg Phe Pro
100    105    110
Pro Pro Thr Pro Ala Gly Leu Thr Pro His Ser Ser Trp Leu Gly Ser
115    120    125
Cys Ile Ser Ala Gly Arg Leu Asp Ser Gly Ala Leu Ala Gly Ala Arg
130    135    140
Gly Gln Glu Pro Ala Val Ala Cys Val Val His Ser Cys Leu Cys Cys
145    150    155    160
Leu Tyr Leu Thr Ala Pro Ser Arg
165

```

<210> 543  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<400> 543  
 nnaaagccgg acatgaatac ccgcattgct ggcaaaactg tcctgaccat cattctggcc  
 60  
 gggggcaaaag gcagccgcct ggccccgatg accgatcagg tggccaaacc agccgtgccg  
 120  
 tttatgggga cgtaccgcct gattgacttt tcgctgtcca acattgtcca cagcggcttg  
 180  
 caggacgtct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggctggg  
 240  
 gggcgctcct gggatctgga ccgcacccgc ggtggcctga aggtcatgcc gcccttttcc  
 300  
 ggccctgccg atgaggacgg tggcttttcc gaaggcaacg cacacgcgt  
 349

<210> 544  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 544  
 Xaa Lys Pro Asp Met Asn Thr Arg Ile Ala Gly Lys Thr Val Leu Thr  
 1 5 10 15  
 Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp  
 20 25 30  
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile  
 35 40 45  
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp  
 50 55 60  
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly  
 65 70 75 80  
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met  
 85 90 95  
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly  
 100 105 110  
 Asn Ala His Ala  
 115

<210> 545  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<400> 545  
 catgatgcaa aaacagacat gcttatttca aaatataaaa gtgaaaaaga tcgttttagca  
 60  
 caagaaattg ttggtgtcat cacagggttct gcaatgccgg gtggttcagc aaaccgtatc  
 120  
 ccaaataaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaaaca  
 180

atgtataacg aactcaaaac agtggattta actattcaaa atgctggcgg tgtacgcgca  
 240  
 gatattttac cggggaatgt aacctttaac gatgcttata ctttcttacc tttcgggaat  
 300  
 acgttatata cctataaaat ggaaagtcca ttagtgaaac aagtgcttga agatgcaatg  
 360  
 ctatttgctt tgggtcccc ccccccccc  
 390

<210> 546

<211> 130

<212> PRT

<213> Homo sapiens

<400> 546

His	Asp	Ala	Lys	Thr	Asp	Met	Leu	Ile	Ser	Lys	Tyr	Lys	Ser	Glu	Lys
1				5					10					15	
Asp	Arg	Leu	Ala	Gln	Glu	Ile	Val	Gly	Val	Ile	Thr	Gly	Ser	Ala	Met
		20						25					30		
Pro	Gly	Gly	Ser	Ala	Asn	Arg	Ile	Pro	Asn	Lys	Ala	Gly	Ser	Asn	Pro
		35					40					45			
Glu	Gly	Ser	Ile	Ala	Thr	Arg	Phe	Ile	Ala	Glu	Thr	Met	Tyr	Asn	Glu
	50				55				60						
Leu	Lys	Thr	Val	Asp	Leu	Thr	Ile	Gln	Asn	Ala	Gly	Gly	Val	Arg	Ala
65				70					75					80	
Asp	Ile	Leu	Pro	Gly	Asn	Val	Thr	Phe	Asn	Asp	Ala	Tyr	Thr	Phe	Leu
		85					90						95		
Pro	Phe	Gly	Asn	Thr	Leu	Tyr	Thr	Tyr	Lys	Met	Glu	Ser	Ser	Leu	Val
		100					105						110		
Lys	Gln	Val	Leu	Glu	Asp	Ala	Met	Leu	Phe	Ala	Leu	Gly	Pro	Pro	Pro
		115					120					125			
Pro	Pro														
	130														

<210> 547

<211> 306

<212> DNA

<213> Homo sapiens

<400> 547

aagcttggtt ttctgatttt tattcaaatc tctatcatgg atgaagcatg cagtttcaga  
 60  
 atcagttcag tgttgacaac atatcaagat attctgcagt caatctcaat gtatgttcac  
 120  
 gaagcctcca acatattttg tgggatacca tctttgtcag gcattgtgct aggcactgtc  
 180  
 cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc  
 240  
 tcaaactttc atgtttgtgt atacaaatca gctgaggcct tactaaact cnnnnncenn  
 300  
 nncenn  
 306

<210> 548



<211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 548  
 Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr  
 1 5 10 15  
 Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn  
 20 25 30  
 Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val  
 35 40 45  
 Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser  
 50 55 60  
 Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu  
 65 70 75 80  
 Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa Xaa  
 85 90

<210> 549  
 <211> 780  
 <212> DNA  
 <213> Homo sapiens

<400> 549  
 nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttgtaaat  
 60  
 gttttaatca tacacatatt gtctgtaagt atgaagagaa aggcataatca gaaatatttc  
 120  
 aattcagcga tttgaaatgt ttactttctg tttattgaaa atttttgttc tttttcacca  
 180  
 tggtattttt ttctcctcgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg  
 240  
 gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tatcgcttgt  
 300  
 tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt  
 360  
 aagattttcta aggatgcagg gatgcccac cagggccagc catgcttctg caaatatgca  
 420  
 cagggggcag acagcgtaga gcccatgttc cggcatctca agaacacata ttctggccta  
 480  
 cagcttatta tcgtcatcct gccggggaag acaccagtgt atgcggaagt gaaacgtgta  
 540  
 ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaca  
 600  
 tctcctcaaa ctctgtcaaa cttgtgccta aagataaatg ttaaactcgg agggatcaat  
 660  
 aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga  
 720  
 gccgatgtca ctcatccacc tgctggtgat ggaaagaagc cttctattgc tgctgttgta  
 780

<210> 550  
 <211> 192  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 550

```

Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
 1           5           10           15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
          20           25           30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
          35           40           45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
 50           55           60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
 65           70           75           80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
          85           90           95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
          100          105          110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
          115          120          125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
          130          135          140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
          145          150          155          160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
          165          170          175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
          180          185          190

```

&lt;210&gt; 551

&lt;211&gt; 291

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 551

```

nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gctcggtgcc
60
gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttcgag
120
gaaccgtect cgtcgtaaat cgcaccggtc ccgccggccc cgacgactgc agtaccacg
180
actagttcgt cgtcggggcg ctgaccgatg cgcccatcgg cgggctcatc tggtggcgc
240
tagcgggggc ttcgatgtcc ccataccaca gcgtccgcta aattgccnc c
291

```

&lt;210&gt; 552

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 552

```

Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
 1           5           10           15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

```

```

      20      25      30
Pro Thr Asn Ser Ala Pro Ser Glu Pro Ser Ser Ser Ser Ile Ala
      35      40      45
Pro Val Pro Pro Ala Pro Thr Thr Ala Val Pro Thr Thr Ser Ser Ser
      50      55      60
Ser Gly Arg
65

```

<210> 553  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

```

<400> 553
ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata
60
gtatctaaag ccaaaccgaa aattgggtgca tatcatttca ctacaattaa acctaactta
120
ggtgttgttt ccacaaaaga tcaacgtagt tttgttatgg cagatttacc aggtttaatt
180
gaaggtgcat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca
240
aaagtatttg ttcacatgat tgatatgagc ggttctgaag gtagagaacc tattgaagat
300
tataaagtca ttaatcaaga attagctgcg tacgagcaac gtttagaaga tagacctcaa
360
atcgtagtag ctaacaagat ggatttacct gaatcacaag ataatttaaa cttgtttaaa
420
gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcg t
471

```

<210> 554  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

```

<400> 554
Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr
1      5      10      15
Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His
20      25      30
Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln
35      40      45
Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser
50      55      60
Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr
65      70      75      80
Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu
85      90      95
Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu
100      105      110
Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp
115      120      125
Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly

```

130	135	140
Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg		
145	150	155

<210> 555  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 555  
 tctagagatt gagaacaatt atggatacag aaatggttga ttccgtcaaa tatattcgag  
 60  
 attcgggaatc atgtgaggct cgcgtgctgg agatcttagc cagaaggccg tccatgatgg  
 120  
 tgcagatctt gcgtggcgac ggcttaatta acgaagacca gagattagtc agattatggc  
 180  
 ttaataaaagt acctagaatt gtctgcctgc ttctccggct tagtgtgttc gtcgctgcgg  
 240  
 caataggtgc ccgtgcggta tggggcgccg cttccggtaa tcccgatctt gttcacgcgt  
 300

<210> 556  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 556  
 Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu  
 1 5 10 15  
 Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met  
 20 25 30  
 Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg  
 35 40 45  
 Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu  
 50 55 60  
 Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val  
 65 70 75 80  
 Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala  
 85 90

<210> 557  
 <211> 678  
 <212> DNA  
 <213> Homo sapiens

<400> 557  
 atcttcccgg tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag  
 60  
 gccctcacga cgatgcaccc gctcaccggg gaggtcatca gcgaggacga gcaggtctac  
 120  
 gtgttcccgg ctaccacta tgctgccggc ccggaacgta tggagcgggc catagcgtcc  
 180  
 atccagcagg agctcgagga gcgcctggcc gttctagagc gtgatgggaa actgttggag  
 240

gcccaacggt tacgtatgcg tactacctac gatatcgaga tgatgcagca ggtcgggtgcc  
 300  
 tgtgctggca tcgaaaacta ttcgcggcac atcgacggac gcgctcccgg ctacgccccg  
 360  
 aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atcccacgtg  
 420  
 accgtcccgc agattggcgg gatgtatgag ggggacatga gccgcaagcg gacattggta  
 480  
 gaacatgggt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc  
 540  
 acccagcgga tcggccagac tgtctacctg tccgccacgc ccggttcgta cgagaccgaa  
 600  
 cgagctcacg gcgtcgctga acaaatcatt cgtccgacag gtctggtgga tccggagatt  
 660  
 atcgtcaagc ctacgcgt  
 678

&lt;210&gt; 558

&lt;211&gt; 226

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 558

Ile Phe Pro Val Tyr Glu Glu Asn Ala Leu Arg Val Glu Phe Phe Gly  
 1 5 10 15  
 Asp Glu Ile Glu Ala Leu Thr Thr Met His Pro Leu Thr Gly Glu Val  
 20 25 30  
 Ile Ser Glu Asp Glu Gln Val Tyr Val Phe Pro Ala Thr His Tyr Val  
 35 40 45  
 Ala Gly Pro Glu Arg Met Glu Arg Ala Ile Ala Ser Ile Gln Gln Glu  
 50 55 60  
 Leu Glu Glu Arg Leu Ala Val Leu Glu Arg Asp Gly Lys Leu Leu Glu  
 65 70 75 80  
 Ala Gln Arg Leu Arg Met Arg Thr Thr Tyr Asp Ile Glu Met Met Gln  
 85 90 95  
 Gln Val Gly Ala Cys Ala Gly Ile Glu Asn Tyr Ser Arg His Ile Asp  
 100 105 110  
 Gly Arg Ala Pro Gly Ser Ala Pro Asn Cys Leu Leu Asp Tyr Phe Pro  
 115 120 125  
 Glu Asp Phe Val Leu Val Ile Asp Glu Ser His Val Thr Val Pro Gln  
 130 135 140  
 Ile Gly Gly Met Tyr Glu Gly Asp Met Ser Arg Lys Arg Thr Leu Val  
 145 150 155 160  
 Glu His Gly Phe Arg Leu Pro Ser Ala Met Asp Asn Arg Pro Leu Lys  
 165 170 175  
 Phe Asp Glu Phe Thr Gln Arg Ile Gly Gln Thr Val Tyr Leu Ser Ala  
 180 185 190  
 Thr Pro Gly Ser Tyr Glu Thr Glu Arg Ala His Gly Val Val Glu Gln  
 195 200 205  
 Ile Ile Arg Pro Thr Gly Leu Val Asp Pro Glu Ile Ile Val Lys Pro  
 210 215 220  
 Thr Arg  
 225

<210> 559  
 <211> 335  
 <212> DNA  
 <213> Homo sapiens

<400> 559  
 ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggagggt ttgtgataaa  
 60  
 tggaatgcag tcagagggaa ggaactgccn gcttaaagtg tcctatgctg cgctttccag  
 120  
 agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg  
 180  
 tatggtgagg caagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa  
 240  
 ctaaagtgtg tccaggagct gaagccctta atcagctagg gctcacacag agtcaaggta  
 300  
 ggggtcaaaaa cattcagtct gggaccatat ctaga  
 335

<210> 560  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 560  
 Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met  
 1 5 10 15  
 Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp  
 20 25 30  
 Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe  
 35 40 45  
 Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr  
 50 55 60  
 Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly  
 65 70 75 80  
 Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg  
 85 90

<210> 561  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

<400> 561  
 ngcgcgcccc ctctccgat ggcgggcgag atccagccca agcctctgac ccgcaagccg  
 60  
 atcctgctgc agcggatgga ggggtcccag gaggtggtga atatggccgt gatcgtgccc  
 120  
 aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttcgtgtttg gttaaagaga  
 180  
 gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttta tattgtcaga  
 240  
 agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgacgat  
 300

gacccctgttt gtcctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc  
 360  
 ctggcactgc tctgagagtg ggcagcgctt gggaggttat cggaccagtg ctgtggcctc  
 420  
 aggcctgcaa tttgatgttg aaacccggca tgtgtttatc ggtgaccact caggcca  
 477

<210> 562  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<400> 562  
 Xaa Ala Pro Pro Pro Pro Met Ala Ala Glu Ile Gln Pro Lys Pro Leu  
 1 5 10 15  
 Thr Arg Lys Pro Ile Leu Leu Gln Arg Met Glu Gly Ser Gln Glu Val  
 20 25 30  
 Val Asn Met Ala Val Ile Val Pro Lys Glu Glu Gly Val Ile Ser Val  
 35 40 45  
 Ser Glu Asp Arg Thr Val Arg Val Trp Leu Lys Arg Asp Ser Gly Gln  
 50 55 60  
 Tyr Trp Pro Ser Val Tyr His Ala Met Pro  
 65 70

<210> 563  
 <211> 403  
 <212> DNA  
 <213> Homo sapiens

<400> 563  
 ccattggcaga cagggagctg agcggcctgc ggaccaggt gcaccagagc atggtgcccc  
 60  
 tgctcctaca cctgaaggac caatgcccaa ctgtcgccac gggcaatgcc caccccaaga  
 120  
 aaaaggaaggg aaaaggcctc aaccttggcc agggctggaa cccacaggag gccagggtac  
 180  
 ggggcagacg gatggcagca gcaactgctg agagtgggg gagctccac ggggcagcaa  
 240  
 gtggcgggca gagggctctg ccatctgcac tggtttctgt gaccacagtt ggcctgccccg  
 300  
 ctccccact gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa  
 360  
 aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat  
 403

<210> 564  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 564  
 Met Ala Asp Arg Glu Leu Ser Gly Leu Arg Thr Gln Val His Gln Ser  
 1 5 10 15  
 Met Val Pro Leu Leu Leu His Leu Lys Asp Gln Cys Pro Thr Val Ala

```

      20      25      30
Thr Gly Asn Ala His Pro Lys Lys Arg Lys Gly Lys Gly Leu Asn Leu
      35      40      45
Gly Gln Gly Trp Asn Pro Gln Glu Ala Arg Val Arg Gly Arg Arg Met
      50      55      60
Ala Ala Ala Leu Pro Glu Ser Trp Gly Ser Ser His Gly Ala Ala Ser
65      70      75      80
Gly Gly Gln Arg Val Trp Pro Ser Ala Leu Val Ser Val Thr Thr Val
      85      90      95
Gly Leu Pro Ala Pro Pro Leu His His
      100      105

```

&lt;210&gt; 565

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 565

```

nctctccat ggagcagccc catcttcact cttcacctgg ggccaggcct tccacagcag
60
ccaccaccca gcgaccacag agaggctgcg cggaggacac aggagagagg gagcccacgg
120
gcacgatctc caccggcttt cccagctccc tgggtcagcc ccacgggacc tctcctctc
180
tctcccacat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
240
gcttgggccc cacagacctg gacaatgtcc cagtgagggc tggaggtgct agaagggcac
300
aggaggcccc n
311

```

&lt;210&gt; 566

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 566

```

Met Glu Gln Pro His Leu His Ser Ser Pro Gly Ala Arg Pro Ser Thr
  1      5      10      15
Ala Ala Thr Thr Gln Arg Pro Gln Arg Gly Cys Ala Glu Asp Thr Gly
      20      25      30
Glu Arg Glu Pro Thr Gly Thr Ile Ser Thr Gly Phe Pro Ser Ser Leu
      35      40      45
Gly Gln Pro His Gly Thr Ser Pro Pro Leu Ser His Ile Ser Lys Pro
      50      55      60
Ala Leu His Ile Val Arg Ala Val Ile Arg Met Glu Arg Gly Leu Gly
65      70      75      80
Arg Thr Asp Leu Asp Asn Val Pro Val Arg Ala Gly Gly Ala Arg Arg
      85      90      95
Ala Gln Glu Ala Pro
      100

```

&lt;210&gt; 567

&lt;211&gt; 929



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 567

atcacatcgg tcgctgaacc ccgacgagcc tcacctgtgc gaaatattca tccttgagat  
 60  
 cagcccacgt gccgtcgacc tctacctcgg tgagggtcgc gggcgggtac caacagccga  
 120  
 cctcgtcctc ggctccactc atggcggcaa gttccgctgc cagtccgggg atcgtcgggg  
 180  
 catgggcat gatgagcagg ttatccacat cgtcgtcgat ttctccgatg cgccgacgca  
 240  
 cggatcagt gccgcagtaa tagagggctc gcatgaattc gaccggacaa tccagttgga  
 300  
 ggcagtccca ggtctggcgg gtgcgtaggg catcgagac cagagcatgt ccaacattgc  
 360  
 gcagtccaa acgcgtgccg acctcacggg cctgacggcg cccacgtcg gtgagcggac  
 420  
 gctcccgatc cccgcccgga gcatgggatg cgggctgtgc atgtctcatg aggaacagag  
 480  
 tgtgcatgga tccatcggtg cacttcgcgg tcgccgcggg tctacgatgt tggcatgccg  
 540  
 ttgacggatt tgggcattga tgaggcgcgt acctaccgcc cgaacgtccc tgaacccgat  
 600  
 ggtttcgact ctttttgggc cgagaccctc gatgagtatt ccggcggtcc ccaagatctg  
 660  
 acggcgggtgc ctttcgataa ccgtcaggct ctgatagata cctgggattt gtcgtgggtg  
 720  
 gggatcaca actctcgggt gagcgggtga ttacatgcc cagccgctgt gaacggccca  
 780  
 ttcccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca  
 840  
 gtcttcgctg ctgctggcta tgcacatata gtcgtcgatc cacgtgggtca ggggtggggc  
 900  
 caccacaacct tgacggaaaa ctgtccgga  
 929

&lt;210&gt; 568

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 568

Met Pro Leu Thr Asp Leu Gly Ile Asp Glu Ala Arg Thr Tyr Arg Pro  
 1 5 10 15  
 Asn Val Pro Glu Pro Asp Gly Phe Asp Ser Phe Trp Ala Glu Thr Leu  
 20 25 30  
 Asp Glu Tyr Ser Gly Val Pro Gln Asp Leu Thr Ala Val Pro Phe Asp  
 35 40 45  
 Asn Arg Gln Ala Leu Ile Asp Thr Trp Asp Leu Ser Trp Val Gly Tyr  
 50 55 60  
 His Asn Ser Arg Val Ser Gly  
 65 70

<210> 569  
 <211> 371  
 <212> DNA  
 <213> Homo sapiens

<400> 569  
 ncgcaaactt caacgggtgcc atctgccata ttccagggat gccagatttg gatggaaaat  
 60  
 accatatcac tctcgattca gaattcgtac ttgatttagt ggcctttaac aaaacgctac  
 120  
 ctgtcgatta cttaatggtc gaaggaacgg aacttggtga ttcaaactg gaagaactac  
 180  
 ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaac  
 240  
 tcaaggaaca accaacagcc gttgctctct tctcgatgt tgataaacgg ccagagatta  
 300  
 aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcggtactt  
 360  
 cccatgtcta n  
 371

<210> 570  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 570  
 Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe  
 1 5 10 15  
 Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu  
 20 25 30  
 Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro  
 35 40 45  
 Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys  
 50 55 60  
 Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp  
 65 70 75 80  
 Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp  
 85 90 95  
 Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa  
 100 105 110

<210> 571  
 <211> 407  
 <212> DNA  
 <213> Homo sapiens

<400> 571  
 nacgcgtatc ttcgctggtc cacaccagac gtggcattaa acgacgtcac aagaacgaca  
 60  
 ccgggccttg acggggccac gcacgaagag gccaaagacac tgaccgagac tactgtttcc  
 120  
 gttccacact ccttcgccga cctcggcgtc cgagaagata tctgccaggc gctggaaggg  
 180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tcccgattgc cgtcgagggc  
 240  
 acggatctta ttgggcaggc gcgtactggc actggcaaaa cactcgcctt cggcatcacc  
 300  
 atcttgagc gcataccct gcccggtgac gaagggtggg aagaactcac caccaaaggc  
 360  
 aagcccccaa gcactcgtga tgtgcccta cccgggagct aggtcgg  
 407

<210> 572

<211> 100

<212> PRT

<213> Homo sapiens

<400> 572

Leu	Thr	Glu	Thr	Thr	Val	Ser	Val	Pro	Thr	Ser	Phe	Ala	Asp	Leu	Gly
1				5				10						15	
Val	Arg	Glu	Asp	Ile	Cys	Gln	Ala	Leu	Glu	Gly	Val	Gly	Ile	Val	Ser
	20						25					30			
Pro	Phe	Pro	Ile	Gln	Ala	Met	Ser	Ile	Pro	Ile	Ala	Val	Glu	Gly	Thr
	35					40					45				
Asp	Leu	Ile	Gly	Gln	Ala	Arg	Thr	Gly	Thr	Gly	Lys	Thr	Leu	Ala	Phe
	50				55					60					
Gly	Ile	Thr	Ile	Leu	Gln	Arg	Ile	Thr	Leu	Pro	Gly	Asp	Glu	Gly	Trp
65				70				75						80	
Glu	Glu	Leu	Thr	Thr	Lys	Gly	Lys	Pro	Pro	Ser	Thr	Arg	Asp	Val	Pro
			85					90						95	
Leu	Pro	Gly	Ser												
			100												

<210> 573

<211> 393

<212> DNA

<213> Homo sapiens

<400> 573

acgcgtctac cgtaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg  
 60  
 actacgaggt cgccggacta atgtggctcg ctgctgcccg gccagatggg gccggcatcg  
 120  
 tcgaggtgct cgaccacggc aagggatggc tcaccgaacc cgaattgtcc actgggcacc  
 180  
 ccaccgcga ggcagccgag gactttggcc gccgactggc tcacaccac gcagccggg  
 240  
 cctcacacct gggggctgca cctgacgggt ttgttcccga cgatgggtat atcggccgtg  
 300  
 ctcccctgcc actgccgtcc gaaccaatct cctcctgggg agagttttac gctcagtgcc  
 360  
 gcatcgaacc atatatggac agtctcgagc ctg  
 393

<210> 574

<211> 124

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 574

```

Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
 1           5           10           15
Val Ala Gly Leu Met Trp Leu Ala Ala Arg Pro Asp Gly Ala Gly
      20           25           30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
      35           40           45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
      50           55           60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
      65           70           75           80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
      85           90           95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
      100          105          110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
      115          120

```

&lt;210&gt; 575

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 575

```

nntatccatg cagacatggg accaggggtct ctgagggcag gaagcaaagt gggtgagggg
60
gatgggacaa gatgccctgg tgctaaggcc tctggagctg gagctgggta tagggatgat
120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctgggag ccagtgggct
180
tatggggctg gcaatgtgct gggttatgag gatggatcag aacttccagg gcctcagggg
240
actgggggtca gaacagccta tggagaaagg tcaaggggcc ttgggcctag gagtacaggg
300
ccaggggggtg aggcaggctt tagagatggt tcaggaggcc tccaaggaat gggatcagca
360
gatgggcccc gt
372

```

&lt;210&gt; 576

&lt;211&gt; 124

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 576

```

Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
 1           5           10           15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
      20           25           30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
      35           40           45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```

```

      50              55              60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65              70              75              80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
      85              90              95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
      100              105              110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
      115              120

```

&lt;210&gt; 577

&lt;211&gt; 432

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 577

```

nagcgcaatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagcgcc gggcgcggat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgtcgctctt tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagtct ccaaaccctg catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtag accgcgaggt acgccaccta caagattccc tcaacgccgc catgaccgcg
300
ccaaagcaag gcccgaaacg caccctggag tcagcggtag tggccctgct ggactacatc
360
gacgaccgtc cagacggttt tcggatcacc tcgcgagact cctcggtcgg ttcagccacc
420
ggttcgtagc cg
432

```

&lt;210&gt; 578

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 578

```

Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
1              5              10              15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
      20              25              30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
      35              40              45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
      50              55              60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
65              70              75              80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
      85              90              95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
      100              105              110
Ala Thr Gly Ser Tyr Ala

```

115

<210> 579  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 579  
 ggccccaac actccgacct cagctggtcc agcatgctgg gcaccgtgct gctgctggcc  
 60  
 ctgctcccag ggatcaccac cttaccacgc gggccacctg ctcccccggt ccccgcggcg  
 120  
 cccggccctt ggctgcgcag acccctcttc agcctgaagc tgtccgacac agaggacgtc  
 180  
 tttcctcgcc gcgcggggcc gctcgaggtc ccggccgaca gccgcgtgtt cgtgcaggcg  
 240  
 gccttgccc gtccctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccg  
 300  
 tcctcacgcc cggccccggg  
 320

<210> 580  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 580  
 Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr  
 1 5 10 15  
 Leu Pro Ser Gly Pro Pro Ala Pro Pro Phe Pro Ala Ala Pro Gly Pro  
 20 25 30  
 Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp  
 35 40 45  
 Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg  
 50 55 60  
 Val Phe Val Gln Ala Ala Leu Ala Arg Pro Ser Pro Arg Trp Gly Leu  
 65 70 75 80  
 Ala Leu His Arg Cys Ser Val Thr Pro Ser Ser Arg Pro Ala Pro  
 85 90 95

<210> 581  
 <211> 419  
 <212> DNA  
 <213> Homo sapiens

<400> 581  
 nacgacggca accattcgct gtggaaggag ctgaacggcc agctcgacgt gcagtttttc  
 60  
 cagtcgggca tgggcttcaa gacgccagta cgcattgcaca gcgtcgaccc caagaccgac  
 120  
 gaagcccgcg aggtgcattt ccgcccgtcg ctgttcaact atgccaagac cacggtggac  
 180  
 accaagcagc tgaccggcga cctgggtttc tccggtttca agctgttcaa ggcgccggaa  
 240

ctggatcgcc atgacgtgct gtcgtttctc ggcgccagtt acttccgtgc ggtggacgca  
 300  
 acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc  
 360  
 gaggaattcc ccgacttcac gcagttctgg ttcgaaaccc cgagcaagga cccacgcgt  
 419

<210> 582

<211> 139

<212> PRT

<213> Homo sapiens

<400> 582

Xaa	Asp	Gly	Asn	His	Ser	Leu	Trp	Lys	Glu	Leu	Asn	Gly	Gln	Leu	Asp
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Val	Gln	Phe	Phe	His	Val	Gly	Met	Gly	Phe	Lys	Thr	Pro	Val	Arg	Met
			20					25						30	
His	Ser	Val	Asp	Pro	Lys	Thr	Arg	Glu	Ala	Arg	Glu	Val	His	Phe	Arg
			35				40					45			
Pro	Ser	Leu	Phe	Asn	Tyr	Ala	Lys	Thr	Thr	Val	Asp	Thr	Lys	Gln	Leu
		50				55					60				
Thr	Gly	Asp	Leu	Gly	Phe	Ser	Gly	Phe	Lys	Leu	Phe	Lys	Ala	Pro	Glu
65				70						75				80	
Leu	Asp	Arg	His	Asp	Val	Leu	Ser	Phe	Leu	Gly	Ala	Ser	Tyr	Phe	Arg
			85						90					95	
Ala	Val	Asp	Ala	Thr	Arg	Gln	Tyr	Gly	Leu	Ser	Ala	Arg	Gly	Leu	Ala
			100					105					110		
Ile	Asp	Thr	Tyr	Ala	Lys	Lys	Arg	Glu	Glu	Phe	Pro	Asp	Phe	Thr	Gln
		115					120					125			
Phe	Trp	Phe	Glu	Thr	Pro	Ser	Lys	Asp	Pro	Arg					
		130					135								

<210> 583

<211> 407

<212> DNA

<213> Homo sapiens

<400> 583

cttttgatca atgctgatgg cacgaagcta tcgaaaaggt cgggtgatgt ccgcgtagct  
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 gattatatgg agcagggatg ggagccggag acgctggtga acctagttgc cctcacgggc  
 120  
 tatagctatg cgaatttgga gcatgctgat catgatgtca agacgatgaa cgaactcatc  
 180  
 cgtgactttg agcttactcg tatctcccat acgcgagcca cactcccat ggacaagctt  
 240  
 gtgtttttga acaagcatca cttgacaaat aagctggcgc tcgccacgac gtgtgagcag  
 300  
 accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat  
 360  
 tcagatgatt atatcctgcg cgtcgtaaca ctgggacccc aacgcgt  
 407

<210> 584

<211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 584  
 Leu Leu Ile Asn Ala Asp Gly Thr Lys Leu Ser Lys Arg Ser Gly Asp  
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 Val Arg Val Ala Asp Tyr Met Glu Gln Gly Trp Glu Pro Glu Thr Leu  
           20                  25                  30  
 Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His  
           35                  40                  45  
 Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu  
           50                  55                  60  
 Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu  
   65                  70                  75                  80  
 Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr  
           85                  90                  95  
 Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile  
           100                  105                  110  
 Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val  
           115                  120                  125  
 Val Thr Leu Gly Pro Gln Arg  
           130                  135

<210> 585  
 <211> 502  
 <212> DNA  
 <213> Homo sapiens

<400> 585  
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 gatattttgt tgtgcgcggt gggattgttg gttcagcacc gtgacatcac tgaggagatt  
 120  
 cgggctcggt accgacattt cgttgtcgac gaataccagg acgtttctcc gctgcagcat  
 180  
 aggttgcttg aactgtggtt tggcgatcga aatgatgtat gcgtcgtggg agatccgcac  
 240  
 caggccattc actcttatgc aggcgcacga gctgactacc tcctcgactt cgttgccgat  
 300  
 catcctggcg ctaaacgcat cgatttggtt cgcaactacc gctccactcc cgagatcggt  
 360  
 cagttggcca atgaagttct tgtcaaccgt atgactccag aggaggcttt ggaacatggc  
 420  
 aggggagtc cattggtttc gcggggtcga tccgggtccc agcccatcta tcaggtctc  
 480  
 ggggacgatg cctccgaagc tt  
 502

<210> 586  
 <211> 167  
 <212> PRT  
 <213> Homo sapiens



<400> 586  
 Xaa Arg Val Leu Ala Gly Tyr Glu Ala Val Lys Arg Glu Arg Cys Val  
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 Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln  
 20 25 30  
 His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val  
 35 40 45  
 Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu  
 50 55 60  
 Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His  
 65 70 75 80  
 Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp  
 85 90 95  
 Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn  
 100 105 110  
 Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val  
 115 120 125  
 Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr  
 130 135 140  
 Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu  
 145 150 155 160  
 Gly Asp Asp Ala Ser Glu Ala  
 165

<210> 587  
 <211> 746  
 <212> DNA  
 <213> Homo sapiens

<400> 587  
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 gagctgtgag aggtggacga ggacgagtgt gcatcgagcc cctgccagca tgggggcca  
 120  
 tgcctgcagc gctctgaccc ggccctctac ggggggtgtcc aggccgcctt ccctggcgcc  
 180  
 ttcagcttcc gccatgctgc gggtttccctg tgccactgcc ctcttggtt tgagggagcc  
 240  
 gactgcggtg tggaggtgga cgagtgtgcc tcacggccat gcctcaatgg aggccactgc  
 300  
 caggacctgc ccaatggctt ccagtgtcac tgcccagatg gctacgcagg gccgacatgt  
 360  
 gaggaagatg tggatgaatg cctgtccgat ccctgcctgc acggcggaac ctgcagtgc  
 420  
 actgtggcag gctatatctg caggtgcccc gagacctggg gtgggcgcga ctgttctgtg  
 480  
 cagctcactg gctgccaggg ccacacctgc ccgctggctg ccacctgcat ccctatcttc  
 540  
 gactctgggg tccacagtta cgtctgccac tgcccacctg gtacctatgg accgttctgt  
 600  
 ggccagaata ccaccttctc tgtgatggct gggagcccca ttcaggcatc agtgccagct  
 660  
 ggtggccccc tgggtctggc actgaggttt cgcaccacac tgcccgtgg gaccttggcc  
 720

actcgcaatg acaccaagga aagctt  
746

<210> 588

<211> 248

<212> PRT

<213> Homo sapiens

<400> 588

Ala	Ser	Cys	Leu	Glu	Gly	Leu	Gly	Ser	Phe	Arg	Cys	Leu	Cys	Trp	Pro
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Gly	Tyr	Ser	Gly	Glu	Leu	Cys	Glu	Val	Asp	Glu	Asp	Glu	Cys	Ala	Ser
		20					25					30			
Ser	Pro	Cys	Gln	His	Gly	Gly	Arg	Cys	Leu	Gln	Arg	Ser	Asp	Pro	Ala
		35					40					45			
Leu	Tyr	Gly	Gly	Val	Gln	Ala	Ala	Phe	Pro	Gly	Ala	Phe	Ser	Phe	Arg
	50					55				60					
His	Ala	Ala	Gly	Phe	Leu	Cys	His	Cys	Pro	Pro	Gly	Phe	Glu	Gly	Ala
65					70					75					80
Asp	Cys	Gly	Val	Glu	Val	Asp	Glu	Cys	Ala	Ser	Arg	Pro	Cys	Leu	Asn
				85					90					95	
Gly	Gly	His	Cys	Gln	Asp	Leu	Pro	Asn	Gly	Phe	Gln	Cys	His	Cys	Pro
		100						105					110		
Asp	Gly	Tyr	Ala	Gly	Pro	Thr	Cys	Glu	Glu	Asp	Val	Asp	Glu	Cys	Leu
		115					120					125			
Ser	Asp	Pro	Cys	Leu	His	Gly	Gly	Thr	Cys	Ser	Asp	Thr	Val	Ala	Gly
	130					135					140				
Tyr	Ile	Cys	Arg	Cys	Pro	Glu	Thr	Trp	Gly	Gly	Arg	Asp	Cys	Ser	Val
145					150					155					160
Gln	Leu	Thr	Gly	Cys	Gln	Gly	His	Thr	Cys	Pro	Leu	Ala	Ala	Thr	Cys
				165					170					175	
Ile	Pro	Ile	Phe	Glu	Ser	Gly	Val	His	Ser	Tyr	Val	Cys	His	Cys	Pro
		180						185					190		
Pro	Gly	Thr	His	Gly	Pro	Phe	Cys	Gly	Gln	Asn	Thr	Thr	Phe	Ser	Val
		195					200					205			
Met	Ala	Gly	Ser	Pro	Ile	Gln	Ala	Ser	Val	Pro	Ala	Gly	Gly	Pro	Leu
	210					215					220				
Gly	Leu	Ala	Leu	Arg	Phe	Arg	Thr	Thr	Leu	Pro	Ala	Gly	Thr	Leu	Ala
225					230					235					240
Thr	Arg	Asn	Asp	Thr	Lys	Glu	Ser								
					245										

<210> 589

<211> 381

<212> DNA

<213> Homo sapiens

<400> 589

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ccagtacctc tgcaagccac tatgagtgtc gcaactggta tccagccatc gcctgttaat  
120  
gtggttggtg taacttcagc tttaggtcag cagccttcca tttccagttt ggctcaaccc  
180

cagctaccat attctcaggc ggctcctcca gtgcaaactc cccttccagg ggcaccacca  
 240  
 cccaacagt tacagtatgg acaacagcaa ccaatgggtt ctacacagat ggccccaggc  
 300  
 catgtcaaat cagtgaactca aaatcctgct tcagagtatg tacaacagca gccaatctt  
 360  
 caaacagcaa tgcctccgg a  
 381

<210> 590

<211> 127

<212> PRT

<213> Homo sapiens

<400> 590

Ile	Ser	Gln	Val	Gln	Leu	Gln	Ser	Gln	Glu	Leu	Ser	Tyr	Gln	Gln	Lys
1				5					10					15	
Gln	Gly	Leu	Gln	Pro	Val	Pro	Leu	Gln	Ala	Thr	Met	Ser	Ala	Ala	Thr
		20						25					30		
Gly	Ile	Gln	Pro	Ser	Pro	Val	Asn	Val	Val	Gly	Val	Thr	Ser	Ala	Leu
	35						40					45			
Gly	Gln	Gln	Pro	Ser	Ile	Ser	Ser	Leu	Ala	Gln	Pro	Gln	Leu	Pro	Tyr
	50					55					60				
Ser	Gln	Ala	Ala	Pro	Pro	Val	Gln	Thr	Pro	Leu	Pro	Gly	Ala	Pro	Pro
65					70					75				80	
Pro	Gln	Gln	Leu	Gln	Tyr	Gly	Gln	Gln	Gln	Pro	Met	Val	Ser	Thr	Gln
				85					90					95	
Met	Ala	Pro	Gly	His	Val	Lys	Ser	Val	Thr	Gln	Asn	Pro	Ala	Ser	Glu
			100						105				110		
Tyr	Val	Gln	Gln	Gln	Pro	Ile	Leu	Gln	Thr	Ala	Met	Ser	Ser	Gly	
		115					120						125		

<210> 591

<211> 684

<212> DNA

<213> Homo sapiens

<400> 591

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 aagcaggaat acaagcgcgga gtcgttcacc ctgttctccg agctgctgga ctcgatcaag  
 120  
 cgcgattcga ttcgggtcct cttccacgtc cagggggccgg gggaaaaatc cgtatcgaaa  
 180  
 naaaaagcgc gcctgcgtca ggaagccgaa gccctggccc agcgcatgca gttcgagcac  
 240  
 gctgaagccc caggcctgga cgcgccggaa atcctcggtg aagaagtcga tgcgcacctg  
 300  
 gccaccgcgc cggtacgcaa cgagcagaag ctggggccgta acgaactgtg ctactgcggt  
 360  
 tcgggcaaga agtacaagca ctgccacggt cagatcagct aaggtcttta ccggatactg  
 420  
 aaatacctgc gccgcgaccg gcattagccg tcgcggcggt tttccatttg aaacactgcc  
 480

cttgtgacgg cagtgcagat atcacattaa aaggagggca ttcattgggtg ttggttctgg  
 540  
 gtccttgaggc tacgttgac cgggttgccg gttttgaact cggatcgcc tcggccggta  
 600  
 tcaagcgccc tgggcgcaag gatgtggtgg cgatgcgctg cgccgaaggt tccacgggtg  
 660  
 cgggggtggt taccctcaac gcgt  
 684

<210> 592  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 592  
 Ser Thr Met Asp His Leu Arg His Gly Ile His Leu Arg Gly Tyr Ala  
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 Gln Lys Asn Pro Lys Gln Glu Tyr Lys Arg Glu Ser Phe Thr Leu Phe  
 20 25 30  
 Ser Glu Leu Leu Asp Ser Ile Lys Arg Asp Ser Ile Arg Val Leu Phe  
 35 40 45  
 His Val Gln Gly Pro Gly Glu Lys Ser Val Ser Lys Xaa Lys Ala Arg  
 50 55 60  
 Leu Arg Gln Glu Ala Glu Ala Leu Ala Gln Arg Met Gln Phe Glu His  
 65 70 75 80  
 Ala Glu Ala Pro Gly Leu Asp Ala Pro Glu Ile Leu Gly Glu Glu Val  
 85 90 95  
 Asp Val Ala Leu Ala Thr Ala Pro Val Arg Asn Glu Gln Lys Leu Gly  
 100 105 110  
 Arg Asn Glu Leu Cys Tyr Cys Gly Ser Gly Lys Lys Tyr Lys His Cys  
 115 120 125  
 His Gly Gln Ile Ser  
 130

<210> 593  
 <211> 615  
 <212> DNA  
 <213> Homo sapiens

<400> 593  
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 120  
 gataccatcc ccgcgccgct aggccagcca cgatggtcga cggccaccat ccagacccca  
 180  
 gtcataccta ctacacgtgg tcgattcgtg atcggtcccg tcatgatgag caccatcgac  
 240  
 ccgtttggca tggcccgcca tcacaccgat ctcggtcagg ttgccgaagt cattgtcagc  
 300  
 ccaaggatcg tcgatttggg cgcctccggg gagctcgggg gtcagggtt cgacacaagg  
 360  
 tcctcagcga tccatgccgg acgacgtggt cccgacgatg ccatggtgag cgattggcac  
 420

accggagact cgggtgcgacg cattcactgg cgctccaccg ctcaccgcgg ggacctcatg  
 480  
 gtccgatgcg aggagcaggc ctggaaccca tccgtcgtca tcgtgttgga ttctcgggct  
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 cggcggtcacg ctggaactgg ccccgcgcga tcctttgaat gggccgtcaa cgcgggtggca  
 600  
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 615

<210> 594  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 594  
 Xaa Arg Val Gln Thr Ala Arg Ser Leu Ala Pro Val Arg Ile Ala Leu  
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 Gly Ser Gln Thr Cys Glu Thr Val Thr Val Glu Arg Arg Gly Gly Leu  
 20 25 30  
 Pro Leu Arg Ala Ala Arg Phe Thr Asp Thr Ile Pro Ala Pro Leu Gly  
 35 40 45  
 Gln Pro Arg Trp Ser Thr Ala Thr Ile Gln Thr Pro Val Ile Pro Thr  
 50 55 60  
 Thr Arg Gly Arg Phe Val Ile Gly Pro Val Met Met Arg Thr Ile Asp  
 65 70 75 80  
 Pro Phe Gly Met Ala Arg His His Thr Asp Leu Gly Gln Val Ala Glu  
 85 90 95  
 Val Ile Val Thr Pro Arg Ile Val Asp Leu Gly Ala Ser Gly Glu Leu  
 100 105 110  
 Gly Gly Gln Gly Phe Asp Thr Arg Ser Ser Ala Ile His Ala Gly Arg  
 115 120 125  
 Arg Gly Pro Asp Asp Ala Met Val Arg Asp Trp His Thr Gly Asp Ser  
 130 135 140  
 Val Arg Arg Ile His Trp Arg Ser Thr Ala His Arg Gly Asp Leu Met  
 145 150 155 160  
 Val Arg Cys Glu Glu Gln Ala Trp Asn Pro Ser Val Val Ile Val Leu  
 165 170 175  
 Asp Ser Arg Ala Arg Arg His Ala Gly Thr Gly Pro Asp Ala Ser Phe  
 180 185 190  
 Glu Trp Ala Val Asn Ala Val Ala Ser Ile Ser Thr Arg  
 195 200 205

<210> 595  
 <211> 303  
 <212> DNA  
 <213> Homo sapiens

<400> 595  
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 60  
 cccatggggc catcgagaccg cgcgcgcgg gggcggttcgc cagggcctcc gcagaagccc  
 120  
 gcctgtgccc gcaaccgccc cgaaattctc tccctggcac cgtgtccgct ttacggagcc  
 180

cggagcaagg ctcagaaaaa tgtcccagcc aaaaacatgg tacatgctg tcatcaggca  
 240  
 agtcttcaaa gagcggctgg gaccaggggc cgagggacct cgtttagagg cggcttaggg  
 300  
 gga  
 303

<210> 596  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<400> 596  
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 20 25 30  
 Ala Arg Leu Cys Pro Gln Pro Pro Arg Asn Ser Leu Pro Gly Thr Val  
 35 40 45  
 Ser Ala Leu Arg Ser Pro Glu Gln Gly Ser Glu Lys Cys Pro Ser Gln  
 50 55 60  
 Lys His Gly Thr Cys Leu Ser Ser Gly Lys Ser Ser Lys Ser Gly Trp  
 65 70 75 80  
 Asp Gln Gly Pro Arg Asp Leu Val  
 85

<210> 597  
 <211> 2709  
 <212> DNA  
 <213> Homo sapiens

<400> 597  
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 aagaaccaca tgggtggagaa gacctacgaa tgtaaagaat gcgggaaatc ctttggcgat  
 120  
 ctcgtgtccc ggaggaaaca catgaggatt cacatcgtca agaaaccgt ggaatgtcgg  
 180  
 cagtgcggga agaccttccg aaaccagtcc atccttaaga ctcacatgaa ctctcacact  
 240  
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 300  
 accgcacaca ggaagataca cacgcaagag agacgctacg aatgcgccgc ctgcgggaaa  
 360  
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 420  
 gttgagtgtg ggcattgtgg caaggccttc aggaaccagt caacgctgaa gacgcacatg  
 480  
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 540  
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 600  
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 660

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720  
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780  
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840  
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960  
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1020  
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1080  
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1140  
ctcatgacgg aatcacact aaagagagaa atcagtgaag taaggaacgt ggaaggctcat  
1200  
gaatgggccg caaaccacgg ccagctgctt gtctttgtat ggcttgccag ctaacaatag  
1260  
tggttccatc tttaaggaag aagaatgttt gatggagaaa atttgtggcc aatgaagtct  
1320  
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1380  
acgggttctc agtcgggcga cgatttggct gtctaggcgt catttgcaa tgtctagaga  
1440  
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1500  
gatgctgcta agtcggctcc agcacacagg agccccccac aacgaagagt tagtgcccc  
1560  
aaacgtcact gttgctgagg ttgaaaataa tcatgcagtc attcctcaat tactgcctgc  
1620  
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1680  
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1740  
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1800  
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1860  
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1980  
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2100  
ttctcagtac cactttgtta ctggtacctg atgcacacgg attgcgacca gagcatgatg  
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2220  
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2280

tcagattagt aagggtgtgct aatctaaatt ttaaaaaatc tcttacaggt tttcttgag  
 2340  
 ctggtacat ccatgtctca cagccctggc cactgacaga tcagcagatg tcaccacgtg  
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 2460  
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 2580  
 agcgaccctg gcctcccctg tggcctcttt gagtgtctgc agcagccctg gacttccaga  
 2640  
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 2700  
 aaaaaaaaaa  
 2709

<210> 598

<211> 240

<212> PRT

<213> Homo sapiens

<400> 598

Xaa	Ala	Cys	Thr	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Trp	Lys	Ser	Asn	Phe	1	5	10	15
Asn	Leu	His	Lys	Lys	Asn	His	Met	Val	Glu	Lys	Thr	Tyr	Glu	Cys	Lys	20	25	30	
Glu	Cys	Gly	Lys	Ser	Phe	Gly	Asp	Leu	Val	Ser	Arg	Arg	Lys	His	Met	35	40	45	
Arg	Ile	His	Ile	Val	Lys	Lys	Pro	Val	Glu	Cys	Arg	Gln	Cys	Gly	Lys	50	55	60	
Thr	Phe	Arg	Asn	Gln	Ser	Ile	Leu	Lys	Thr	His	Met	Asn	Ser	His	Thr	65	70	75	80
Gly	Glu	Lys	Pro	Tyr	Gly	Cys	Asp	Leu	Cys	Gly	Lys	Ala	Phe	Ser	Ala	85	90	95	
Ser	Ser	Asn	Leu	Thr	Ala	His	Arg	Lys	Ile	His	Thr	Gln	Glu	Arg	Arg	100	105	110	
Tyr	Glu	Cys	Ala	Ala	Cys	Gly	Lys	Val	Phe	Gly	Asp	Tyr	Leu	Ser	Arg	115	120	125	
Arg	Arg	His	Met	Ser	Val	His	Leu	Val	Lys	Lys	Arg	Val	Glu	Cys	Arg	130	135	140	
His	Cys	Gly	Lys	Ala	Phe	Arg	Asn	Gln	Ser	Thr	Leu	Lys	Thr	His	Met	145	150	155	160
Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asp	His	Cys	Gly	Lys	165	170	175	
Ala	Phe	Ser	Ile	Gly	Ser	Asn	Leu	Asn	Val	His	Arg	Arg	Ile	His	Thr	180	185	190	
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Leu	Val	Cys	Gly	Lys	Ala	Phe	Ser	Asp	195	200	205	
His	Ser	Ser	Leu	Arg	Ser	His	Val	Lys	Thr	His	Arg	Gly	Glu	Lys	Leu	210	215	220	
Phe	Xaa	Cys	His	Pro	Cys	Gly	Lys	Gly	Ser	Ser	Glu	Arg	Ala	Xaa	Leu	225	230	235	240



<210> 599  
 <211> 340  
 <212> DNA  
 <213> Homo sapiens

<400> 599  
 acgcgtgcct cgcgactcct gacgtcgtgg tggctgcgct cggtcgtgtc actcctcttg  
 60  
 ttcggcgtca tggcgcaggt gctaggcgtg gccgtgcac tgagtctgca ccgctttgcc  
 120  
 caggcatgtt tgccgggccc catcccttgc acttcagtc cgtggcctat cggccgaggc  
 180  
 gcaggcctgc agttggagcc gtgcgtgggt gtcccgcgcg aggagcgtgt tggcagacta  
 240  
 tggggctcgt cggaggacga ggatgtgagt ggcgatggct ttgcgcgact gggcgtattc  
 300  
 caccgcgcga tgggtctcca gatcgtccag ggcgatgatca  
 340

<210> 600  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 600  
 Met Pro Trp Thr Ile Trp Ser Thr Ile Ala Gly Trp Asn Thr Pro Ser  
 1 5 10 15  
 Arg Ala Lys Pro Ser Pro Leu Thr Ser Ser Ser Ser Asp Glu Pro His  
 20 25 30  
 Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn  
 35 40 45  
 Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly  
 50 55 60  
 Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys  
 65 70 75 80  
 Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp  
 85 90 95  
 Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg  
 100 105 110

<210> 601  
 <211> 421  
 <212> DNA  
 <213> Homo sapiens

<400> 601  
 gccggcggca gcgacatctc gctcaacgtc ggctg'gcgcg gcctgacttc gcgtctttct  
 60  
 ccgcgtcca ccattttgat ggacggcgtc ccgctggcgg tcgcgcctta cggccagccg  
 120  
 cagctgtcga tggccccgct gtctatcggg aatctgcaat cgggtggacgt ggtgcgcggc  
 180  
 ggcggcgcgg tcgcgtacgg gccgcagaac gtcggcggcg tgatcaactt cgttaccgca  
 240

gacattccca aaacgtttgg cggcgccgcc agcgtaaaaa cccaggggtgc cagccacggc  
 300  
 ggccctgaaga ccctgaccag cgcctccgtg ggcggcaccg cagacaacgg cctcggcgcc  
 360  
 gagctgctct actccggcct gcacggccag ggctaccgag acaacaacga caacaccgac  
 420  
 n  
 421

<210> 602  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 602  
 Ala Gly Gly Ser Asp Ile Ser Leu Asn Val Gly Val Arg Gly Leu Thr  
 1 5 10 15  
 Ser Arg Leu Ser Pro Arg Ser Thr Ile Leu Met Asp Gly Val Pro Leu  
 20 25 30  
 Ala Val Ala Pro Tyr Gly Gln Pro Gln Leu Ser Met Ala Pro Leu Ser  
 35 40 45  
 Ile Gly Asn Leu Gln Ser Val Asp Val Val Arg Gly Gly Gly Ala Val  
 50 55 60  
 Arg Tyr Gly Pro Gln Asn Val Gly Gly Val Ile Asn Phe Val Thr Arg  
 65 70 75 80  
 Asp Ile Pro Lys Thr Phe Gly Gly Ala Ala Ser Val Gln Thr Gln Gly  
 85 90 95  
 Ala Ser His Gly Gly Leu Lys Thr Leu Thr Ser Ala Ser Val Gly Gly  
 100 105 110  
 Thr Ala Asp Asn Gly Leu Gly Ala Glu Leu Leu Tyr Ser Gly Leu His  
 115 120 125  
 Gly Gln Gly Tyr Arg Asp Asn Asn Asp Asn Thr Asp  
 130 135 140

<210> 603  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<400> 603  
 nagggcggca tgcacgaaag cttgcgcaaa cgctcgctgg aaggcttgga caagatcggc  
 60  
 ttgcacggcc tggccatcgg cggctctgtcg gtgggcgagc ccaagcacga gatgatcaag  
 120  
 gtgctggatt acctgccggg cctgatgccg gctgacaaac ctcgttacct tatgggcggt  
 180  
 ggcaaaccgg aagacctcgt agagggtgtg cgccgcgggtg tggacatgtt cgattgcgtg  
 240  
 atgccaaccc gtaatgcccg caatgggcat ctgttcatcg atacaggcgt gctgaagatc  
 300  
 cgtaacgcg  
 309

<210> 604

<211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 604  
 Xaa Gly Gly Met His Glu Ser Leu Arg Lys Arg Ser Leu Glu Gly Leu  
 1 5 10 15  
 Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly  
 20 25 30  
 Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu  
 35 40 45  
 Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu  
 50 55 60  
 Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val  
 65 70 75 80  
 Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly  
 85 90 95  
 Val Leu Lys Ile Arg Asn Ala  
 100

<210> 605  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<400> 605  
 acgcgttcac gatagggtag ttgcctatatt caacgcgggc ggtattttcc tgcacaacaa  
 60  
 actggcccaa ggctgggcta tagtcagggtg catagtactt ggtgaagtag cgtacgtccg  
 120  
 caccacatc acatttcagt accttggcta tcttcaatcg gaaaaaaga ttggagtaaa  
 180  
 tggtgagttt tggtaatggc aacgccgttt gactggaaga gttttggaag gtaatgaccg  
 240  
 attcccagtg caaagggtccc catgctacat cctgcgacaa tgaggccgtt agcacgttta  
 300  
 ttgcctcgct gctttgccga acgccaacct ctgtaccgat acgctgatac tgattgttga  
 360  
 tggatataggc ttgcgccagg taggtataat tggtaattc gtccatggca atgcgcagtg  
 420  
 aagtcttg  
 428

<210> 606  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 606  
 Met Asp Glu Leu Thr Asn Tyr Thr Tyr Leu Ala Gln Ala Tyr Thr Ile  
 1 5 10 15  
 Asn Asn Gln Tyr Gln Arg Ile Gly Thr Glu Val Gly Val Arg Gln Ser  
 20 25 30  
 Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

```

      35              40              45
Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
  50              55              60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
  65              70              75              80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
      85              90              95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
      100              105              110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
      115              120              125
Asn Tyr Pro Ile Val Asn Ala
      130              135

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<210> 607  
 <211> 366  
 <212> DNA  
 <213> Homo sapiens

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<400> 607
gatcacgatg aattgtgggc gtacacgtac gagaatgtga tggcgctaaa cttgccgctt
  60
gacattgtgt gtaaaggatt ctttagaaaa ttggaaaacg tagtgaccgg agtcaatttg
  120
gttttcaacg gcaaacatta tcaaattgta aagaaagagg atgacctatt caaattgacc
  180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attggaaata cttgtacttg
  240
acaacgcacg gtgtgtacaa cgtgttcacc aacagctttc attcgagctg tccatttttg
  300
ttggggcacca cgttgccgca gacattcaag aagcccaccg acgaaaagta tttgcccgag
  360
gacgcg
  366

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<210> 608  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

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<400> 608
Asp His Asp Glu Leu Trp Ala Tyr Thr Tyr Glu Asn Val Met Ala Leu
  1              5              10              15
Asn Leu Pro Pro Asp Ile Val Cys Lys Gly Phe Phe Arg Lys Leu Glu
      20              25              30
Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
      35              40              45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
      50              55              60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
  65              70              75              80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
      85              90              95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro

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100 105 110  
 Thr Asp Glu Lys Tyr Leu Pro Glu Asp Ala  
 115 120

<210> 609  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 609  
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 60  
 tgggtcgggtt ggaacgagtc cgtcatgagc ccggtcgcca tggacgactc cagcagtcgg  
 120  
 taccacgcct ggaagcagga cccccacgcg acggaatcgc cggcttccaa gtcgtcggcc  
 180  
 ccgaagcctc aaacttcccc cgccccgtac gccgggcccgg ctccgaagac accggccaca  
 240  
 cctggaccat ctggggcggg ggcgcgcggg tgggtggtggc ggggtggagcc g  
 291

<210> 610  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

<400> 610  
 Met Ser Pro Val Ala Met Asp Asp Ser Ser Ser Pro Tyr Pro Ala Trp  
 1 5 10 15  
 Lys Gln Asp Pro His Ala Thr Glu Ser Pro Ala Ser Lys Ser Ser Pro  
 20 25 30  
 Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys  
 35 40 45  
 Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp  
 50 55 60  
 Trp Arg Val Glu Pro  
 65

<210> 611  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 611  
 nnnatcttgt gtcgattttc ggtcgcatat actatggggg agtattgtat aatgcggcgg  
 60  
 tgtacccaag tagagaggtg ttcgatgccca cacagtcggg aagaaaagaa gcaagcactg  
 120  
 acgcgcatca ggcgcatcaa aggtcaggta gcgactcttg agcaagcgt tgatgcaggt  
 180  
 gcgaaatgtc ctgcaattct tcagcagctt gcggccgttc gtggcgcagt caacggattg  
 240  
 atggcaacgg ttctggagag ctatctgcgg gaagagtttc ccagtagcga aatcaggagc  
 300

gattcgcaga acaagtccat tgacgagacc atctctatcg tccgctccta tctgcggtag  
 360  
 aggcaccagg gtgtcctcgg tgagggcaaa ttt  
 393

<210> 612  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 612  
 Xaa Ile Leu Cys Arg Phe Ser Val Ala Tyr Thr Met Gly Glu Tyr Cys  
 1 5 10 15  
 Ile Met Arg Arg Cys Thr Gln Val Glu Arg Cys Ser Met Pro His Ser  
 20 25 30  
 Pro Glu Glu Lys Lys Gln Ala Leu Thr Arg Ile Arg Arg Ile Lys Gly  
 35 40 45  
 Gln Val Ala Thr Leu Glu Gln Ala Leu Asp Ala Gly Ala Lys Cys Pro  
 50 55 60  
 Ala Ile Leu Gln Gln Leu Ala Ala Val Arg Gly Ala Val Asn Gly Leu  
 65 70 75 80  
 Met Ala Thr Val Leu Glu Ser Tyr Leu Arg Glu Glu Phe Pro Ser Ser  
 85 90 95  
 Glu Ile Arg Ser Asp Ser Gln Asn Lys Ser Ile Asp Glu Thr Ile Ser  
 100 105 110  
 Ile Val Arg Ser Tyr Leu Arg  
 115

<210> 613  
 <211> 567  
 <212> DNA  
 <213> Homo sapiens

<400> 613  
 gaaaatgctc ctggcgccctc aggggaaggctc cttctcaaag aaaaggatgg ggctgaatcg  
 60  
 ctggaaacgg ttcacaagga agccgagtcc caagcctact tttggctcctg acagtgtgga  
 120  
 acactggata aagagagtgg agaaagccctc agagtgttgca gtgtcaaatg cattttttac  
 180  
 tagaaattca gatttaccta gaagtccctg gggccaaatc acagatttga aaacatctga  
 240  
 gcaaatagag gatcatgatg aaatctatgc agaagctcag gagctgggtca atgactgggtt  
 300  
 agacacccaaa cttaagcaag aattagcaag tgaggaagaa ggtgatgcta aaaacactgt  
 360  
 gtcaagtgtc actattatgc cggaagccaa tggccatttg aaatatgaca agtttgatga  
 420  
 tttatgtggc tatttggagg aagaagagga aagtaccacc gttcaaaaat ttatagacca  
 480  
 tctgtccat aaaaatgtgg tagattctgc aatgatggaa gatcttggaa ggaaggaaaa  
 540  
 ccaagacaag aagcagcaga aggatcc  
 567

<210> 614  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 614  
 Met Leu Leu Ala Pro Gln Gly Arg Ser Phe Ser Lys Lys Arg Met Gly  
 1 5 10 15  
 Leu Asn Arg Trp Lys Arg Phe Thr Arg Lys Pro Ser Pro Lys Pro Thr  
 20 25 30  
 Phe Gly Pro Asp Ser Val Glu His Trp Ile Lys Arg Val Glu Lys Ala  
 35 40 45  
 Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu  
 50 55 60  
 Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln  
 65 70 75 80  
 Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn  
 85 90 95  
 Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu  
 100 105 110  
 Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala  
 115 120 125  
 Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu  
 130 135 140  
 Glu Glu Glu Glu Glu Ser Thr Thr Val Gln Lys Phe Ile Asp His Leu  
 145 150 155 160  
 Leu His Lys Asn Val Val Asp Ser Ala Met Met Glu Asp Leu Gly Arg  
 165 170 175  
 Lys Glu Asn Gln Asp Lys Lys Gln Gln Lys Asp  
 180 185

<210> 615  
 <211> 685  
 <212> DNA  
 <213> Homo sapiens

<400> 615  
 nnacgcgtgc tgccctaagt gacggattcc atgtcgggtgc gagtcgggtc ggggccgatg  
 60  
 ggccatgaac gggccctagc gagggccgga ctcgcccccg tggccggatg cgacgaggcg  
 120  
 gggcggggcg cgtgtgcagg gccattggta gccgcagctg tcattcttga tgatcgaga  
 180  
 tccggcagga ttgcggggct agcagattcc aagacactat ctgcggccaa gagagaggcc  
 240  
 ctgtttaacg tcatcatgga taaagctttg gcagtgtcgt gggtagctgt agaagccgac  
 300  
 gaatgcgac gggtggggat gcaggaggca gatatcagcg gcttgaggcg tgccgtggtg  
 360  
 aggttgggag ttgaaccggg ctacgtgctg tcggacggtt tcccggtcga cggactgacg  
 420  
 gttcccgatc tgggaatgtg gaagggcgat tcagtgtgtg cgtgtgtggc agctgcctcc  
 480

atcgtggcca aagtggccag ggatcgcatc atgatcgcta tggacgccga gattcctggt  
 540  
 tacgattttg cgggtgcacaa ggggtacgcg acagccttac accagcgctcg tctgaaggag  
 600  
 ttaggaccgt ctcgtcagca ccggatgagc tacgccaatg tgcgacgagc ggctaggctt  
 660  
 cattcatcat gagtgccgaa gatct  
 685

<210> 616

<211> 213

<212> PRT

<213> Homo sapiens

<400> 616

Met	Ser	Val	Arg	Val	Gly	Ser	Gly	Pro	Met	Gly	His	Glu	Arg	Ala	Leu
1				5					10					15	
Ala	Arg	Ala	Gly	Leu	Gly	Pro	Val	Ala	Gly	Cys	Asp	Glu	Ala	Gly	Arg
			20					25					30		
Gly	Ala	Cys	Ala	Gly	Pro	Leu	Val	Ala	Ala	Ala	Val	Ile	Leu	Asp	Asp
		35					40					45			
Arg	Arg	Ser	Gly	Arg	Ile	Ala	Gly	Leu	Ala	Asp	Ser	Lys	Thr	Leu	Ser
	50					55					60				
Ala	Ala	Lys	Arg	Glu	Ala	Leu	Phe	Asn	Val	Ile	Met	Asp	Lys	Ala	Leu
65					70					75				80	
Ala	Val	Ser	Trp	Val	Arg	Val	Glu	Ala	Asp	Glu	Cys	Asp	Arg	Leu	Gly
			85					90						95	
Met	Gln	Glu	Ala	Asp	Ile	Ser	Gly	Leu	Arg	Arg	Ala	Val	Val	Arg	Leu
			100					105					110		
Gly	Val	Glu	Pro	Gly	Tyr	Val	Leu	Ser	Asp	Gly	Phe	Pro	Val	Asp	Gly
		115					120					125			
Leu	Thr	Val	Pro	Asp	Leu	Gly	Met	Trp	Lys	Gly	Asp	Ser	Val	Cys	Ala
	130					135					140				
Cys	Val	Ala	Ala	Ala	Ser	Ile	Val	Ala	Lys	Val	Ala	Arg	Asp	Arg	Ile
145					150					155				160	
Met	Ile	Ala	Met	Asp	Ala	Glu	Ile	Pro	Gly	Tyr	Asp	Phe	Ala	Val	His
			165					170						175	
Lys	Gly	Tyr	Ala	Thr	Ala	Leu	His	Gln	Arg	Arg	Leu	Lys	Glu	Leu	Gly
		180					185					190			
Pro	Ser	Arg	Gln	His	Arg	Met	Ser	Tyr	Ala	Asn	Val	Arg	Arg	Ala	Ala
		195				200						205			
Arg	Leu	His	Ser	Ser											
		210													

<210> 617

<211> 337

<212> DNA

<213> Homo sapiens

<400> 617

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 gctcgtttcc cggcttcaac cccatcgctg agctgtcgct gtcgttccac aacctcgctg  
 120



tcggcgccaa cgccagcgc caggccatgt tcctcgaaaa cgtttccggc cttcccggag  
 180  
 cgaatcctcc gaaacttcga cctgtcccaa caagactctg cactcgtgat ttcataaagg  
 240  
 gctgcaacgt cgtgccaatc gagatggccg aggagttcca gcgtcgcggc gtccgcgtcg  
 300  
 tctcgatcat ctcgctggcg cactcgcagg cgtcgac  
 337

<210> 618  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 618  
 Xaa Thr Cys Leu Ala Arg Gly Thr Arg Gly Ser Trp Ser Arg Lys Cys  
 1 5 10 15  
 Gly Arg Ala Thr Ala Arg Phe Pro Ala Ser Thr Pro Ser Ser Cys  
 20 25 30  
 Arg Cys Arg Ser Thr Thr Ser Ser Ser Ala Pro Thr Ala Ser Ala Arg  
 35 40 45  
 Pro Cys Ser Ser Lys Thr Phe Pro Ala Phe Pro Glu Arg Ile Leu Arg  
 50 55 60  
 Asn Phe Asp Leu Ser Gln Gln Asp Ser Ala Leu Val Ile Ser Ser Ser  
 65 70 75 80  
 Ala Ala Thr Ser Cys Gln Ser Arg Trp Pro Arg Ser Ser Ser Val Ala  
 85 90 95  
 Ala Ser Ala Ser Ser Arg Ser Ser Arg Trp Arg Thr Arg Arg Arg Arg  
 100 105 110

<210> 619  
 <211> 425  
 <212> DNA  
 <213> Homo sapiens

<400> 619  
 acgcgttttt tatgccgatc ttatgctcta acctagaaac aatatcagct acaaacctaa  
 60  
 tagctataag ataatttcg aaagcatcaa taggagtttt gatcatttcc gcatacctaa  
 120  
 gttttatagc atctttgtca gaaggcaaac ctgccaaacc agatgaatcg atgccactct  
 180  
 caaacttgct caaatgttca attaaatcat ccaagttgtg gccatgctta ccgcttccag  
 240  
 attttgaatg aatcattact ttaattgatt tttcaatcgc taaatggaat tcccagcaag  
 300  
 caatagaagc ccgctcattt ttaaagctca gtatgtcact aatgcctttt tcgaagtggc  
 360  
 tccatattcc ctgcgccata ttagaagctg actgggttga atggcttgcc atgttcaaat  
 420  
 ctaga  
 425

<210> 620

<211> 137  
 <212> PRT  
 <213> Homo sapiens

<400> 620  
 Met Ala Ser His Ser Asn Gln Ser Ala Ser Asn Met Ala Gln Gly Ile  
 1 5 10 15  
 Trp Ser His Phe Glu Lys Gly Ile Ser Asp Ile Leu Ser Phe Lys Asn  
 20 25 30  
 Glu Arg Ala Ser Ile Ala Cys Trp Glu Phe His Leu Ala Ile Glu Lys  
 35 40 45  
 Ser Ile Lys Val Met Ile His Ser Lys Ser Gly Ser Gly Lys His Gly  
 50 55 60  
 His Asn Leu Asp Asp Leu Ile Glu His Leu Ser Lys Phe Glu Ser Gly  
 65 70 75 80  
 Ile Asp Ser Ser Gly Leu Ala Gly Leu Pro Ser Asp Lys Asp Ala Ile  
 85 90 95  
 Lys Leu Arg Tyr Ala Glu Met Ile Lys Thr Pro Ile Asp Ala Phe Glu  
 100 105 110  
 Tyr Tyr Leu Ile Ala Ile Arg Phe Val Ala Asp Ile Val Ser Arg Leu  
 115 120 125  
 Glu His Lys Ile Gly Ile Lys Asn Ala  
 130 135

<210> 621  
 <211> 453  
 <212> DNA  
 <213> Homo sapiens

<400> 621  
 cccggcaagg gagccatctt gacgaatatg tccttgtggt ggttcgacca attggccgac  
 60  
 atcgtcgata accatctcgt gagcgtggat gtccccgccg aggtcgcagg gcgcgccatg  
 120  
 gtcgttgagg aactcgacat gttccccggtc gaatgcgtcg tgcggggcta cctcaccggt  
 180  
 tcagggtggg ccgaatatca gcgcaaccag gccgtgtgcg gaatccgcct tcccagggg  
 240  
 ctgcagaatg ggtccccgct cgaagagccc attttcaccc cggcaattaa ggccccgcag  
 300  
 ggagaacatg acgagaacat cgactatcta cgcttggttag aactcgtcgg tccngatgn  
 360  
 tcagcgcagc tgcattgacct ttcgtgcggt gtctaccagc gtgcagagga gatcgtcgg  
 420  
 aagcagggca tcctcctggc ggataccaag ctt  
 453

<210> 622  
 <211> 151  
 <212> PRT  
 <213> Homo sapiens

<400> 622  
 Pro Gly Lys Gly Ala Ile Leu Thr Asn Met Ser Leu Trp Trp Phe Asp

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      1           5           10           15
Gln Leu Ala Asp Ile Val Asp Asn His Leu Val Ser Val Asp Val Pro
      20           25           30
Ala Glu Val Ala Gly Arg Ala Met Val Val Glu Glu Leu Asp Met Phe
      35           40           45
Pro Val Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Trp Ala
      50           55           60
Glu Tyr Gln Arg Asn Gln Ala Val Cys Gly Ile Arg Leu Pro Glu Gly
      65           70           75           80
Leu Gln Asn Gly Ser Arg Leu Glu Glu Pro Ile Phe Thr Pro Ala Ile
      85           90           95
Lys Ala Pro Gln Gly Glu His Asp Glu Asn Ile Asp Tyr Leu Arg Leu
      100          105          110
Val Glu Leu Val Gly Pro Xaa Xaa Ser Ala Gln Leu His Asp Leu Ser
      115          120          125
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Leu Leu Ala Asp Thr Lys Leu
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&lt;210&gt; 623

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 623

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&lt;210&gt; 624

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 624

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Gly Ala Glu Leu Val Lys Ser Val Val Asn Ser Ile Thr Cys Val Ser
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&lt;210&gt; 628

&lt;211&gt; 1294

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 628

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 Glu His Ser Leu His Val Gln Asp Pro  
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749

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Lys Val Asp Arg Ser Thr Gln Asp Glu Leu Ser Thr Lys Cys Val His		1215
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Cys Thr Asp Lys Tyr Asp Phe Thr Thr His Ile Gln Arg Gly Leu His		1260
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&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 629

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&lt;210&gt; 630

&lt;211&gt; 137

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 630

Xaa Ala Phe Ala Glu Glu Gly Thr Gly Ala Ser Thr Phe Gln Leu Ser

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Ile Ala Cys Gly Ile Trp Phe Ser Asn Val Ser Gly Gly Ile Ala Trp
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Phe Val Ala Ala Ile Gly Gly Ala Asp Met Pro Val Val Ile Ser Met
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Leu Asn Ser Tyr Ser Gly Trp Ala Ala Ala Phe Ser Gly Phe Ser Leu
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His Ile Pro Val Leu Ile Val Thr Gly
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&lt;210&gt; 631

&lt;211&gt; 275

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 631

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 632

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Glu Arg Asp Gln Tyr Lys Leu Met Ala Asn Gln Leu Arg Glu Arg His
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Gln	Asn	Gln	Val	Leu	Phe	Phe	Phe	Ala	Ala	Ile	Ile	Phe	Thr	Val	Ser
			85					90					95		
Val	Ala	Leu	His	Leu	Phe	Ser	Ile	Asp	Glu	Glu	Gln	Tyr	Ser	Pro	Gln
		100					105					110			
Gln	Glu	Arg	Ser	Ala	Glu	Glu	Pro	Gly	Ala	Leu	Asp	Gly	Gly	Glu	Pro
	115					120					125				
His	Gly	Val	Pro	Ala	Phe	Pro	Asp	Glu	Val	Gln	Ser	Glu	His	Glu	Leu
	130				135				140						
Ala	Leu	Asp	Tyr	Pro	Asp	Val	Asp	Ile	Met	Arg	Ser	Lys	Ser	Asp	Ser
145				150					155					160	
Ala	Leu	His	Val	Pro	Asp	Thr	Ala	Leu	Asp	Leu	Glu	Pro	Glu	Leu	Leu
		165					170						175		
Phe	Leu	His	Asp	Ile	Glu	Pro	Ser	Ile	Phe	His	Asp	Ala	Ser	Tyr	Pro
	180					185					190				
Ala	Thr	Pro	Arg	Ser	Thr	Ser	Gln	Glu	Leu	Ala	Lys	Thr	Lys	Leu	Pro
	195					200					205				
Arg	Leu	Ala	Thr	Phe	Leu	Lys	Glu	Ala	Ala	Lys	Glu	Asp	Glu	Thr	Leu
	210				215						220				
Leu	Asp	Asn	His	Leu	Asn	Glu	Ala	Lys	Val	Pro	Asn	Gly	Ser	Gly	Ser
225				230					235					240	
Pro	Thr	Lys	Asp	Ala	Leu	Gly	Gly	Tyr	Thr	Arg	Val	Asp	Thr	Lys	Pro
		245					250						255		
Ser	Ala	Thr	Ser	Ser	Ser	Met	Arg	Arg	Arg	Arg	His	Ala	Phe	Arg	Arg
	260					265					270				
Gln	Ala	Ser	Ser	Thr	Phe	Ser	Tyr	Tyr	Gly	Lys	Leu	Gly	Ser	His	Cys
	275					280					285				
Tyr	Arg	Tyr	Arg	Arg	Ala	Asn	Ala	Val	Val	Leu	Ile	Lys	Pro	Ser	Arg

```

      290              295              300
Ser Met Ser Asp Leu Tyr Asp Met Gln Lys Arg Gln Arg Gln His Arg
305              310              315              320
His Arg Asn Gln Ser Gly Ala Thr Thr Ser Ser Gly Asp Thr Glu Ser
      325              330              335
Glu Glu Gly Glu Gly Glu Thr Thr Val Arg Leu Leu Trp Leu Ser Met
      340              345              350
Leu Lys Met Pro Arg Glu Leu Met Arg Leu Cys Leu Cys His Leu Leu
      355              360              365
Thr Trp Phe Ser Val Ile Ala Glu Ala Val Phe Tyr Thr Asp Phe Met
      370              375              380
Gly Gln Val Ile Phe Glu Gly Asp Pro Lys Ala Pro Ser Asn Ser Thr
385              390              395              400
Ala Trp Gln Ala Tyr Asn Ala Gly Val Lys Met Gly Cys Trp Gly Leu
      405              410              415
Val Ile Tyr Ala Ala Thr Gly Ala Ile Cys Ser Ala Leu Leu Gln Lys
      420              425              430
Tyr Leu Asp Asn Tyr Asp Leu Ser Val Arg Val Ile Tyr Val Leu Gly
      435              440              445
Thr Leu Gly Phe Ser Val Gly Thr Ala Val Met Ala Met Phe Pro Asn
      450              455              460
Val Tyr Val Ala Met Val Thr Ile Ser Thr Met Gly Ile Val Ser Met
465              470              475              480
Ser Ile Ser Tyr Cys Pro Tyr Ala Leu Leu Gly Gln Tyr His Asp Ile
      485              490              495
Lys Gln Tyr Ile His His Ser Pro Gly Asn Ser Lys Arg Gly Phe Gly
      500              505              510
Ile Asp Cys Ala Ile Leu Ser Cys Gln Val Tyr Ile Ser Gln Ile Leu
      515              520              525
Val Ala Ser Ala Leu Gly Gly Val Val Asp Ala Val Gly Thr Val Arg
      530              535              540
Val Ile Pro Met Val Ala Ser Val Gly Ser Phe Leu Gly Phe Leu Thr
545              550              555              560
Ala Thr Phe Leu Val Ile Tyr Pro Asp Val Ser Glu Glu Ala Lys Glu
      565              570              575
Glu Gln Lys Gly Leu Ser Ser Pro Leu Ala Gly Glu Gly Arg Ala Gly
      580              585              590
Gly Asn Ser Glu Lys Pro Thr Val Leu Lys Leu Thr Arg Lys Glu Gly
      595              600              605
Leu Gln Gly Pro Val Glu Thr Glu Ser Val Val
      610              615

```

&lt;210&gt; 637

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 637

```

ngaaaaacag gatgaatccc gtatcattct taagcccgaa aagtactgaa tgtcgtcttc
60
tctcgcgtcg tgatgatctg gaaaggaaaa atcatcgtga ctactacatc acccgctact
120
acgcaaagac cgtcagttgg caggaaagtt ggttcctggt cccttaatcc atgggtgtttt
180

```

tgtaggcctt tattattttt cggaatggtt cggtttattg cgattccagt attcctcact  
 240  
 gtgccgaata tcattaatat cggaatccaa gccgcggtgg tggcgattat ggccttcggt  
 300  
 atgaccttcg tcacgttac ctccggcatt gatttgtctg tgggttcggt cgcagctctt  
 360  
 tcagccatgg  
 370

<210> 638

<211> 99

<212> PRT

<213> Homo sapiens

<400> 638

Met Ile Trp Lys Gly Lys Ile Ile Val Thr Thr Thr Ser Pro Ala Thr  
 1 5 10 15  
 Thr Gln Arg Pro Ser Val Gly Arg Lys Val Gly Ser Trp Ser Leu Asn  
 20 25 30  
 Pro Trp Cys Phe Cys Arg Pro Leu Leu Phe Phe Gly Met Val Arg Phe  
 35 40 45  
 Ile Ala Ile Pro Val Phe Leu Thr Val Pro Asn Ile Ile Asn Ile Gly  
 50 55 60  
 Ile Gln Ala Ala Val Val Ala Ile Met Ala Phe Gly Met Thr Phe Val  
 65 70 75 80  
 Ile Val Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Val Ala Ala Leu  
 85 90 95  
 Ser Ala Met

<210> 639

<211> 330

<212> DNA

<213> Homo sapiens

<400> 639

nacgcgtcga tgggcaacta catcttcagt cgggatgccc tggtcgaggc actcttcgca  
 60  
 gactcccagt ccgtgagtc gcgtcatgac atgggtggcg acatcatccc gagattcgtc  
 120  
 gaggcgggg acgcgcaggt ctacgacttc tgtgacaacc aggtgcccg aaccaccgag  
 180  
 aaggatcggg actactggcg ggacgtggga actatcgatg cctaccacga cgcgcacatg  
 240  
 gacctcgtgt cgggtggaacc ggagttcaac ctctacaacc ccgactggcc gatctggagc  
 300  
 atccaggaac aggcaccggg agcgaaattt  
 330

<210> 640

<211> 110

<212> PRT

<213> Homo sapiens

&lt;400&gt; 640

Xaa Ala Ser Met Gly Asn Tyr Ile Phe Ser Arg Asp Ala Leu Val Glu  
 1 5 10 15  
 Ala Leu Phe Ala Asp Ser Gln Ser Ala Glu Ser Arg His Asp Met Gly  
 20 25 30  
 Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr  
 35 40 45  
 Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp  
 50 55 60  
 Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met  
 65 70 75 80  
 Asp Leu Val Ser Val Glu Pro Glu Phe Asn Leu Tyr Asn Pro Asp Trp  
 85 90 95  
 Pro Ile Trp Ser Ile Gln Glu Gln Ala Pro Gly Ala Lys Phe  
 100 105 110

&lt;210&gt; 641

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 641

cgcgtgaccg gcgcggagaa cgtgcgcaag atcctcatgg gcgagcacca cctcgtgagc  
 60  
 accgagtggc ctgcgagcac ccgcatgttg ctggggcccca acacgggtgtc caattccatt  
 120  
 ggcgacatcc accgcaacaa gcgcaaggtc ttctccaaga tcttcagcca cgaggccctg  
 180  
 gagagttacc tgcccaagat ccagctgggtg atccaggaca cactgcgcgc ctggagcagc  
 240  
 caccgccagg ccattcaacgt gtaccaggag gcgcagaagc tgaccttcg catggccatc  
 300  
 cgggtgctgc tgggcttcag catccctgag gaggaccttg ggcacctctt tgaggtctac  
 360  
 cagcagtttg tggacaatgt cttctccctg cctgtcgacc tgcccttcag tggctaccgg  
 420  
 cggggcattc aggctcggca gatcctgcag aaggggctgg agaaggccat ccgggagaag  
 480  
 ctgcagtga c  
 491

&lt;210&gt; 642

&lt;211&gt; 163

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 642

Arg Val Thr Gly Ala Glu Asn Val Arg Lys Ile Leu Met Gly Glu His  
 1 5 10 15  
 His Leu Val Ser Thr Glu Trp Pro Arg Ser Thr Arg Met Leu Leu Gly  
 20 25 30  
 Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg  
 35 40 45  
 Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu



```

      50              55              60
Pro Lys Ile Gln Leu Val Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser
65              70              75              80
His Pro Glu Ala Ile Asn Val Tyr Gln Glu Ala Gln Lys Leu Thr Phe
      85              90              95
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp
      100              105              110
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe
      115              120              125
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln
      130              135              140
Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys
145              150              155              160
Leu Gln Cys

```

<210> 643  
 <211> 628  
 <212> DNA  
 <213> Homo sapiens

```

<400> 643
nagatctttg acatctacgt ggtcacgct gactacctgc ccctaggggc tgagcaggat
60
gccatcacgc tgcggaagg ccagtatgtg gaggtcctgg atgcagccca cccactgctg
120
tggcttgctc gcaccaagcc caccaagtcc agccccctcac ggcagggctg ggtgtcacca
180
gcctacctgg acaggaggct caagctgtca cctgagtggg gggccgctga ggccccctgag
240
ttccctgggg aggtgtgtc tgaagacgaa tacaaggcaa ggctgagctc tgtgatccag
300
gagctgctga gttctgagca ggccttcgtg gaggagctgc agttcctgca gagccaccac
360
ctgcagcacc tggagcgctg cccccacgtg cccatagctg tggccggcca gaaggcagtc
420
atcttcgca atgtgcggga catcgccgc ttccacagca gcttcctgca ggagttgcag
480
cagtgcgaca cggacgacga cgtggccatg tgcttcatca agaaccaggc ggcctttgag
540
cagtacctgg agttcctggt gggacgtgtg caggctgagt cggtggtcgt cagcacggcc
600
atccaggagt tctacaagaa atacgcgt
628

```

<210> 644  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

```

<400> 644
Xaa Ile Phe Asp Ile Tyr Val Val Thr Ala Asp Tyr Leu Pro Leu Gly
1              5              10              15
Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr Val Glu Val

```

```

      20      25      30
Leu Asp Ala Ala His Pro Leu Arg Trp Leu Val Arg Thr Lys Pro Thr
      35      40      45
Lys Ser Ser Pro Ser Arg Gln Gly Trp Val Ser Pro Ala Tyr Leu Asp
      50      55      60
Arg Arg Leu Lys Leu Ser Pro Glu Trp Gly Ala Ala Glu Ala Pro Glu
65      70      75      80
Phe Pro Gly Glu Ala Val Ser Glu Asp Glu Tyr Lys Ala Arg Leu Ser
      85      90      95
Ser Val Ile Gln Glu Leu Leu Ser Ser Glu Gln Ala Phe Val Glu Glu
      100      105      110
Leu Gln Phe Leu Gln Ser His His Leu Gln His Leu Glu Arg Cys Pro
      115      120      125
His Val Pro Ile Ala Val Ala Gly Gln Lys Ala Val Ile Phe Arg Asn
      130      135      140
Val Arg Asp Ile Gly Arg Phe His Ser Ser Phe Leu Gln Glu Leu Gln
145      150      155      160
Gln Cys Asp Thr Asp Asp Val Ala Met Cys Phe Ile Lys Asn Gln
      165      170      175
Ala Ala Phe Glu Gln Tyr Leu Glu Phe Leu Val Gly Arg Val Gln Ala
      180      185      190
Glu Ser Val Val Val Ser Thr Ala Ile Gln Glu Phe Tyr Lys Lys Tyr
      195      200      205
Ala

```

&lt;210&gt; 645

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 645

```

atccataggc attgccagag tattcacttc ctgttgaggagg cacacagggg agaggcctgt
60
gaggggaagg gcatcaatgc agggctgggg tgtgggaagg tctgcagggc tggcaatggg
120
caagctcagg aatgggtgggg gagacagttg gagccacggc agggacaatg gagctcagaa
180
ggtcctctctg tcattcccttt tggaacccat tgatctggaa aatttggggc agtgcctttt
240
tccgtaggta ctggaggcac tggcttgaca tactacagcc ctcccaggag gccagaagg
300
tagatgttat aactaccccc atttccaga tgaagaaact gagcctctgg gatctgcgga
360
agctcccaga gctggagcag ttagtccctg ggcctacac tcacagcaca gtttccc
417

```

&lt;210&gt; 646

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 646

```

Met Val Gly Glu Thr Val Gly Ala Thr Ala Gly Thr Met Glu Leu Arg

```

```

      1           5           10           15
Arg Ser Leu Cys His Pro Phe Trp Asn Pro Leu Ile Trp Lys Ile Trp
      20           25           30
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu
      35           40           45
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile
      50           55           60
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu
      65           70           75           80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser
      85           90           95

```

&lt;210&gt; 647

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 647

```

acgcggtttcg gttcttgagc gttccacca attcagcggg ggtgagcggc ccctgtgcat
60
cgcgacagcag ggtgatcaga taggcgatat ccgcctcgtt cagttgcacg gtgtcgttat
120
cggtagccat gcgtggcgaa ctcttttggc atgggaaaat cgggtgaggc caacgggcac
180
agcaacagga cgtgtccctt gcggcacgtg gcaacacgtc agtatagcgc gtttcgcccg
240
ggatttccgt tgaatgaagg caagaagtcg ggcacgcac cacctgctac cgctcggtgg
300
tacgatagcc gcggcgccac caggttggtt acattccaaa cgcaacgcag gaacccgcac
360
gaacagcggtt ttctgcaaca aaccccttat gacgctggct ctcgggcatt tcagtgtcga
420
c
421

```

&lt;210&gt; 648

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 648

```

Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro
      1           5           10           15
Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe
      20           25           30
Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala
      35           40           45
Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr
      50           55           60
Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr
      65           70           75           80
Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg
      85           90

```

<210> 649  
 <211> 563  
 <212> DNA  
 <213> Homo sapiens

<400> 649  
 cgcaacatgc ataaacacat gtgctcctcc gagactcagc tacttccttt gccctctctg  
 60  
 gacctcagtg tccaggcttg tgcatttagg ggctcagggt tgggctctgt gcctatgagc  
 120  
 cagtctatgt gtgcactgtc tgtctgtctg tccgtctgcc agcaaccttc aaggccccag  
 180  
 gaggggaagg caccaatgga aggtgggggc agggaaggag gtagcgttga caagttccaa  
 240  
 tgtctggctt tccctcctgg aaaccccgag ctggggctgg ccccccttc ccttcctgtc  
 300  
 tctctcgctc aagcacgtcc cttctaagag cccctctctg cagacgcccc cagtgaacc  
 360  
 aagcctagat tcgctgccaa gaaggccgac attttttaga cttgccacgt taaagggggc  
 420  
 tgcacaggca cgcaactcaa tccccccctc catgtcctcc gcctgtgcac attcaggcaa  
 480  
 cccgaaacac acaaagacac ggttggacac agcggccacc tgtgcacaca ggaggtagca  
 540  
 catggagcgc atctgacccc ggg  
 563

<210> 650  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 650  
 Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro  
 1 5 10 15  
 Ser Leu Asp Leu Ser Val Gln Ala Cys Ala Phe Arg Gly Ser Gly Leu  
 20 25 30  
 Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu  
 35 40 45  
 Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met  
 50 55 60  
 Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu  
 65 70 75 80  
 Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu  
 85 90 95  
 Pro Val Ser Leu Ala Gln Ala Arg Pro Phe  
 100 105

<210> 651  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 651

gaattcttca acaagctctc ctgctctagg atcaaggata gacctataca aggtccaaac  
60  
cataatggag tccatggggg caaagttatc tcttgagct cagcagttga tggatatggg  
120  
taggtgtcag cagcggaatt gtattcccat tggagagcag cttcagtcgg tgttgggcaa  
180  
ttctggatac aagcatatga ttggactaca atcctcatct accttaggaa ccttaaacaa  
240  
gtcgtcctcc acaccttttc cttttagaac tggattgaca tctgggaacg tgactgaaaa  
300  
cttacaagcg tacattgata aaagtacaca actgcctggg ggagagaatt c  
351

<210> 652  
<211> 95  
<212> PRT  
<213> Homo sapiens

<400> 652  
Met Glu Ser Met Gly Ser Lys Leu Ser Pro Gly Ala Gln Gln Leu Met  
1 5 10 15  
Asp Met Val Arg Cys Gln Gln Arg Asn Cys Ile Pro Ile Gly Glu Gln  
20 25 30  
Leu Gln Ser Val Leu Gly Asn Ser Gly Tyr Lys His Met Ile Gly Leu  
35 40 45  
Gln Ser Ser Ser Thr Leu Gly Thr Leu Asn Lys Ser Ser Ser Thr Pro  
50 55 60  
Phe Pro Phe Arg Thr Gly Leu Thr Ser Gly Asn Val Thr Glu Asn Leu  
65 70 75 80  
Gln Ala Tyr Ile Asp Lys Ser Thr Gln Leu Pro Gly Gly Glu Asn  
85 90 95

<210> 653  
<211> 399  
<212> DNA  
<213> Homo sapiens

<400> 653  
nncccgggtg gggctggggg ggggccagca tcagaggagg acatgaccaa gctgtgcaac  
60  
caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgtcga  
120  
cactcttctc ctggagaggg agcgagcccc caaatgttcc aactgtgtc ccaggggccc  
180  
ccctctgccc gccctccctg tcgagttcct cctacaactc cacttaatgg gggctcctggc  
240  
tcccttcccc cagaaccacc ctcaatttcc caggccttcc ccactctagc aggccctggg  
300  
gggcttttcc cccaaggct tgetgaccea gtcccttctg ggggcagtag cagcccccgt  
360  
ttctcccaa ggggcaatgc cccctctcca gcccacct  
399

<210> 654

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 654

```

Xaa Pro Gly Gly Ala Gly Val Gly Pro Ala Ser Glu Glu Asp Met Thr
 1             5             10             15
Lys Leu Cys Asn His Arg Arg Lys Ala Val Ala Met Ala Thr Leu Tyr
      20             25             30
Arg Ser Met Glu Thr Thr Cys Ser His Ser Ser Pro Gly Glu Gly Ala
      35             40             45
Ser Pro Gln Met Phe His Thr Val Ser Pro Gly Pro Pro Ser Ala Arg
      50             55             60
Pro Pro Cys Arg Val Pro Pro Thr Thr Pro Leu Asn Gly Gly Pro Gly
65             70             75             80
Ser Leu Pro Pro Glu Pro Pro Ser Val Ser Gln Ala Phe Pro Thr Leu
      85             90             95
Ala Gly Pro Gly Gly Leu Phe Pro Pro Arg Leu Ala Asp Pro Val Pro
      100            105            110
Ser Gly Gly Ser Ser Ser Pro Arg Phe Leu Pro Arg Gly Asn Ala Pro
      115            120            125
Ser Pro Ala Pro Pro
      130

```

&lt;210&gt; 655

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 655

```

tgaaggaaat tctctatggc ttgtgttcat catgtagaac agcccatgag gagaatagga
60
gatgaggtgg gaagtgcact gggatctggg ggaagaagcc cgggggtcaa gactcagcta
120
ctgactgcat ggtgtcaaag gattcgggca tctctctga ggctgagtct tcagatgaca
180
gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg
240
cttgacaaat gcaagggtgcc atacaaacag gaactgcaca atctcacgcg cgggcctact
300
cagcattgtt atttttacct ttacatctat atgaagatgt agttccattc cttttaactg
360
ttgttttc
368

```

&lt;210&gt; 656

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 656

```

Met Ala Cys Val His His Val Glu Gln Pro Met Arg Arg Ile Gly Asp
 1             5             10             15
Glu Val Gly Ser Ala Leu Gly Ser Gly Gly Arg Ser Pro Gly Phe Lys

```

```

      20      25      30
Thr Gln Leu Leu Thr Ala Trp Cys Gln Arg Ile Arg Ala Ser Ser Leu
      35      40      45
Arg Leu Ser Leu Gln Met Thr Val Arg Thr Gly Thr Pro Ala Leu Pro
      50      55      60
Phe Ser Arg Gly Val Trp Ala Pro Met Ser Met Leu Asp Lys Cys Lys
      65      70      75      80
Val Pro Tyr Lys Gln Glu Leu His Asn Leu Thr Ala Arg Pro Thr Gln
      85      90      95
His Cys Tyr Phe Tyr Leu Tyr Ile Tyr Met Lys Met
      100      105

```

&lt;210&gt; 657

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 657

```

gtcgaccacg gcatgaaaaa gccgggggatg atcctcatca acaaccctg gggcgagtc
60
aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cggtgtcgag
120
cgtattcagg acagcgacct ggacgtggtg ccgcaattga ccccgctga aaaacgccgg
180
tgccgacacc ttgctgatgg tcggcaacgt cggcccttcg gcacaggtgg tcaagtcct
240
ggaccgcatg ggttgggacg tgctgtggt gtctcactgg gggccggccg gnggtcgctt
300
tggcgagctg gcggggccta acgcttctcg
330

```

&lt;210&gt; 658

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 658

```

Met Lys Lys Pro Gly Met Ile Leu Ile Asn Asn Pro Trp Gly Glu Ser
  1      5      10      15
Asn Glu Ala Gly Phe Lys Arg Ala Leu Glu Glu Arg Gly Met Ala Asn
      20      25      30
Ala Gly Val Glu Arg Ile Gln Asp Ser Asp Leu Asp Val Val Pro Gln
      35      40      45
Leu Thr Pro Pro Glu Lys Arg Arg Cys Arg His Leu Ala Asp Gly Arg
      50      55      60
Gln Arg Arg Pro Phe Gly Thr Gly Gly Gln Val Pro Gly Pro His Gly
      65      70      75      80
Leu Gly Arg Ala Cys Gly Val Ser Leu Gly Ala Gly Arg Xaa Ser Leu
      85      90      95
Trp Arg Ala Gly Gly Ala
      100

```

&lt;210&gt; 659

&lt;211&gt; 1505

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 659

gccaggatca tgccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg  
60  
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac  
120  
aaccctgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt  
180  
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240  
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300  
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360  
acactgacct ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct  
420  
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480  
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540  
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660  
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720  
aagaagatat acgatggagg tgcccgacac gaggacgagg tacaatctta tccttccaag  
780  
cacgactatg tgtaatgtc taagacctct cagcacgggc ggaagaaact cccggagagc  
840  
tcacccaaaa aacaaggaga tcccatctag atttcttctt gcttttgact cacagctgga  
900  
agttagaaaa gcctcgattt catctttgga gaggccaagt ggtcttagcc tcagtctctg  
960  
tctctaataa ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac  
1020  
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1080  
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1140  
ataaacccat tgatgatcta tttcccagct tatccccaag aaaacttttg aaaggaaaga  
1200  
gtagacccaa agatgttatt ttctgtgtt tgaattttgt ctccccacc ccaacttggc  
1260  
tagtaataaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag  
1320  
cccatgatct cggttttctt acactgtgat cttaaaagtt accaaaccaa agtcattttc  
1380  
agtttgaggc aaccaaacct ttctactgct gttgacatct tcttattaca gcaacaccat  
1440  
tctaggagtt tcctgagctc tccactggag tcctccctt ctgtcgtctt ctgcagcgg  
1500



tacc

1505

&lt;210&gt; 660

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 660

```

Met Ser Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
 1           5           10       15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20           25           30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
 35           40           45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50           55           60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
 65           70           75           80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
 85           90           95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100          105          110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115          120          125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130          135          140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145          150          155          160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165          170          175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180          185          190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195          200          205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210          215          220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225          230          235          240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245          250          255
Lys His Asp Tyr Val
260

```

&lt;210&gt; 661

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 661

```

nnacgcgtgt agtttggtgta tcggcgcgga actcgccgcg tctgatctcg aggagcttcc
60
cccatgggacg agattttaac cttgcttgcc ggaggcggtg acgacgagcc agagtggcat
120

```

gacaaggcat tatgtgcca gactgatccg gaggcattct tccctgaaaa gggtaggatcc  
 180  
 acccgtgagg ccaagcgcat ctgtgagtc tgtgaggtcc gccaggagtg cttggagtac  
 240  
 gcccttgcca atgacgagag gttcggaaac tggggcggat tgtccgagat ggagaggcgt  
 300  
 cggctgcgca agcgggcggt acctgacgtc ggagcgcggt tattgacacg gcccggtaaa  
 360  
 atgccctgtc tgcccgggat ggctgtctgc acgatgcggc atatgcgatg atcgagacg  
 420  
 tgggtgtgcat cccgtgctcc atgacgtcga c  
 451

<210> 662

<211> 85

<212> PRT

<213> Homo sapiens

<400> 662

Met	Asp	Glu	Ile	Leu	Thr	Leu	Leu	Ala	Gly	Gly	Gly	Asp	Asp	Glu	Pro
1				5					10					15	
Glu	Trp	His	Asp	Lys	Ala	Leu	Cys	Ala	Gln	Thr	Asp	Pro	Glu	Ala	Phe
		20						25					30		
Phe	Pro	Glu	Lys	Gly	Gly	Ser	Thr	Arg	Glu	Ala	Lys	Arg	Ile	Cys	Glu
		35				40						45			
Ser	Cys	Glu	Val	Arg	Gln	Glu	Cys	Leu	Glu	Tyr	Ala	Leu	Ala	Asn	Asp
		50				55					60				
Glu	Arg	Phe	Gly	Ile	Trp	Gly	Gly	Leu	Ser	Glu	Met	Glu	Arg	Arg	Arg
65					70					75				80	
Leu	Arg	Lys	Arg	Ala											

<210> 663

<211> 552

<212> DNA

<213> Homo sapiens

<400> 663

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 60  
 ccctacgacg tgctcgtcgt aggggagggt cccgccggtg ccgcggccgc cgtgtacgcg  
 120  
 gctcgtaagg gcattcgac cgccatggtc gggctctcga tcggcggcca ggtactcgat  
 180  
 accgaggcca tcgacaacct catctcgggt ccgcacacca ccggtccgcg tctggccgac  
 240  
 gccctccgca gccacgtcaa cgactacaac attgacgtta ttgagcgtca gaccgccagc  
 300  
 gccatagaga ccaccggcgg tatgaccacc gtgcatctga ccgacggcga cctgcggggc  
 360  
 cgctcagtca tcgtggccac cgggtgccgc tggcgcaacc ttggcgtaacc tggcgaggag  
 420  
 gaataccgca ccaaggggtg gacctactgc ccgcactgcg atggcccgtt attcacaggc  
 480

aaaaagggtgg ccgtcgtcgg aggtggaaac tccggtattg aggccgctat cgacctcgcc  
540

ggcgtcgtcg ac  
552

<210> 664

<211> 184

<212> PRT

<213> Homo sapiens

<400> 664

Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu  
1 5 10 15  
Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala  
20 25 30  
Gly Ala Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala  
35 40 45  
Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile  
50 55 60  
Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp  
65 70 75 80  
Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg  
85 90 95  
Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His  
100 105 110  
Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly  
115 120 125  
Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Glu Tyr Arg Thr  
130 135 140  
Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly  
145 150 155 160  
Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala  
165 170 175  
Ile Asp Leu Ala Gly Val Val Asp  
180

<210> 665

<211> 352

<212> DNA

<213> Homo sapiens

<400> 665

acgcgtacag ttcgccgtcg aggttgaaca ccacgatcgg tgtaccggtc acttcgtcga  
60  
acacgtcttt catttcgccc ggcagcagtt cggcgccggc gcagacaaag gtccaggcct  
120  
cgctcacgcg gtggccccgg ccagcggttt ttccaggatc tcgaaacgca ggtcgtcgcg  
180  
cttgggggatg ccgaatcggt cgtcgccata cgggaacggc ttcttgatgc cggtgcgacg  
240  
gtagccgcgg cgctcgtaga agcgatcaga tcgcgcgcac gtcgatcact gtcactctgca  
300  
ttaccggcac gttccattcg cgcgcggcgt gggcttcggc ggcgtccatc aa  
352

<210> 666  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 666  
 Met Glu Arg Ala Gly Asn Ala Asp Asp Ser Asp Arg Arg Ala Arg Asp  
 1 5 10 15  
 Leu Ile Ala Ser Thr Ser Ala Ala Ala Thr Cys Ala Pro Ala Ser Arg  
 20 25 30  
 Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr  
 35 40 45  
 Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg  
 50 55 60  
 Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Arg Thr Ala Ala Gly  
 65 70 75 80  
 Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly  
 85 90 95  
 Val Gln Pro Arg Arg Arg Thr Val Arg  
 100 105

<210> 667  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 667  
 nacgcgtacg aatcgggtgtt gcgtcgcaac ccaggggagg ccgagttcca ccaggctgtg  
 60  
 cgggagatct ttgaatctct cggcccggtg ctcgacaaga atccgcagta cgtggaggca  
 120  
 gccgtgttgt cgcgcatctg cgaaccggaa cgccagatca ttttccgggt gccgtgggtt  
 180  
 gacgacgagg gcaagatccg tatcaaccgt ggcttcgcg ttgaatatc gtcggtactg  
 240  
 gggccgtata aggggtggatt gcgattccac ccctcgggtg acttaggaac gattaagttc  
 300  
 cttggttttg agcagatctt caaaaatgct ctgactggca tgccgatcgg tggcggaag  
 360  
 ggtgggtcgg actttgatcc ccatgacgcg t  
 391

<210> 668  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 668  
 Xaa Ala Tyr Glu Ser Val Leu Arg Arg Asn Pro Gly Glu Ala Glu Phe  
 1 5 10 15  
 His Gln Ala Val Arg Glu Ile Phe Glu Ser Leu Gly Pro Val Leu Asp  
 20 25 30  
 Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

```

      35              40              45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly
  50              55              60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu
65              70              75              80
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly
      85              90              95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr
      100              105              110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His
      115              120              125
Asp Ala
      130

```

<210> 669  
 <211> 707  
 <212> DNA  
 <213> Homo sapiens

```

<400> 669
nngagtccgt tccccgtcta agctcatcgt ggtggtgctg gcatggccgt caacaaggga
60
attgagaaca cccttgctgc ctteggccac gcggtcgagg tgggatgcac ctaccttgaa
120
actgacgttc acgcgaccag cgacgggggtg ctagtggcct tccacgatcc gatactcgat
180
cgcgtcactg aatcaggcgg agtcatcgcc gccatgccgt ggcaacaagg caaacaagcc
240
aagggttggtg gcgaaccgat cccacacctta gatgagattt tcgacgcctt tcccgcgcg
300
ttcatcaata tcgacatcaa gcatgatggc gccaccatgc cgctcatcga cgttctttcc
360
cgtcaccggg cttggagtcg ggtttgcgtc gggtcgttca gcagtaaagc catccagacc
420
ttccgtcgcc tggttcaggg acgcactgcg actgcagtgg ggtcgggtggg agtcnnggct
480
gggctgtcat cagccctcat agcatgcaga tggcacagtc ccatgggaat gcgtaccagg
540
tgccgcaccg cttgaccggg tnatgggggtg ccccttgatga caccgacctt cattaaagct
600
gcccacgtc aggggcgagc tgttcatgtc tggacgggta atgagatctc tgagggtcga
660
gaactgatgg atatgggggt cgacggcatc gtcacagatc gtccgga
707

```

<210> 670  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

```

<400> 670
Met Ala Val Asn Lys Gly Ile Glu Asn Thr Leu Ala Ala Phe Gly His
  1              5              10              15
Ala Val Glu Val Gly Cys Thr Tyr Leu Glu Thr Asp Val His Ala Thr

```

```

      20      25      30
Ser Asp Gly Val Leu Val Ala Phe His Asp Pro Ile Leu Asp Arg Val
      35      40      45
Thr Glu Ser Gly Gly Val Ile Ala Ala Met Pro Trp His Lys Val Lys
      50      55      60
Gln Ala Lys Val Gly Gly Glu Pro Ile Pro Thr Leu Asp Glu Ile Phe
65      70      75      80
Asp Ala Phe Pro Asp Ala Phe Ile Asn Ile Asp Ile Lys His Asp Gly
      85      90      95
Ala Thr Met Pro Leu Ile Asp Val Leu Ser Arg His Arg Ala Trp Ser
      100      105      110
Arg Val Cys Val Gly Ser Phe Ser Ser Lys Arg Ile Gln Thr Phe Arg
      115      120      125
Arg Leu Val Gln Gly Arg Thr Ala Thr Ala Val Gly Ser Val Gly Val
      130      135      140
Xaa Ala Gly Leu Ser Ser Ala Leu Ile Ala Cys Arg Trp His Ser Pro
145      150      155      160
Met Gly Met Arg Thr Arg Cys Arg Thr Ala
      165      170

```

&lt;210&gt; 671

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 671

```

acgcgtgggc cttcgggttg atgggatcag aaggggacgg gacctgtaga aaggggcctg
60
cagctcagag catggggcgg ctttggtca ctacgctgc agctgtgaat tcgttctccg
120
gtgctggaga gggatctggt tatctccatt ctctgtctc cacgtggaaa ggaaggacgt
180
gcgctctcat cctacgtggt ttgagaaatc gcattgtccc cagctctgcg ggaggatctg
240
gggacgcagt ggggaaccag acaggcagtt ggaggtctag tgcgcgccag aagccagttc
300
ccacccaggg tgccatttgc tgggcgcctt agggagctgc gtgggcatcc agaggagtga
360
gtcgccccct gctctgctca gtgcccactt ccccgggcag ggcaggcggtt attaacgtag
420
agggagaaca cccatgcaca caac
444

```

&lt;210&gt; 672

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 672

```

Met Gly Ser Glu Gly Asp Gly Thr Cys Arg Lys Gly Pro Ala Ala Gln
1      5      10      15
Ser Met Gly Arg Pro Trp Leu Thr Thr Pro Ala Ala Val Asn Ser Phe
      20      25      30
Ser Gly Ala Gly Glu Gly Ser Gly Tyr Leu His Ser Leu Val Ser Thr

```

```

      35          40          45
Trp Lys Gly Arg Thr Cys Ala Leu Ile Leu Arg Val Leu Arg Asn Arg
      50          55          60
Ile Val Pro Ser Ser Ala Gly Gly Ser Gly Asp Ala Val Gly Asn Gln
65          70          75          80
Thr Gly Ser Trp Arg Ser Ser Ala Arg Gln Lys Pro Val Pro Thr Gln
      85          90          95
Gly Ala Ile Cys Trp Ala Pro
      100

```

<210> 673  
 <211> 452  
 <212> DNA  
 <213> Homo sapiens

```

<400> 673
acgcgtccct gcagaaatcc tctcggccta ggatcatccgc aagatgtggc agggcatgca
60
ccgtgaaagc cttcaagtct gccgcagcaa gaccgcacgc ctgctgaaat tcgcagttgt
120
gccgcggtcc ctgatgcgga caaactcggc caccacgatc agcctgacgc ttgcggacca
180
acgttcaaat actgtgcact tgaaacgtcc gggccgcac acctgggtga ctttgtgcga
240
ccgacattac ttatgttcac gctctttcag ttcttgtcaa taccgtatatt ttcgtcgacg
300
tctccatcag aaaaatgtcg gtgttaccgc accgcagacg atgcgtaccc ttgcgtgacg
360
gatggaggcc ttgaaaagtg cattagccac tactgggcga atctacggca aaaagctgtt
420
actaggcggg gattggggag gcccgtagtg gc
452

```

<210> 674  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

```

<400> 674
Met Trp Gln Gly Met His Arg Glu Ser Leu Gln Val Cys Arg Ser Lys
1          5          10          15
Thr Ala Arg Leu Leu Lys Phe Ala Val Val Pro Arg Ser Leu Met Arg
      20          25          30
Thr Asn Ser Ala Thr Thr Ile Ser Leu Thr Leu Ala Asp Gln Arg Ser
      35          40          45
Asn Thr Val His Leu Lys Arg Pro Gly Arg Ile Thr Trp Val Thr Leu
50          55          60
Cys Asp Arg His Tyr Leu Cys Ser Arg Ser Phe Ser Ser Cys Gln Tyr
65          70          75          80
Arg Ile Phe Arg Arg Arg Leu His Gln Lys Asn Val Gly Val Thr Ala
      85          90          95
Pro Gln Thr Met Arg Thr Leu Ala Leu Thr Met Glu Ala Leu Lys Ser
      100          105          110
Ala Leu Ala Thr Thr Gly Arg Ile Tyr Gly Lys Lys Leu Leu Leu Gly

```

115  
Gly Asp Trp Gly Gly Pro  
130

120

125

&lt;210&gt; 675

&lt;211&gt; 8564

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 675

atgtcgggct ccacacagct tgtggcacag acgtggaggg ccactgagcc ccgctacccg  
60  
ccccacagcc ttctctaccc agtgcagatc gcccgacgc acacggacgt cgggctcctg  
120  
gagtaccagc accactcccg cgactatgcc tccacctgt cgccgggctc catcatccag  
180  
ccccagcggc ggaggccctc cctgctgtct gagttccagc ccgggaatga acgggtcccag  
240  
gagctccacc tgcggccaga gtccactca tacctgcccg agctggggaa gtcagagatg  
300  
gagttcattg aaagcaagcg ccctcggcta gagctgctgc ctgacccct gctgcgaccg  
360  
tcaccctgc tggccacggg ccagcctgcg ggatctgaag acctcaccaa ggaccgtagc  
420  
ctgacgggca agctggaacc ggtgtctccc ccagcccc cgcacactga ccctgagctg  
480  
gagctggtgc cgccacggct gtccaaggag gagctgatcc agaacatgga ccgcgtggac  
540  
cgagagatca ccatggtaga gcagcagatc tctaagctga agaagaagca gcaacagctg  
600  
gaggaggagg ctgccaaagg gcccgagcct gagaagcccg tgtcaccgcc gcccatcgag  
660  
tcgaagcacc gcagcctggt gcagatcatc tacgacgaga accggaagaa ggctgaagct  
720  
gcacatcgga ttctggaagg cctggggccc caggtggagc tgccgctgta caaccagccc  
780  
tccgacaccc ggcagtatca tgagaacatc aaaataaacc aggcgatgag gaagaagcta  
840  
atcttgact tcaagaggag gaatcacgct cggaacaat gggagcagaa gttctgccag  
900  
cgctatgacc agctcatgga ggcctgggaa aaaaagggtg agcgcatcga gaacaacccc  
960  
cggcggcggg ccaaggagag caagggtgcg gagtactacg aaaagcagtt ccctgagatc  
1020  
cgcaagcagc gcgagctgca ggagcgcagc cagggcaggg tgggccagcg gggcagtg  
1080  
ctgtccatgt cggccgcccg cagcagacag gaggtgtcag agatcatcga tggcctctca  
1140  
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1200  
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1260  
aagggtgtaca aagaccgcca ggtcatgaac atgtggagtg agcaggagaa ggagaccttc  
1320



cgggagaagt tcatgcagca tcccaagaac tttggcctga tcgcatcatt cctggagagg  
1380  
aagacagtgg ctgagtgcgt cctctattac tacctgacta agaagaatga gaactataag  
1440  
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1500  
cagcagcagc agcagcagca gcagcagcag cagcccatgc cccgcagcag ccaggaggag  
1560  
aaagatgaga aggagaagga aaaggaggcg gagaaggagg aggagaagcc ggaggtggag  
1620  
aacgacaagg aagacctcct caaggagaag acagacgaca cctcagggga ggacaacgac  
1680  
gagaaggagg ctgtggcctc caaaggccgc aaaactgcc aagccaggg aagacgcaa  
1740  
ggccgcatca cccgtcaat ggctaagtag gccaacagcg aggaggccat cccccccag  
1800  
cagagcgccg agctggcctc catggagctg aatgagagtt ctgctggac agaagaagaa  
1860  
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1920  
atggtgggct ccaagactgt gtgcagtgat aagaacttct acttcaacta caagaagg  
1980  
cagaacctcg atgagatctt gcagcagcac aagctgaaga tggagaagga gaggaacgcg  
2040  
cggaggaaga agaagaaagc gccggcgccg gccagcgagg aggtgcatt cccgccgtg  
2100  
gtggaggatg aggagatgga ggctcgccg gtgagcgga atgaggagg gatggtggag  
2160  
gaggctgaag ccttacatgc ctctgggaat gaggtgccca gagggaatg cagtggccca  
2220  
gccactgtca acaacagctc agacaccgag agcatccct ctctcacac ggaggccg  
2280  
aaggacacag ggcagaatgg gcccaagccc ccagccaccc tggcgccga cgggccaccc  
2340  
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2460  
cctgtggtcc ccaaggagga gaaggaggag gagaccgag cagcgcccc agtggaggag  
2520  
ggggaggagc agaagcccc cgcggtgag gagctggcag tggacacagg gaaggccgag  
2580  
gagcccgtca agagcgagtg cacggaggaa gccgaggagg ggccggccaa gggcaaggac  
2640  
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2700  
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2760  
acctgcagtg cagacgaggt ggatgaggcc gagggcgccg acaagaaccg gctgctgtcc  
2820  
ccaaggccca gcctctcac cccgactggc gacccccggg ccaatgcctc accccagaag  
2880  
ccactggacc tgaagcagct gaagcagcga gcggctgcca tccccccat ccaggtcacc  
2940

aaagtccatg agcccccccg ggaggacgca gctcccacca agccagctcc cccagcccca  
3000  
ccgccaccgc aaaacctgca gccggagagc gacgcccctc agcagcctgg cagcagcccc  
3060  
cggggcaaga gcaggagccc ggcaccccc ggcgacaagg aggccttcgc agccgaggcc  
3120  
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<211> 2518

<212> PRT

<213> Homo sapiens

<400> 676

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Pro	Arg	Tyr	Pro	His	Ser	Leu	Ser	Tyr	Pro	Val	Gln	Ile	Ala	Arg	
			20				25					30			
Thr	His	Thr	Asp	Val	Gly	Leu	Leu	Glu	Tyr	Gln	His	His	Ser	Arg	Asp
		35				40					45				
Tyr	Ala	Ser	His	Leu	Ser	Pro	Gly	Ser	Ile	Ile	Gln	Pro	Gln	Arg	Arg
	50				55					60					
Arg	Pro	Ser	Leu	Leu	Ser	Glu	Phe	Gln	Pro	Gly	Asn	Glu	Arg	Ser	Gln
65				70				75					80		
Glu	Leu	His	Leu	Arg	Pro	Glu	Ser	His	Ser	Tyr	Leu	Pro	Glu	Leu	Gly
			85				90					95			
Lys	Ser	Glu	Met	Glu	Phe	Ile	Glu	Ser	Lys	Arg	Pro	Arg	Leu	Glu	Leu
		100					105					110			
Leu	Pro	Asp	Pro	Leu	Leu	Arg	Pro	Ser	Pro	Leu	Leu	Ala	Thr	Gly	Gln
		115				120						125			
Pro	Ala	Gly	Ser	Glu	Asp	Leu	Thr	Lys	Asp	Arg	Ser	Leu	Thr	Gly	Lys
	130				135					140					
Leu	Glu	Pro	Val	Ser	Pro	Pro	Ser	Pro	Pro	His	Thr	Asp	Pro	Glu	Leu
145				150				155					160		
Glu	Leu	Val	Pro	Pro	Arg	Leu	Ser	Lys	Glu	Glu	Leu	Ile	Gln	Asn	Met

783

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Glu Leu Asn Glu Ser Ser Arg Trp Thr Glu Glu Glu Met Glu Thr Ala		
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Lys Lys Gly Leu Leu Glu His Gly Arg Asn Trp Ser Ala Ile Ala Arg		
625	630	635
Met Val Gly Ser Lys Thr Val Ser Gln Cys Lys Asn Phe Tyr Phe Asn		
645	650	655
Tyr Lys Lys Arg Gln Asn Leu Asp Glu Ile Leu Gln Gln His Lys Leu		
660	665	670
Lys Met Glu Lys Glu Arg Asn Ala Arg Arg Lys Lys Lys Lys Ala Pro		
675	680	685
Ala Ala Ala Ser Glu Glu Ala Ala Phe Pro Pro Val Val Glu Asp Glu		
690	695	700
Glu Met Glu Ala Ser Gly Val Ser Gly Asn Glu Glu Glu Met Val Glu		
705	710	715
Glu Ala Glu Ala Leu His Ala Ser Gly Asn Glu Val Pro Arg Gly Glu		
725	730	735
Cys Ser Gly Pro Ala Thr Val Asn Asn Ser Ser Asp Thr Glu Ser Ile		
740	745	750
Pro Ser Pro His Thr Glu Ala Ala Lys Asp Thr Gly Gln Asn Gly Pro		
755	760	765
Lys Pro Pro Ala Thr Leu Gly Ala Asp Gly Pro Pro Pro Gly Pro Pro		
770	775	780
Thr Pro Pro Arg Arg Thr Ser Arg Ala Pro Ile Glu Pro Thr Pro Ala		
785	790	795
Ser Glu Ala Thr Gly Ala Pro Thr Pro Pro Pro Ala Pro Pro Ser Pro		
805	810	815
Ser Ala Pro Pro Pro Val Val Pro Lys Glu Glu Lys Glu Glu Glu Thr		
820	825	830
Ala Ala Ala Pro Pro Val Glu Glu Gly Glu Glu Gln Lys Pro Pro Ala		
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Ala Glu Glu Leu Ala Val Asp Thr Gly Lys Ala Glu Glu Pro Val Lys		
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Ser Glu Cys Thr Glu Glu Ala Glu Glu Gly Pro Ala Lys Gly Lys Asp		
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Ala Glu Ala Ala Glu Ala Thr Ala Glu Gly Ala Leu Lys Ala Glu Lys		
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Lys Glu Gly Gly Ser Gly Arg Ala Thr Thr Ala Lys Ser Ser Gly Ala		
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Pro Gln Asp Ser Asp Ser Ser Ala Thr Cys Ser Ala Asp Glu Val Asp		
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Glu Ala Glu Gly Gly Asp Lys Asn Arg Leu Leu Ser Pro Arg Pro Ser		
930	935	940
Leu Leu Thr Pro Thr Gly Asp Pro Arg Ala Asn Ala Ser Pro Gln Lys		
945	950	955
Pro Leu Asp Leu Lys Gln Leu Lys Gln Arg Ala Ala Ala Ile Pro Pro		
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Ile Gln Val Thr Lys Val His Glu Pro Pro Arg Glu Asp Ala Ala Pro		
980	985	990
Thr Lys Pro Ala Pro Pro Ala Pro Pro Pro Gln Asn Leu Gln Pro		
995	1000	1005
Glu Ser Asp Ala Pro Gln Gln Pro Gly Ser Ser Pro Arg Gly Lys Ser		
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Arg Ser Pro Ala Pro Pro Ala Asp Lys Glu Ala Phe Ala Ala Glu Ala		

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 Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu Pro Phe  
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 Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro Leu Pro Leu Gly  
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                                  1090                      1095                      1100  
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 Pro Tyr Ser Glu His Ala Lys Ala Pro Val Gly Pro Val Thr Met Gly  
                                  1140                      1145                      1150  
 Leu Pro Leu Pro Met Asp Pro Lys Lys Leu Ala Pro Phe Ser Gly Val  
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 Lys Gln Glu Gln Leu Ser Pro Arg Gly Gln Ala Gly Pro Pro Glu Ser  
                                  1170                      1175                      1180  
 Leu Gly Val Pro Thr Ala Gln Glu Ala Ser Val Leu Arg Gly Thr Ala  
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 Leu Gly Ser Val Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser Thr  
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 Gly Thr Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile Ile  
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 Gly Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser Leu  
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 Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu Ser  
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 Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp Gly Arg  
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 Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys Arg Thr Tyr  
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 Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser Ser Ala Ser Ile  
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 Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu Arg His Ser Pro His  
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 Thr Leu Ser Asp Ser Glu  
 2515

&lt;210&gt; 677

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 677

gtaatgcaag gtgaacgccc aatggctgcg cagaacaaga gcattgggtca gttcaccctt  
 60  
 gagggatatag ctccggcagc ccgtgggtgtt ccacagattg aagttacttt cgatatcgat  
 120  
 gccaacggta ttttgaatgt gagcgcaaag gataaggcta ccggtaagga acagaagatt  
 180  
 cgcacgaag cttcaagtgg tttgagtcag gaagaaatcg acagaatgaa agctgaggca  
 240  
 gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct  
 300  
 gactcaatga tttccccccc cgaaaactcc tgaaagacaa cgatn  
 345

&lt;210&gt; 678

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 678

Val Met Gln Gly Glu Arg Pro Met Ala Ala Gln Asn Lys Ser Ile Gly  
 1                      5                      10                      15  
 Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln

```

                20                25                30
Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
                35                40                45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
                50                55                60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
65                70                75                80
Glu Gln Asn Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
                85                90                95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
                100                105                110

```

<210> 679  
 <211> 362  
 <212> DNA  
 <213> Homo sapiens

```

<400> 679
acgcgtgacg tcaccgctcc atggggaaga tgacgactat ccctgtgaaa gtaaagcata
60
atgggaaaaa tgtacgttaa atgtgctaac gcgcagtatg atgtatctat gaatcttgag
120
ggtacaggcc tggatttcaa gcgtgccatt gctgacgtca cgcattgtgcc acccgaacgc
180
caaaaagtac tcatcaaggg aggattgcta aaagacgata cccattagg taaagtgggt
240
gcgcgtgcag gacagcagtt catggtgctg ggtgctgtgg gtgagctgcc caaggcccca
300
gaaaaacctg tgctgttcct ggaggatttg ccggaagacg agctcaacaa ggctaaggat
360
cc
362

```

<210> 680  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

```

<400> 680
Met Gly Lys Met Tyr Val Lys Cys Ala Asn Ala Gln Tyr Asp Val Ser
 1                5                10                15
Met Asn Leu Glu Gly Thr Gly Leu Asp Phe Lys Arg Ala Ile Ala Asp
                20                25                30
Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
                35                40                45
Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
50                55                60
Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
65                70                75                80
Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
                85                90                95
Lys Ala Lys Asp
                100

```

<210> 681  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 681  
 acgcgtccaa atggacaaac gcttgatgat ttctaccatg aaattagagc aaaatatcca  
 60  
 gaacaattac tgatggcaga ctgttcaaca gtagaagaaa tgattcacgc tgatgaactc  
 120  
 ggttttgatt ttatcggaag tacttttagta ggatatacaa aacaaagtaa aggtgacaaa  
 180  
 atcgaagaaa atgactttga aatcttgaga acagtttttag aacgaattaa acatccacta  
 240  
 attgcagaag gcaatatcga tacacctgaa aagggtgaaac gtgtgcttga gttaggcgcg  
 300  
 tatagtgtcg ttgtagggtc agcgattact cgtccacaac tcatcacgaa aaaattt  
 357

<210> 682  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 682  
 Thr Arg Pro Asn Gly Gln Thr Leu Asp Asp Phe Tyr His Glu Ile Arg  
 1 5 10 15  
 Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu  
 20 25 30  
 Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr  
 35 40 45  
 Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn  
 50 55 60  
 Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu  
 65 70 75 80  
 Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu  
 85 90 95  
 Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro  
 100 105 110  
 Gln Leu Ile Thr Lys Lys Phe  
 115

<210> 683  
 <211> 411  
 <212> DNA  
 <213> Homo sapiens

<400> 683  
 ntctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg  
 60  
 aatattgttt tgcccgcagc gtggttgcatt gattgcgtca gttaccctaa aaaccatgta  
 120  
 ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt  
 180

aattacccca aacaatactt attagcaatt catcatgcaa tttcagcgca cagtgtcagt  
 240  
 ggtaaaatac aggcaatgag tttagaagct caaatagtgc aagatgcaga tagattggat  
 300  
 gcgctagggg caattggcgt ggctcgttgc attcaagtaa gtagccagtt acagcgccca  
 360  
 ctatattctg aagttgaccc cttcagcgag acacgatctc tagtctgcat g  
 411

<210> 684

<211> 137

<212> PRT

<213> Homo sapiens

<400> 684

Xaa	Ser	Asp	Arg	Val	Val	Lys	Leu	Ala	Thr	Leu	Ile	Ala	Glu	Asp	Glu
1				5					10					15	
Gln	Ala	Glu	Met	Asn	Ile	Val	Leu	Pro	Ala	Ala	Trp	Leu	His	Asp	Cys
			20					25					30		
Val	Ser	Tyr	Pro	Lys	Asn	His	Val	Leu	Arg	Ala	Gln	Ser	Ala	Leu	His
		35				40					45				
Ala	Ala	Asp	Lys	Ala	Ile	Val	Phe	Leu	Arg	Ser	Ile	Asn	Tyr	Pro	Lys
	50					55					60				
Gln	Tyr	Leu	Leu	Ala	Ile	His	His	Ala	Ile	Ser	Ala	His	Ser	Val	Ser
65					70					75				80	
Gly	Lys	Ile	Gln	Ala	Met	Ser	Leu	Glu	Ala	Gln	Ile	Val	Gln	Asp	Ala
			85						90					95	
Asp	Arg	Leu	Asp	Ala	Leu	Gly	Ala	Ile	Gly	Val	Ala	Arg	Cys	Ile	Gln
			100				105						110		
Val	Ser	Ser	Gln	Leu	Gln	Arg	Pro	Leu	Tyr	Ser	Glu	Val	Asp	Pro	Phe
		115				120							125		
Ser	Glu	Thr	Arg	Ser	Leu	Val	Cys	Met							
		130				135									

<210> 685

<211> 417

<212> DNA

<213> Homo sapiens

<400> 685

acgcgttgcg ttgcggagtg aaccggaac gatggatgga ttgacactat tcggcctggt  
 60  
 cgccgtcact gcgatgctgg tctgctatgc catggaggac cgcagccact ggttcgtgct  
 120  
 gctgttcgcg gccgcttggc gctcggttcg gcctacggct tcctccaagg cgcttgccg  
 180  
 ttcggcttcg tcgaggcgat atgggcgctc gttgcctcg cggtggtgga cgatcaggcc  
 240  
 gcgatgaccg catcgtccgg cttaagccc gaaacgaaac cgaccagtgc gctggtttga  
 300  
 tgggcggcgc gtcgctggat gcacagcgtc tcgacgcgag cgtgatgatg gcctcagcgc  
 360  
 gtgcatgccg acgctgtcgc tcatcgcgct acgctcgacc acggcgcgcg gcaatag  
 417

<210> 686  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 686  
 Met Pro Trp Arg Thr Ala Ala Thr Gly Ser Cys Cys Cys Ser Arg Pro  
 1 5 10 15  
 Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val  
 20 25 30  
 Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly  
 35 40 45  
 Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu  
 50 55 60  
 Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln  
 65 70 75 80  
 Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg  
 85 90 95  
 Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile  
 100 105 110

<210> 687  
 <211> 412  
 <212> DNA  
 <213> Homo sapiens

<400> 687  
 nnacgcgtga ccgaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgca  
 60  
 gacggcatcg atattccgtc tggggcgatt attgaaagct gccgcacctt atcagccggt  
 120  
 ctcatgaaa cccacggtgg tcgcacgata gagcttcggg taccacctgc gtgcgcgggt  
 180  
 caattggcgg ccattgagtc gggccccaac caccaccggg gcactccgcc caatgtggcc  
 240  
 gagaccgacc ctgtcacctt cctgcagttg gcaactggct tctcacactg gccagaaatg  
 300  
 cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc  
 360  
 ccagtcgttg atatggccgg gggtttccgc gacatttttg ccgacgacta ga  
 412

<210> 688  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

<400> 688  
 Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala  
 1 5 10 15  
 Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu  
 20 25 30  
 Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg

```

      35              40              45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
  50              55              60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
  65              70              75              80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
      85              90              95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
      100              105              110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
      115              120              125
Phe Arg Asp Ile Phe Ala Asp Asp
      130              135

```

&lt;210&gt; 689

&lt;211&gt; 499

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 689

```

cgcgctcgcgg tactcgacgt cgattttcat cacggtaacg gcaccagaa cattttttac
60
ccgcgcaatg acgtgatgtt catatcgctg cacggcgagc cggccgtgtc ctatccctac
120
tattcgggggt tcagcgatga agtcggcgca ggtgttggcg aagggttcaa cctcaactac
180
ccgctgccga aaaacaccgc ctgggatacc taccgcgacg ccctgctgca tgctgcagg
240
aaactccagc aattctcgcc gcaggtattg gtgatctcac tgggggtcga caccttcaag
300
gacgacccga tcagtcactt cctgctggaa ggcgaggatt tcacgggat cggcgagctg
360
atagcgagtg tgggttgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
420
atcggaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcg cttgagcatcc
480
gcccgaagac ggcgtgata
499

```

&lt;210&gt; 690

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 690

```

Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
  1              5              10              15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
      20              25              30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
      35              40              45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
      50              55              60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg

```



```

65          70          75          80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
          85          90          95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
          100          105          110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
          115          120          125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
          130          135          140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145          150          155

```

<210> 691  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

```

<400> 691
ntgctgctg aaaacgtgca gcgcggcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggcccctg ggagttggcc tgcgacatcg cgctgccgtg cgccaccag
120
aacgaactgg acgccgacgc cgccgcacg ctgctgcgca acggctgcct ttgcgtggct
180
ggaggcgcgca atatgccgcc cgcgcttgag gctgtggata tctttatcga ggcggggcatt
240
ctgttcgcgc ccggcaaggc atccaatgcc ggcggcgctg ccgtgagtgg cctggaaatg
300
tcgcagaacg ccatgcgcct gctgtggacc gccggc
336

```

<210> 692  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

```

<400> 692
Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
1      5      10      15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
20     25     30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
35     40     45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
50     55     60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65     70     75     80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
85     90     95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
100    105    110

```

<210> 693  
 <211> 580

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 693

```

ngggcaaccc ggaaggtccg gcgtcccagc cgcctacctc gctggggaccc tggctcttgct
60
gtcccccgct ggccctcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg
120
gccacctgcg cactcaacca gtggggccctg gacttcgagg gcaatttgca aagaatttta
180
aagagtattg aaattgccaa aaacagagga gcaagataca ggcttggacc agagctggaa
240
atatgcggct gcggatgttg ggatcattat tacgagtcgg acaccctctt gcactcgttt
300
caagtcctag cggcccttgt ggagtcctcc gtcactcagg acatcatctg cgacgtgggg
360
atacctgtaa tgcaccgaaa cgtccgctac aactgcagag tgatattcct caacaggaag
420
atcctgctca tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc
480
tggttcaccc cgtggtcgag gagtcggtga gtcgggtgcc tgaccactcc tgggatgtgc
540
gttaagcacc tccgctgtgt gtagccttgg gtcctgatca
580

```

&lt;210&gt; 694

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 694

```

Met Gly Arg Lys Val Thr Val Ala Thr Cys Ala Leu Asn Gln Trp Ala
1           5           10           15
Leu Asp Phe Glu Gly Asn Leu Gln Arg Ile Leu Lys Ser Ile Glu Ile
20          25          30
Ala Lys Asn Arg Gly Ala Arg Tyr Arg Leu Gly Pro Glu Leu Glu Ile
35          40          45
Cys Gly Cys Gly Cys Trp Asp His Tyr Tyr Glu Ser Asp Thr Leu Leu
50          55          60
His Ser Phe Gln Val Leu Ala Ala Leu Val Glu Ser Pro Val Thr Gln
65          70          75          80
Asp Ile Ile Cys Asp Val Gly Ile Pro Val Met His Arg Asn Val Arg
85          90          95
Tyr Asn Cys Arg Val Ile Phe Leu Asn Arg Lys Ile Leu Leu Ile Arg
100         105         110
Pro Lys Met Ala Leu Ala Asn Glu Gly Asn Tyr Arg Glu Leu Arg Trp
115         120         125
Phe Thr Pro Trp Ser Arg Ser Arg
130         135

```

&lt;210&gt; 695

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 695

ntggtgactc aggcgtccaa tggcacgatg gctgacgtcg tcaatatgcc gtcctcgacc  
60  
atcatggctc tgtcgagggc tgattacctg ctcgatatcg agacttcggt gcccggatc  
120  
ggcgacaagt tcgtcccggc cgtctggggc aaactcaaac tcggcaagga caacgagcac  
180  
accgctctgc cctggtactt cggcccgttc gtcgtgacgt acaacaagga cattttcaag  
240  
gatgttggcc tcgatcccg aatcccgcg aagacgatga ccgagtacct cgacttcgcc  
300  
aagaaaatca ccgctgccgg caagcaggcg gtctatggca acacgtcgtg gtacatgctc  
360  
gcggaatggc gtgccctcgg cgtcaaggtc atgaatgacg acttcaccaa gttcactttt  
420  
gcctcggaat ccaacgcgt  
439

&lt;210&gt; 696

&lt;211&gt; 146

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 696

Xaa	Val	Thr	Gln	Ala	Ser	Asn	Gly	Thr	Met	Ala	Asp	Val	Val	Asn	Met
1				5					10					15	
Pro	Ser	Ser	Thr	Ile	Met	Ala	Leu	Ser	Arg	Ala	Asp	Tyr	Leu	Leu	Asp
			20					25					30		
Ile	Glu	Thr	Ser	Val	Pro	Gly	Ile	Gly	Asp	Lys	Phe	Val	Pro	Asp	Val
		35					40					45			
Trp	Gly	Lys	Leu	Lys	Leu	Gly	Lys	Asp	Asn	Glu	His	Thr	Ala	Leu	Pro
	50					55				60					
Trp	Tyr	Phe	Gly	Pro	Phe	Val	Val	Thr	Tyr	Asn	Lys	Asp	Ile	Phe	Lys
65					70				75					80	
Asp	Val	Gly	Leu	Asp	Pro	Glu	Ile	Pro	Pro	Lys	Thr	Met	Thr	Glu	Tyr
				85				90					95		
Leu	Asp	Phe	Ala	Lys	Lys	Ile	Thr	Ala	Ala	Gly	Lys	Gln	Ala	Val	Tyr
			100					105					110		
Gly	Asn	Thr	Ser	Trp	Tyr	Met	Leu	Ala	Glu	Trp	Arg	Ala	Leu	Gly	Val
		115					120					125			
Lys	Val	Met	Asn	Asp	Asp	Phe	Thr	Lys	Phe	Thr	Phe	Ala	Ser	Glu	Ser
	130					135					140				
Asn	Ala														
145															

&lt;210&gt; 697

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 697

nggcaataac gccgtcgtcg aaatccgttc ccttgatctc gaacatgccg atgaagcggg  
60

tgtcggtgat ggggtcggag atgtcgccct cccacaactt gaacttgatc ggaccaaccc  
 120  
 tttccaccct ggagagactc gcctgccttg aaagtcttct tgcccttctt gggcaactga  
 180  
 tcgccctccc gaacgagata atccaagctc aagcgaccgc ccaccttgtc gcgcgcctcc  
 240  
 acaccgacgg aatgcgatgc cgggatcgca tcgatgctag cggcgggtgcg tgcaatgaca  
 300  
 atcttgtctt cacgcagcga tacgggcccg ccgttggaat cgaacacaaa caccttgaag  
 360  
 gcgttgtn  
 368

<210> 698

<211> 108

<212> PRT

<213> Homo sapiens

<400> 698

Met	Pro	Met	Lys	Arg	Leu	Ser	Val	Met	Gly	Ser	Glu	Met	Ser	Pro	Ser
1				5					10					15	
His	Asn	Leu	Asn	Leu	Ile	Gly	Pro	Thr	Leu	Ser	Thr	Leu	Glu	Arg	Leu
			20					25					30		
Ala	Cys	Leu	Glu	Ser	Leu	Leu	Ala	Leu	Leu	Gly	Gln	Leu	Ile	Ala	Leu
		35					40					45			
Pro	Asn	Glu	Ile	Ile	Gln	Ala	Ala	Thr	Ala	His	Leu	Val	Ala	Arg	
	50					55				60					
Leu	His	Thr	Asp	Gly	Met	Arg	Cys	Arg	Asp	Arg	Ile	Asp	Ala	Ser	Gly
65				70					75					80	
Gly	Ala	Cys	Asn	Asp	Asn	Leu	Val	Phe	Thr	Gln	Arg	Tyr	Gly	Pro	Ala
			85					90						95	
Val	Gly	Ile	Glu	His	Lys	His	Leu	Glu	Gly	Val	Val				
			100					105							

<210> 699

<211> 363

<212> DNA

<213> Homo sapiens

<400> 699

nacgcgtaca caaatagtat cggaatcatt tcctatcatg ctgctatgac gagatttctc  
 60  
 cacacctcag attggcaact ggggatgact cggcactacc tgctgaagcg cggcgacgac  
 120  
 gacccacagg cacggtttac tgccgatcga atcgagacgg tgcgcaggct gggcgacgtt  
 180  
 gcccggaagg agggctgcga gtttgtcgtc gtcgccggag atgtcttcga aaccacaaat  
 240  
 gtctccactc agatcattgc ccgcgcgtgt gaggcgatag cctccattga tctccccgtg  
 300  
 tacctgctgc ccggaatatc cgacagctta gagccggggt gtctctggga tgggccagaa  
 360  
 ttc  
 363

<210> 700  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 700  
 Xaa Ala Tyr Thr Asn Ser Ile Gly Ile Ile Ser Tyr His Ala Ala Met  
 1 5 10 15  
 Thr Arg Phe Leu His Thr Ser Asp Trp Gln Leu Gly Met Thr Arg His  
 20 25 30  
 Tyr Leu Ser Lys Arg Gly Asp Asp Pro Gln Ala Arg Phe Thr Ala  
 35 40 45  
 Asp Arg Ile Glu Thr Val Arg Arg Leu Gly Asp Val Ala Arg Lys Glu  
 50 55 60  
 Gly Cys Glu Phe Val Val Val Ala Gly Asp Val Phe Glu Thr His Asn  
 65 70 75 80  
 Val Ser Thr Gln Ile Ile Ala Arg Ala Cys Glu Ala Ile Ala Ser Ile  
 85 90 95  
 Asp Leu Pro Val Tyr Leu Leu Pro Gly Asn His Asp Ser Leu Glu Pro  
 100 105 110  
 Gly Cys Leu Trp Asp Gly Pro Glu Phe  
 115 120

<210> 701  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens

<400> 701  
 nacgcgtccg ggcacaccgt caccgaggcg acgttccacg gccaccccac gctgatctat  
 60  
 ttgggctacg tccattgcgc ggatgtctgc ccgctgacac tgggcaacat ggtctcggcc  
 120  
 ctcgatcgcc tgggctcccg ggcggacggc atcggtccga tcttcatctc cgtcgatccg  
 180  
 gcccgcgaca caccgcgct ggtcggacag tatgtcgcgc atttctcgcc gcggatcgtc  
 240  
 gggctgaccg gcaccgcagc gcagctggcg ccggtactgg cggagttcca catcaccgcg  
 300  
 cgcgccgaac ctgcggcaca cgacatggcc gccgacatgt atgccgtcga ccacagcgcc  
 360  
 ctctctatc tgatggacgg caacaaccgc ctgttgcggg tgatggcggt cagcgccgac  
 420  
 gctgcctcgc tgacgcacca gctggcgggc ggctggccg gggcaagaat gagaccatga  
 480  
 aagcgatcgg accgacggac gccccgaac aggcagcgcc gggctggctg ttcggcatca  
 540  
 tctgctgct cggcatcgcc ggcattgctg atttcgtcga ccggt  
 585

<210> 702  
 <211> 159  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 702

```

Xaa Ala Ser Gly His Thr Val Thr Glu Ala Thr Phe His Gly His Pro
 1           5           10           15
Thr Leu Ile Tyr Phe Gly Tyr Val His Cys Ala Asp Val Cys Pro Leu
 20           25           30
Thr Leu Gly Asn Met Val Ser Ala Leu Asp Arg Leu Gly Ser Arg Ala
 35           40           45
Asp Gly Ile Val Pro Ile Phe Ile Ser Val Asp Pro Ala Arg Asp Thr
 50           55           60
Pro Ala Leu Val Gly Gln Tyr Val Ala His Phe Ser Pro Arg Ile Val
 65           70           75           80
Gly Leu Thr Gly Thr Ala Ala Gln Leu Ala Pro Val Leu Ala Glu Phe
 85           90           95
His Ile Thr Ala Arg Ala Glu Pro Ala Ala His Asp Met Ala Ala Asp
100           105           110
Met Tyr Ala Val Asp His Ser Ala Leu Leu Tyr Leu Met Asp Gly Asn
115           120           125
Asn Arg Leu Leu Arg Val Met Ala Val Ser Ala Asp Ala Ala Ser Leu
130           135           140
Thr His Gln Leu Ala Ala Gly Leu Ala Gly Ala Arg Met Arg Pro
145           150           155

```

&lt;210&gt; 703

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 703

```

ttctctgctc catacacacc tcagcagaat ggcacgccc agcgcaagaa cataactctt
60
attgagatgg cccgaacgat gcttgatgag tacaagactc cgcggaagtt ctggcctgaa
120
gccattgata ctgcttggtca caccatcaac cgcgtttatc ttcacaaggt tttggagaaa
180
acctcttatg agttcctaac tggttaagaaa cccaatgtaa gctatttcag agtatttggt
240
gctaggtgct ggatcaagga tcctcatcac acttcaaaat ttgcaccgaa agcacatgaa
300
gggttttatgc ttggttacgg aaaggattcg cactcctaca gagtcttcaa cctctttcac
360
tataaagtgg ttcaaactgt ggatgtgcn
390

```

&lt;210&gt; 704

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 704

```

Phe Ser Ala Pro Tyr Thr Pro Gln Gln Asn Gly Ile Ala Glu Arg Lys
 1           5           10           15
Asn Ile Thr Leu Ile Glu Met Ala Arg Thr Met Leu Asp Glu Tyr Lys

```

```

      20      25      30
Thr Pro Arg Lys Phe Trp Pro Glu Ala Ile Asp Thr Ala Cys His Thr
      35      40      45
Ile Asn Arg Val Tyr Leu His Lys Val Leu Glu Lys Thr Ser Tyr Glu
      50      55      60
Phe Leu Thr Gly Lys Lys Pro Asn Val Ser Tyr Phe Arg Val Phe Gly
      65      70      75      80
Ala Arg Cys Trp Ile Lys Asp Pro His His Thr Ser Lys Phe Ala Pro
      85      90      95
Lys Ala His Glu Gly Phe Met Leu Gly Tyr Gly Lys Asp Ser His Ser
      100      105      110
Tyr Arg Val Phe Asn Leu Phe His Tyr Lys Val Val Gln Thr Val Asp
      115      120      125
Val Arg
      130

```

<210> 705  
 <211> 513  
 <212> DNA  
 <213> Homo sapiens

```

<400> 705
acgcgtatatt cgtccaaatg attcaaatac aaacgccgcc gttaaaaacg atgcaggcga
60
agacaatgcg aataaaaaag gtggtaaata agcatgagtt ttaaaatgac acaatctcaa
120
tacacaagtc tttatggacc aactgtagga gactccgtga gattaggaga tacgaacttg
180
tttgacaaag ttgagaaaga ctatgcaaatac tatgggggatg aagctacttt cgggtggcga
240
aaatcaattc gtgatgggat ggctcaaaat cctaattgtga caagagatga taaaaatgta
300
gccgatttag ttttaactaa cgcattaatt attgattatg acaagattgt taaagcagat
360
atcgggtatta aaaatgggta tatttttaag attggtaaag ctggaaaccc agatataatg
420
gataacgttg acatcatcat tgggtgcaaca actgatatta ttgctgctga aggtaaaatt
480
gttactgccg gcggtatcga tacacacgtg cac
513

```

<210> 706  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

```

<400> 706
Met Ser Phe Lys Met Thr Gln Ser Gln Tyr Thr Ser Leu Tyr Gly Pro
1      5      10      15
Thr Val Gly Asp Ser Val Arg Leu Gly Asp Thr Asn Leu Phe Ala Gln
20      25      30
Val Glu Lys Asp Tyr Ala Asn Tyr Gly Asp Glu Ala Thr Phe Gly Gly
35      40      45
Gly Lys Ser Ile Arg Asp Gly Met Ala Gln Asn Pro Asn Val Thr Arg

```

```

      50              55              60
Asp Asp Lys Asn Val Ala Asp Leu Val Leu Thr Asn Ala Leu Ile Ile
65              70              75              80
Asp Tyr Asp Lys Ile Val Lys Ala Asp Ile Gly Ile Lys Asn Gly Tyr
      85              90              95
Ile Phe Lys Ile Gly Lys Ala Gly Asn Pro Asp Ile Met Asp Asn Val
      100             105             110
Asp Ile Ile Ile Gly Ala Thr Thr Asp Ile Ile Ala Ala Glu Gly Lys
      115             120             125
Ile Val Thr Ala Gly Gly Ile Asp Thr His Val His
      130             135             140

```

&lt;210&gt; 707

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 707

```

acgcgtggca tcctcagacc accaaagaca atcctgtcct gggaggcagg gagaaagccg
60
gcacactaca cagtgcacag gtgaagccct caggggggtcc tggagcaggg ccacctccct
120
gggggatccc caggtgccat tttcatggca gtgtctatgg acggctcccc ttggcatggg
180
gctgggtggc aatcctggct gtagctgccca cccctgccc tttttgcttc cctccgaggg
240
cattgtgatc atcagtgtga gtctgttggg aaggagagcc aggtccccag gtttgggaaa
300
ggagtagggg ttcccagcct gtctggccat cccccccag cccagccct cctgctgggt
360
gacgtgctca gttcggcccc tgctgtactg ggaggggggt aggagcata
409

```

&lt;210&gt; 708

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 708

```

Met Leu Leu Ala Pro Ser Gln Tyr Ser Arg Gly Arg Thr Glu His Val
 1              5              10              15
Thr Gln Gln Glu Gly Leu Gly Trp Gly Val Met Ala Arg Gln Ala Gly
      20              25              30
Lys Pro Tyr Ser Phe Pro Lys Pro Gly Asp Leu Ala Leu Leu Pro Asn
      35              40              45
Arg Leu Thr Leu Met Ile Thr Met Pro Ser Glu Gly Ser Lys Lys Gly
      50              55              60
Arg Gly Trp Gln Leu Gln Pro Gly Leu Pro Pro Ser Thr Met Pro Arg
65              70              75              80
Gly Ala Val His Arg His Cys His Glu Asn Gly Thr Trp Gly Ser Pro
      85              90              95
Arg Glu Val Ala Leu Leu Gln Asp Pro Leu Arg Ala Ser Pro Val His
      100             105             110
Cys Val Val Cys Arg Leu Ser Pro Cys Leu Pro Gly Gln Asp Cys Leu

```



115 120 125  
 Trp Trp Ser Glu Asp Ala Thr Arg  
 130 135  
 <210> 709  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens  
 <400> 709  
 acgcgtctga cggagagcct cctgagtctc cccacgcaga ggactcagaa agggaaatcgg  
 60  
 tgaccacacc tgggccagcg acgtgtggtg cgccagcctc cccagcggat cacctcctcc  
 120  
 tccccctccca ggaggagagt ttctccgaag tcccatgag tgaagcaagc tcagcgaaag  
 180  
 acactccact ctttaggatg gagggagagg atgcccttgt gactcagtat cagagcaaag  
 240  
 ccagtgacca cgaaggttta ttgtctgacc ccttgagtga ccttcagttg gtctcagatt  
 300  
 ttaaattctcc aatcatggcc gatctgaact taagccttcc ttccattcct gaagtcgcat  
 360  
 cggatgatga aagaatagat caggttgaag atgacggaga tcaggttgaa gatgatggag  
 420  
 agacagcaaa gtcgtcaact ctggacatag gagctttgtc cttgggcttg gtagtcccct  
 480  
 gtcttgagag gggaaagggg cccagtggcg aggcagatag gttggtactg ggggagggcc  
 540  
 tgtgtgattt caggctgcaa gcaccccagg catctgtgac agctccttca gagcagacca  
 600  
 cagagttcgg aattcacaaa ccacatcttg gcaagagctc aagcttggat aaacagctgc  
 660  
 caggccccag tgggtgtgag gaagaaaaac cgatgggaaa tgggagtcca agccccctc  
 720  
 ctggcacatc cctggacaat cctgtaccca gccctcccc ttctgagatc t  
 771

<210> 710  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 710  
 Met Ser Glu Ala Ser Ser Ala Lys Asp Thr Pro Leu Phe Arg Met Glu  
 1 5 10 15  
 Gly Glu Asp Ala Leu Val Thr Gln Tyr Gln Ser Lys Ala Ser Asp His  
 20 25 30  
 Glu Gly Leu Leu Ser Asp Pro Leu Ser Asp Leu Gln Leu Val Ser Asp  
 35 40 45  
 Phe Lys Ser Pro Ile Met Ala Asp Leu Asn Leu Ser Leu Pro Ser Ile  
 50 55 60  
 Pro Glu Val Ala Ser Asp Glu Arg Ile Asp Gln Val Glu Asp Asp  
 65 70 75 80  
 Gly Asp Gln Val Glu Asp Asp Gly Glu Thr Ala Lys Ser Ser Thr Leu

```

<400> 712
Met Ile Met Asn Thr Val Phe Ile Ile Asp Asp His Pro Val Ile Arg
 1             5             10             15
Leu Ala Ile Arg Met Leu Leu Glu His Glu Gly Tyr Lys Val Val Gly
      20             25             30
Glu Thr Asp Asn Gly Cys Asp Ala Ile Gln Met Val Arg Glu Cys Leu
      35             40             45
Pro Asp Leu Ile Ile Leu Asp Ile Ser Ile Pro Lys Leu Asp Gly Leu
      50             55             60
Glu Val Leu Cys Arg Phe Asn Ala Met Asn Thr Ser Met Lys Thr Leu

```

```
<210> 713
<211> 465
<212> DNA
<213> Homo sapiens
```

```
<210> 714
<211> 155
<212> PRT
<213> Homo sapiens
```

804

<210> 715  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 715  
 nnaccggtgg atgccaacga atatcgtggc gagctgaaag tcggcgccat caccaccgcc  
 60  
 cagaccggcc tgctgcctca ggcactggtg cgtttgcgcc aggcagcgcc gacggtggag  
 120  
 tgcaagttgg taccgggggt ttccctggag ttgctcagcc aggtggacgc aggcgagctg  
 180  
 gactcggcga tcatcattcg cccgcccttt gatttgccca aggagttgca cgtacaggta  
 240  
 ctgcgcaagg agccgtttgt gttgatcgtg ccccaggcgg tcgggggtga tgaccggtg  
 300  
 caactgctcg aagctcatcc ccacgtgcgc tacgaccgcg cttcgtttgg cggg  
 354

<210> 716  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 716  
 Xaa Pro Val Asp Ala Asn Glu Tyr Arg Gly Glu Leu Lys Val Gly Ala  
 1 5 10 15  
 Ile Thr Thr Ala Gln Thr Gly Leu Leu Pro Gln Ala Leu Val Arg Leu  
 20 25 30  
 Arg Gln Ala Ala Pro Thr Val Glu Cys Lys Leu Val Pro Gly Val Ser  
 35 40 45  
 Leu Glu Leu Leu Ser Gln Val Asp Ala Gly Glu Leu Asp Ser Ala Ile  
 50 55 60  
 Ile Ile Arg Pro Pro Phe Val Asp Leu Pro Lys Glu Leu His Val Gln Val  
 65 70 75 80  
 Leu Arg Lys Glu Pro Phe Val Leu Ile Val Pro Gln Ala Val Gly Gly  
 85 90 95  
 Asp Asp Pro Leu Gln Leu Leu Glu Ala His Pro His Val Arg Tyr Asp  
 100 105 110  
 Arg Ala Ser Phe Gly Gly  
 115

<210> 717  
 <211> 401  
 <212> DNA  
 <213> Homo sapiens

<400> 717  
 acgcgtatct ttccggtaaa cctactaatt ttctattcaa cgctcgacgc ccaggtaaag  
 60  
 ccgtaagtc atctaaatag gccattctgt ggctctccat cagtaagaac caaatccata  
 120  
 ggagaagttg agcggatagt aatgcacaa attgatgctg agaaaccgaa aaatgggaca  
 180

atataatcaa gctgacaata ctgatcaaac cactcgcacg aaagctacta ccgcttgacc  
 240  
 accaagcaga aaaaaccaat gaaatgctta aaaataaaat cgtccaaagt aaaaagctag  
 300  
 accaggtggg agccagatta aaaataggcc gctctagaaa atgaaaagaa atccaatgag  
 360  
 attcaacggc gtagcaccag cacagcaaca tagccactag t  
 401

<210> 718  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 718  
 Met Leu Leu Cys Trp Cys Tyr Ala Val Glu Ser His Trp Ile Ser Phe  
 1 5 10 15  
 His Phe Leu Glu Arg Pro Ile Phe Asn Leu Ala Thr Thr Trp Ser Ser  
 20 25 30  
 Phe Leu Leu Trp Thr Ile Leu Phe Leu Ser Ile Ser Leu Val Phe Ser  
 35 40 45  
 Ala Trp Trp Ser Ser Gly Ser Ser Phe His Ala Ser Gly Leu Ile Ser  
 50 55 60  
 Ile Val Ser Leu Ile Ile Leu Ser His Phe Ser Val Ser Gln His Gln  
 65 70 75 80  
 Phe Asp Ala Leu Leu Ser Ala Gln Leu Leu Leu Trp Ile Trp Phe Leu  
 85 90 95  
 Leu Met Glu Ser His Arg Met Ala Tyr Leu Asp Asp Leu Thr Ala Leu  
 100 105 110  
 Pro Gly Arg Arg Ala Leu Asn Glu Lys Leu Val Gly Leu Pro Lys Arg  
 115 120 125  
 Tyr Ala  
 130

<210> 719  
 <211> 685  
 <212> DNA  
 <213> Homo sapiens

<400> 719  
 tatatagggc tatctacctt attcacagca cattccatct acacaacctt gtagcgttca  
 60  
 ctcttgaagg cggattttca taggcgctgc gcctctcata ttcaagcatc aaggcaatcc  
 120  
 aatctccctg cggttggaac tgggcaaaag aaagacctct gcagtccagc aacctcatcg  
 180  
 tgcaaatgcc gtggcgtggg caactctgac ggcctggaag ctgcagacct tgtcaaagga  
 240  
 cctcggccga aattcaccct tgatctcttt gtcttgcca actcttgtcc ctgagaatga  
 300  
 aactgtcttc tgagagtcca tcaatgcgac gctgactcgt gagaagtgtc gaatcacgtc  
 360  
 gccattttgg agacctgcca acgcagctct ggaacctgcc aggacgcctt ccacaacacc  
 420

agaacgcagc gactttgcgt taaatccaag ctcaaacacc tcttgctcca caggcctgag  
 480  
 cataaaaaagg tattctgcga cgggaaatgt aaagtctgag cttaggtgca gaggaccgcc  
 540  
 atcgatcagt gtctgatact gcttggtccgc gacttctttg ccgagcaatg ggtatagcgt  
 600  
 tttcaaccaa gtggaagcag tcgtttgctc accctggcga ttccggcgag ttagggacat  
 660  
 gaccacgtca tcgatgggat ttgac  
 685

<210> 720

<211> 161

<212> PRT

<213> Homo sapiens

<400> 720

Met	Ser	Leu	Thr	Arg	Arg	Asn	Arg	Gln	Gly	Glu	Gln	Thr	Thr	Ala	Ser
1				5				10						15	
Thr	Trp	Leu	Lys	Thr	Leu	Tyr	Pro	Leu	Leu	Gly	Lys	Glu	Val	Ala	Asp
		20					25					30			
Lys	Gln	Tyr	Gln	Thr	Leu	Ile	Asp	Gly	Gly	Thr	Leu	His	Leu	Ser	Ser
	35					40					45				
Asp	Phe	Thr	Phe	Pro	Val	Ala	Glu	Tyr	Leu	Phe	Met	Leu	Arg	Pro	Val
	50				55					60					
Glu	Gln	Glu	Val	Phe	Glu	Leu	Gly	Phe	Asn	Ala	Lys	Ser	Leu	Arg	Ser
65				70				75					80		
Gly	Val	Val	Glu	Gly	Val	Leu	Ala	Gly	Ser	Arg	Ala	Ala	Leu	Ala	Gly
			85					90					95		
Leu	Gln	Asn	Gly	Asp	Val	Ile	Gln	His	Phe	Ser	Arg	Val	Ser	Val	Ala
		100					105					110			
Leu	Met	Asp	Ser	Gln	Lys	Thr	Val	Ser	Phe	Ser	Gly	Thr	Arg	Val	Gly
	115					120						125			
Gln	Asp	Lys	Glu	Ile	Lys	Gly	Glu	Phe	Arg	Pro	Arg	Ser	Phe	Asp	Lys
	130				135						140				
Val	Cys	Ser	Phe	Gln	Ala	Val	Arg	Val	Asp	His	Ala	Thr	Ala	Phe	Ala
145				150					155					160	
Arg															

<210> 721

<211> 579

<212> DNA

<213> Homo sapiens

<400> 721

aagcttgagg tcaggggtgtg gcagtgtggc gggagtgtgg aggtcctgcc ctgctcacgg  
 60  
 attgccaca ttgagcgagc ccacaagccc tacacagagg acctcaccgc ccatgtccgc  
 120  
 aggaacgctc tcaggggtggc tgaagtctgg atggatgaat ttaaaagcca cgtctactgg  
 180  
 catggaacat accaggagga ctcaggaatt gacattgggg acatcactgc aaggaaggct  
 240

ctcaggaaac agctgcagtg caagaccttc cggtgggtacc tggtcagcgt gtacccagag  
 300  
 atgaggatgt actccgacat cattgcctat ggagtgcctgc agaattctct gaagactgat  
 360  
 ttgtgtcttg accaggggcc agatacagag aatgtcccca tcatgtacat ctgccatggg  
 420  
 atgacgcctc agaacgtgta ctacacgagc agtcagcaga tccatgtggg cattctgagc  
 480  
 cccaccgtgg atgatgatga caaccgatgc ctggtggacg tcaacagccg gccccggctc  
 540  
 atcgaatgca gctacgcaa agccaagagg atgaagctt  
 579

<210> 722

<211> 193

<212> PRT

<213> Homo sapiens

<400> 722

Lys	Leu	Gly	Ile	Arg	Val	Trp	Gln	Cys	Gly	Gly	Ser	Val	Glu	Val	Leu
1			5				10						15		
Pro	Cys	Ser	Arg	Ile	Ala	His	Ile	Glu	Arg	Ala	His	Lys	Pro	Tyr	Thr
			20				25					30			
Glu	Asp	Leu	Thr	Ala	His	Val	Arg	Arg	Asn	Ala	Leu	Arg	Val	Ala	Glu
			35				40					45			
Val	Trp	Met	Asp	Glu	Phe	Lys	Ser	His	Val	Tyr	Trp	His	Gly	Thr	Tyr
			50				55				60				
Gln	Glu	Asp	Ser	Gly	Ile	Asp	Ile	Gly	Asp	Ile	Thr	Ala	Arg	Lys	Ala
65					70				75					80	
Leu	Arg	Lys	Gln	Leu	Gln	Cys	Lys	Thr	Phe	Arg	Trp	Tyr	Leu	Val	Ser
			85						90					95	
Val	Tyr	Pro	Glu	Met	Arg	Met	Tyr	Ser	Asp	Ile	Ile	Ala	Tyr	Gly	Val
			100				105						110		
Leu	Gln	Asn	Ser	Leu	Lys	Thr	Asp	Leu	Cys	Leu	Asp	Gln	Gly	Pro	Asp
			115				120					125			
Thr	Glu	Asn	Val	Pro	Ile	Met	Tyr	Ile	Cys	His	Gly	Met	Thr	Pro	Gln
			130				135					140			
Asn	Val	Tyr	Tyr	Thr	Ser	Ser	Gln	Gln	Ile	His	Val	Gly	Ile	Leu	Ser
145					150				155					160	
Pro	Thr	Val	Asp	Asp	Asp	Asp	Asn	Arg	Cys	Leu	Val	Asp	Val	Asn	Ser
			165				170							175	
Arg	Pro	Arg	Leu	Ile	Glu	Cys	Ser	Tyr	Ala	Lys	Ala	Lys	Arg	Met	Lys
			180				185						190		

Leu

<210> 723

<211> 384

<212> DNA

<213> Homo sapiens

<400> 723

acgcgtcctc ttacgctcag ttttgacaat gcgtgctggc agccaaccga agccgtaaaa  
 60

ctcaacgaaa tgctctcgct taaaccgtgc gaaggaaccc caccgcaatg gcgcttattc  
 120  
 cgcggaagggg attaccaaat gcgcattgat acgcgctccg gaacgcctac gctgatgctt  
 180  
 accgtacaaa gtgtaaccga caaacctggt acggacgtca ctcgacaatg tcctaaatgg  
 240  
 gacggcaagc ccctcaccct tgacgtaacg aatacattcc cggaaggctc cgtcgtacga  
 300  
 gacttctaca gcaagcaaac cgctatgggtg cagcaaggta aaatcacact tcagcctggc  
 360  
 gctaacagca atggcctgct gctg  
 384

<210> 724

<211> 128

<212> PRT

<213> Homo sapiens

<400> 724

Thr	Arg	Pro	Leu	Thr	Leu	Ser	Phe	Asp	Asn	Ala	Cys	Trp	Gln	Pro	Thr
1				5				10						15	
Glu	Ala	Val	Lys	Leu	Asn	Glu	Met	Leu	Ser	Leu	Lys	Pro	Cys	Glu	Gly
		20						25				30			
Thr	Pro	Pro	Gln	Trp	Arg	Leu	Phe	Arg	Glu	Gly	Asp	Tyr	Gln	Met	Arg
		35				40					45				
Ile	Asp	Thr	Arg	Ser	Gly	Thr	Pro	Thr	Leu	Met	Leu	Thr	Val	Gln	Ser
	50					55					60				
Val	Thr	Asp	Lys	Pro	Val	Thr	Asp	Val	Thr	Arg	Gln	Cys	Pro	Lys	Trp
65				70					75					80	
Asp	Gly	Lys	Pro	Leu	Thr	Leu	Asp	Val	Thr	Asn	Thr	Phe	Pro	Glu	Gly
			85					90					95		
Ser	Val	Val	Arg	Asp	Phe	Tyr	Ser	Lys	Gln	Thr	Ala	Met	Val	Gln	Gln
		100					105					110			
Gly	Lys	Ile	Thr	Leu	Gln	Pro	Ala	Asn	Ser	Asn	Gly	Leu	Leu	Leu	
		115				120					125				

<210> 725

<211> 521

<212> DNA

<213> Homo sapiens

<400> 725

tcattgacttg ctttattgca gtggtctgga actggtggat ggaacgaatt ttatctagag  
 60  
 cctggtgaac agcttcccag gtgtgcattt agggcctcct agggatcatc aaagttttta  
 120  
 gaaaataggt ttccttcttc cacaggcatg gagaaggaag gaaattttgc actggccttt  
 180  
 gggaagctga agaagagctg gggggaggct tgttctgaca aaatagtac tctctccctg  
 240  
 cttgaaatgt cccacagaag gctgtttctg gttcacattt gcccctctag gtccactccc  
 300  
 tccccctcat cctgctcact gccagagaga ctatgctggg agtggtgcat cggtggtctc  
 360



caggcccttt taggctcaag gtgttcattc cctggctcct tccctgccat gtctttgttc  
 420  
 cttctccct ctttccatc ccagcagcca cctctctcct tccaccagac ctgggaacca  
 480  
 tcatcccaac cacaatcacc ccgtggttct attacacgcg t  
 521

<210> 726

<211> 124

<212> PRT

<213> Homo sapiens

<400> 726

Met	Glu	Lys	Glu	Gly	Asn	Phe	Ala	Leu	Ala	Phe	Gly	Lys	Leu	Lys	Lys
1				5					10				15		
Ser	Trp	Gly	Glu	Ala	Cys	Ser	Asp	Lys	Ile	Val	Thr	Leu	Ser	Leu	Leu
			20					25				30			
Glu	Met	Ser	His	Arg	Arg	Leu	Phe	Leu	Val	His	Ile	Cys	Pro	Ser	Arg
		35				40					45				
Ser	Thr	Pro	Ser	Pro	Ser	Ser	Cys	Ser	Leu	Pro	Glu	Arg	Leu	Cys	Trp
	50				55				60						
Glu	Trp	Cys	Ile	Gly	Gly	Leu	Gln	Ala	Leu	Leu	Gly	Ser	Arg	Cys	Ser
65				70					75				80		
Phe	Pro	Gly	Ser	Phe	Pro	Ala	Met	Ser	Leu	Phe	Leu	Pro	Pro	Ser	Phe
			85					90					95		
Pro	Ser	Gln	Gln	Pro	Pro	Ser	Ser	Phe	His	Gln	Thr	Trp	Glu	Pro	Ser
		100				105							110		
Ser	Gln	Pro	Gln	Ser	Pro	Arg	Gly	Ser	Ile	Thr	Arg				
	115					120									

<210> 727

<211> 629

<212> DNA

<213> Homo sapiens

<400> 727

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&lt;210&gt; 730

&lt;211&gt; 797

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 730

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agcagcttcg aacctacacc tgagggttac cagcagggtg cgctctggct ttgcactgca  
3240  
aaaactgggg accagcccc ttctccaca aataaagccc aataaagcct gagaagttag  
3300  
gaaagccata tttgggtata tttgaagtgg aaagtgtgta tgaataacag caagggaaga  
3360  
gcattcttac ataggaggta tgcattctcc cctgagcctt gagaacctgt ctcaacacgg  
3420  
gggcggggag ggggcagctg ttggttcttt ctaacctct ccaggtcagg gaacaaattt  
3480  
gcccctaaac ttccacagga ggcactctac cctctgggcc agagctgggc acagtggcaa  
3540  
agtcagatta gaatttctag agttctaaca gcgattccca accatttcct caacttttct  
3600  
tctgtttccc acatcccaag gcagggaat cctgctgcc tctctcctc ttctaactca  
3660  
gctgtaaggc ggtttaggag ccgctggcag aatcaatggc atcgaccaag ggaggggggg  
3720  
tggcaaggga ttttctgtg cttaactact gatcacggct aagtggaaat cctataaaca  
3780  
cgagcggaaa tcaatggagg ctgcttagcg gccaggggag aggggcggcc cacagattgc  
3840  
atctgacgga tgagcgagag gaagcagcca gggagggtc aaggaagagt agcttagagg  
3900  
agggggaaga aacaggcagc gctggagaga gaggagtcac tgtcagaagg gacactgagg  
3960  
ggagaggcac agtgggccc ggagtggact ccgttagacc cagagttccc tcccccttct  
4020

aggaagtgtac acccctagcc caggcagtgg tcaggatctt cagtctcttg tggcctctct  
 4080  
 ctggagctgt tcacttctag caggcgctga tagtcttgag gccggaaacg ctgtagatac  
 4140  
 acaatcagct tggctggtgc tgtctctgt gcaggcacac ctcaaagccc gagagtctcc  
 4200  
 tcgcgggacc cacagagggg gaaggagacc caccatac actcgcgagg aatgccggga  
 4260  
 gcagttccgg atcccggacc tcggcccgac cctccgcgcg cccggcaggt cccggcacca  
 4320  
 gcggccatat tacgcccgtt gtggcgggtgc cgagagcagg ccaggc  
 4366

<210> 734

<211> 364

<212> PRT

<213> Homo sapiens

<400> 734

Met	Val	Val	Pro	Ser	Leu	Lys	Leu	Gln	Asp	Leu	Ile	Glu	Glu	Ile	Arg
1				5					10					15	
Gly	Ala	Lys	Thr	Gln	Ala	Gln	Glu	Arg	Glu	Val	Ile	Gln	Lys	Glu	Cys
			20					25					30		
Ala	His	Ile	Arg	Ala	Ser	Phe	Arg	Asp	Gly	Asp	Pro	Val	His	Arg	His
		35					40					45			
Arg	Gln	Leu	Ala	Lys	Leu	Leu	Tyr	Val	His	Met	Leu	Gly	Tyr	Pro	Ala
	50				55						60				
His	Phe	Gly	Gln	Met	Glu	Cys	Leu	Lys	Leu	Ile	Ala	Ser	Ser	Arg	Phe
65					70					75				80	
Thr	Asp	Lys	Arg	Val	Gly	Tyr	Leu	Gly	Ala	Met	Leu	Leu	Leu	Asp	Glu
			85						90					95	
Arg	His	Asp	Ala	His	Leu	Leu	Ile	Thr	Asn	Ser	Ile	Lys	Asn	Asp	Leu
			100					105					110		
Ser	Gln	Gly	Ile	Gln	Pro	Val	Gln	Gly	Leu	Ala	Leu	Cys	Thr	Leu	Ser
	115						120					125			
Thr	Met	Gly	Ser	Ala	Glu	Met	Cys	Arg	Asp	Leu	Ala	Pro	Glu	Val	Glu
	130					135					140				
Lys	Leu	Leu	Leu	Gln	Pro	Ser	Pro	Tyr	Val	Arg	Lys	Lys	Ala	Ile	Leu
145				150						155				160	
Thr	Ala	Val	His	Met	Ile	Arg	Lys	Val	Pro	Glu	Leu	Ser	Ser	Val	Phe
			165						170					175	
Leu	Pro	Pro	Cys	Ala	Gln	Leu	Leu	His	Glu	Arg	His	His	Gly	Ile	Leu
		180						185					190		
Leu	Gly	Thr	Ile	Thr	Leu	Ile	Thr	Glu	Leu	Cys	Glu	Arg	Ser	Pro	Ala
	195					200						205			
Ala	Leu	Arg	His	Phe	Arg	Lys	Val	Val	Pro	Gln	Leu	Val	His	Ile	Leu
	210					215						220			
Arg	Thr	Leu	Val	Thr	Met	Gly	Tyr	Ser	Thr	Glu	His	Ser	Ile	Ser	Gly
225				230						235				240	
Val	Ser	Asp	Pro	Phe	Leu	Gln	Val	Gln	Ile	Leu	Arg	Leu	Leu	Arg	Ile
			245						250					255	
Leu	Gly	Arg	Asn	His	Glu	Glu	Ser	Ser	Glu	Thr	Met	Asn	Asp	Leu	Leu
			260					265					270		
Ala	Gln	Val	Ala	Thr	Asn	Thr	Asp	Thr	Ser	Arg	Asn	Ala	Gly	Asn	Ala

275	280	285
Val Leu Phe Glu Thr Val Leu Thr Ile Met Asp Ile Arg Ser Ala Ala		
290	295	300
Gly Leu Arg Val Leu Ala Val Asn Ile Leu Gly Arg Phe Leu Leu Asn		
305	310	315
Ser Asp Arg Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Arg Leu		
	325	330
Val Gln Ser Asp His Ser Ala Val Gln Arg His Arg Pro Thr Val Val		335
	340	345
Glu Cys Leu Arg Glu Thr Asp Ala Ser Leu Ser Arg		350
355	360	

&lt;210&gt; 735

&lt;211&gt; 597

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 735

```

gtcgactagc caaaccgccc gggaaagtct tgtaccaccg atcctggttt atgcggatct
60
catcgccacc atggactcgc gcaatctgga aaccgccaac cttattccag aaaaaataat
120
tgcttggtgt cctcgatccc gctctgaccg cccactggac cgctcaaccc aggacatcct
180
cagtgccatc cacgacgtgg ctgcaccgct ggcactacc atcttcgtgg tgggtgccac
240
agcgcgcgac attctgctga cacacgtgtt cggtatcgag accggacgtg ccacgctcga
300
cgtggatttc gccgttgccg tagaacattg gccgcagttc gaaaacatca agcagcacct
360
gctagccaac gaccatttcg actctgccgc cagcatcacc catcgactgc tctatcgcac
420
gagcgacaac acgatcgccc ggccaatcga tctcatccca ttcggcggca tcgaacagcc
480
gccagccacc atcaaatggc cgcccgacat ggctgtcatg atgaatgttg ctggctacgc
540
agatgcctgg cgggcccag tcgaagtaga gtttgtgccc gggcgagca tacgcgt
597

```

&lt;210&gt; 736

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 736

Met Asp Ser Arg Asn Leu Glu Thr Ala Asn Leu Ile Pro Glu Lys Ile		
1	5	10
Ile Ala Trp Cys Pro Arg Ser Arg Ser Asp Arg Pro Leu Asp Arg Ser		15
	20	25
Thr Gln Asp Ile Leu Ser Ala Ile His Asp Val Ala Ala Pro Leu Ala		30
	35	40
Leu Pro Ile Phe Val Val Gly Ala Thr Ala Arg Asp Ile Leu Leu Thr		45
	50	55
His Val Phe Gly Ile Glu Thr Gly Arg Ala Thr Leu Asp Val Asp Phe		60

```

65              70              75              80
Ala Val Ala Val Glu His Trp Pro Gln Phe Glu Asn Ile Lys Gln His
              85              90              95
Leu Leu Ala Asn Asp His Phe Asp Ser Ala Ala Ser Ile Thr His Arg
              100             105             110
Leu Leu Tyr Arg Thr Ser Asp Asn Thr Ile Ala Arg Pro Ile Asp Leu
              115             120             125
Ile Pro Phe Gly Gly Ile Glu Gln Pro Pro Ala Thr Ile Lys Trp Pro
              130             135             140
Pro Asp Met Ala Val Met Met Asn Val Ala Gly Tyr Ala Asp Ala Trp
145              150              155              160
Arg Ala Ala Val Glu Val Glu Phe Val Pro Gly Arg Ser Ile Arg
              165              170              175

```

<210> 737  
 <211> 497  
 <212> DNA  
 <213> Homo sapiens

```

<400> 737
ntgcgcctgg ccaattccgg cgccatcctc gggcacgatac tggggaaaac ctccatgggtg
60
cgcgccggca tcgttgggta cggatacgat cccaaccctc acgccgaccg tgccgaccta
120
caccctgccc tgtcctggat cagccacgtc accttcgtta aaactgtcag tgtgggggat
180
accatcggtc acggcagaac atggacagcc agcgaaacga caaaaatcgc caccgtccca
240
gtcggttacg ccgacggact gtcccaggga ctgtcaaata aaggacacgt tctcattaga
300
gggtccgttc atcccatcgt cggtcggatac tgcattggacc aattcatggt cgatcttggc
360
cccgattcga acgtcacggt gggagatgag gtggtgctca ttggaacca ggaggacgaa
420
actctgaccg ctgatgacat ggccgaactc ctcggaacca ttagctacga gatcacttgc
480
gccatttcca aacgcgt
497

```

<210> 738  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

```

<400> 738
Xaa Arg Leu Ala Asn Ser Gly Ala Ile Leu Gly His Asp Leu Gly Lys
1              5              10              15
Thr Ser Met Val Arg Ala Gly Ile Val Gly Tyr Gly Tyr Asp Pro Asn
              20              25              30
Pro His Ala Asp Arg Ala Asp Leu His Pro Ala Leu Ser Trp Ile Ser
              35              40              45
His Val Thr Phe Val Lys Thr Val Ser Val Gly Asp Thr Ile Gly Tyr
              50              55              60
Gly Arg Thr Trp Thr Ala Ser Glu Thr Thr Lys Ile Ala Thr Val Pro

```

```

65          70          75          80
Val Gly Tyr Ala Asp Gly Leu Ser Arg Gly Leu Ser Asn Lys Gly His
          85          90          95
Val Leu Ile Arg Gly Ser Val His Pro Ile Val Gly Arg Ile Cys Met
          100          105          110
Asp Gln Phe Met Val Asp Leu Gly Pro Asp Ser Asn Val Thr Val Gly
          115          120          125
Asp Glu Val Val Leu Ile Gly Thr Gln Glu Asp Glu Thr Leu Thr Ala
          130          135          140
Asp Asp Met Ala Glu Leu Leu Gly Thr Ile Ser Tyr Glu Ile Thr Cys
145          150          155          160
Ala Ile Ser Lys Arg
          165

```

&lt;210&gt; 739

&lt;211&gt; 438

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 739

```

cggctgcggg aagagcgggc gcacgcgctc aagaccaagg aaaagctggc acagaccgcc
60
acggcctcat cagcagctgt gggctcaggc cccctcccg aggcggagca ggcgtggccg
120
cagagcagcg gggaggagga gctgcagctc cagctggccc tggccatgag caaggaggag
180
gccgaccagc cccgtcctg cgccccgag gacgacgcc agctccagct ggcccttagt
240
ttgagccgag aagagcatga taaggaggag cggatccgtc gcggggatga cctgcccgtg
300
cagatggcaa tcgaggagag caagagggag actgggggca aggaggagtc gtccctcatg
360
gaccttgctg acgtcttcac gccccagct cctgccccga ccacagaccc ctggggggggc
420
ccagcaccca tggctgct
438

```

&lt;210&gt; 740

&lt;211&gt; 146

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 740

```

Arg Leu Arg Glu Glu Arg Ala His Ala Leu Lys Thr Lys Glu Lys Leu
1          5          10          15
Ala Gln Thr Ala Thr Ala Ser Ser Ala Ala Val Gly Ser Gly Pro Pro
          20          25          30
Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu Glu Leu
          35          40          45
Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp Gln Pro
          50          55          60
Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln Leu Gln Leu Ala Leu Ser
65          70          75          80
Leu Ser Arg Glu Glu His Asp Lys Glu Glu Arg Ile Arg Arg Gly Asp

```

	85		90		95										
Asp	Leu	Arg	Leu	Gln	Met	Ala	Ile	Glu	Glu	Ser	Lys	Arg	Glu	Thr	Gly
			100					105					110		
Gly	Lys	Glu	Glu	Ser	Ser	Leu	Met	Asp	Leu	Ala	Asp	Val	Phe	Thr	Pro
		115				120						125			
Pro	Ala	Pro	Ala	Pro	Thr	Thr	Asp	Pro	Trp	Gly	Gly	Pro	Ala	Pro	Met
	130					135						140			
Ala	Ala														
145															

&lt;210&gt; 741

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 741

```

gcctctctcc gaccgcgttg ttgtaaggat gtcgcgcacgg tgcgcaaaaa tgaatatgtg
60
aatttgccgg tcatctgcct cgtcggggccc actgctagcg gaaaatcagg gctagcgggtg
120
cgagtgtgcc gccgcttgta tgctgatgag caccgccgag aaattattaa tactgactcg
180
atgggtggtgt atcgcgggat ggacattggc actgccaccc ctacactgag cgagcagcgc
240
acggtagtgc atcacctggt gtcgattctt gatgtgactg tgccctcttc gctagtactg
300
atgcagacgc tggcccgatga tgccgtcgag gattgtctgt cgcggtggtgt catcctgtgc
360
ttggtgggag ggtctgcgct gtacaccaag gccatcattg acgaaatgtc catcccgcca
420
actgatccgg aagtgagggc tcggtggcag gagaagctag atgccgaggg gccgcgagtt
480
ctgcatgacg agcttgcccg tcgcatcccc aaggcggctg agtcaatctt gcccggaac
540
ggcaggcgaa tcgtttcgtg ccctcgaagt ttattgaccc tgacagggtc ctttactgcc
600
accgatcccc gacgggaccc tccactggcc aagacggtgc aaatgggctt agaactgtcg
660
cgcaaagaca tagaccagcg tattgccgat cgggttgacc agatgtgggc atacggtttc
720
gtcgac
726

```

&lt;210&gt; 742

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 742

Ala	Ser	Leu	Arg	Pro	Arg	Cys	Cys	Lys	Asp	Val	Ala	Thr	Val	Arg	Lys
1				5				10						15	
Asn	Glu	Tyr	Val	Asn	Leu	Pro	Val	Ile	Cys	Leu	Val	Gly	Pro	Thr	Ala
			20					25					30		
Ser	Gly	Lys	Ser	Gly	Leu	Ala	Val	Arg	Val	Cys	Arg	Arg	Leu	Tyr	Val

```

      35              40              45
Asp Glu His Pro Ala Glu Ile Ile Asn Thr Asp Ser Met Val Val Tyr
  50              55              60
Arg Gly Met Asp Ile Gly Thr Ala Thr Pro Thr Leu Arg Glu Gln Arg
  65              70              75              80
Thr Val Val His His Leu Val Ser Ile Leu Asp Val Thr Val Pro Ser
      85              90              95
Ser Leu Val Leu Met Gln Thr Leu Ala Arg Asp Ala Val Glu Asp Cys
      100             105             110
Leu Ser Arg Gly Val Ile Pro Val Leu Val Gly Gly Ser Ala Leu Tyr
      115             120             125
Thr Lys Ala Ile Ile Asp Glu Met Ser Ile Pro Pro Thr Asp Pro Glu
      130             135             140
Val Arg Ala Arg Trp Gln Glu Lys Leu Asp Ala Glu Gly Pro Arg Val
      145             150             155             160
Leu His Asp Glu Leu Ala Arg Arg Asp Pro Lys Ala Ala Glu Ser Ile
      165             170             175
Leu Pro Gly Asn Gly Arg Arg Ile Val Ser Cys Pro Arg Ser Leu Leu
      180             185             190
Thr Leu Thr Gly Ser Phe Thr Ala Thr Asp Pro Arg Arg Asp Pro Pro
      195             200             205
Leu Ala Lys Thr Val Gln Met Gly Leu Glu Leu Ser Arg Lys Asp Ile
      210             215             220
Asp Gln Arg Ile Ala Asp Arg Val Asp Gln Met Trp Ala Tyr Gly Phe
      225             230             235             240
Val Asp

```

<210> 743  
 <211> 430  
 <212> DNA  
 <213> Homo sapiens

```

<400> 743
naaaaaagtg atggtttcgg atctgtggcc agtcgtcttg caagaaatca ttatgacgtg
  60
gatgagggga acagcancat tcatgttaat caagacattg cgcgcagaac agggacggga
  120
aagctattgg tacgagtgtg cccggcgac gtgtactcag aggagcccga tggcactatt
  180
tccgtggagt acgcagcgtg tctggagtgt ggcacttgtc tggcggttgc tgcgccaggg
  240
tcgcttgaat ggcactatcc cgcaggtgca atgggtatct cgttcagaga aggatgaagt
  300
ccttggtggc gactgtaaag cgacatggcc gtcgctcggg aggaggaatt gtggtgtccg
  360
caccaaatag tgctcaggat gaagttcgtc atggaaatcc ggctccaacc gtttcgggag
  420
ctggtcgcga
  430

```

<210> 744  
 <211> 98  
 <212> PRT



&lt;213&gt; Homo sapiens

&lt;400&gt; 744

Xaa Lys Ser Asp Gly Phe Gly Ser Val Ala Ser Arg Leu Ala Arg Asn  
 1 5 10 15  
 His Tyr Asp Val Asp Glu Gly Asn Ser Xaa Ile His Val Asn Gln Asp  
 20 25 30  
 Ile Ala Arg Arg Thr Gly Thr Gly Lys Leu Leu Val Arg Val Cys Pro  
 35 40 45  
 Ala His Val Tyr Ser Glu Glu Pro Asp Gly Thr Ile Ser Val Glu Tyr  
 50 55 60  
 Ala Ala Cys Leu Glu Cys Gly Thr Cys Leu Ala Val Ala Ala Pro Gly  
 65 70 75 80  
 Ser Leu Glu Trp His Tyr Pro Ala Gly Ala Met Gly Ile Ser Phe Arg  
 85 90 95  
 Glu Gly

&lt;210&gt; 745

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 745

cggccgattg aagcgctcgt gcggtttgag tcggtgatgg atgcggtgga cggtgcttcg  
 60  
 gcgtcgtggg ggcgcattgg gcggtatttc atcgccgagc ttgaacgcag cagcgagttg  
 120  
 tatgagcagg cggcgtttac ccgcgatctg gaaagctcgc tgatcaaggg cctgacctc  
 180  
 gccagccga acaactactc cgaagaactg cgcgacgtac tcggcgtgaa gctgccgcat  
 240  
 tacttgattc gcgcgcggca gtacatccac gacaacgccc gcgaagccgt gcatctggaa  
 300  
 gacctggaaa ccgctgccgg ggtatcgagg ttcaagttgt tcgatgcgtt tcgcaaatac  
 360  
 tt  
 362

&lt;210&gt; 746

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 746

Met Asp Ala Val Asp Gly Ala Ser Ala Ser Trp Trp Arg Met Ala Arg  
 1 5 10 15  
 Tyr Phe Ile Ala Glu Leu Glu Arg Ser Ser Glu Leu Tyr Glu Gln Ala  
 20 25 30  
 Ala Phe Thr Arg Asp Leu Glu Ser Ser Leu Ile Lys Gly Leu Ile Leu  
 35 40 45  
 Ala Gln Pro Asn Asn Tyr Ser Glu Glu Leu Arg Asp Val Leu Gly Val  
 50 55 60  
 Lys Leu Pro His Tyr Leu Ile Arg Ala Arg Gln Tyr Ile His Asp Asn

```

65              70              75              80
Ala Arg Glu Ala Val His Leu Glu Asp Leu Glu Thr Ala Ala Gly Val
              85              90              95
Ser Arg Phe Lys Leu Phe Asp Ala Phe Arg Lys Tyr
              100              105

```

<210> 747  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

```

<400> 747
nacgcgttga tcgccgccga ccgtttcatc ccgcaatcac ccgacatggc ggcctatttt
60
ctgaatgccg atggcacgcc taaagccacc ggcacgctgc tcaagaaccc agcgtggcc
120
gccgtgttca aacgtatcgc caaggaagga ccggacgcgc tgtaccacgg gccgattggc
180
gacgagatcg cgcgcaaggt tcagggcaac cgcaatgcgg gcagcctgtc gcaagcggac
240
ctcaaggctt acaccgcaa ggaacgcacg ccgctgtgca ccgactacaa gcaatatcag
300
gtgtgcggca tgccaccgcc gtcgtcaggc gggattgcgg tggcgcagat cctcggcacg
360
ctgcaggccg tggaagcccg cgaccacgc ctggccatcg ccccatgaa accggt
416

```

<210> 748  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

```

<400> 748
Xaa Ala Leu Ile Ala Ala Asp Arg Phe Ile Pro Gln Ser Pro Asp Met
1      5      10      15
Ala Ala Tyr Phe Leu Asn Ala Asp Gly Thr Pro Lys Ala Thr Gly Thr
      20      25      30
Leu Leu Lys Asn Pro Ala Leu Ala Ala Val Phe Lys Arg Ile Ala Lys
      35      40      45
Glu Gly Pro Asp Ala Leu Tyr His Gly Pro Ile Ala Asp Glu Ile Ala
50      55      60
Arg Lys Val Gln Gly Asn Arg Asn Ala Gly Ser Leu Ser Gln Ala Asp
65      70      75      80
Leu Lys Ala Tyr Thr Ala Lys Glu Arg Thr Pro Leu Cys Thr Asp Tyr
      85      90      95
Lys Gln Tyr Gln Val Cys Gly Met Pro Pro Pro Ser Ser Gly Gly Ile
      100      105      110
Ala Val Ala Gln Ile Leu Gly Thr Leu Gln Ala Val Glu Ala Arg Asp
      115      120      125
Pro Arg Leu Ala Ile Ala Pro Met Lys Pro
      130      135

```

<210> 749  
 <211> 1211

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 749

nagtcctaga cgccagaccc gctcagaccc tcctgccagg tgacagccgc caagatgggg  
60  
tcttggggcc tgctgtggcc tcccctgctg ttcaccgggc tgctcgtccg acccccgggg  
120  
accatggccc aggcccagta ctgctctgtg aacaaggaca tctttgaagt agaggagAAC  
180  
acaaatgtca ccgagccgct ggtggacatc cacgtcccgg agggccagga ggtgaccctc  
240  
ggagccttgt ccacccctt tgcatttcgg atccaggga accagctgtt tctcaacgtg  
300  
actcctgatt acgaggagaa gtcactgctt gaggtcagc tgctgtgtca gagcggaggc  
360  
acattggtga ccagctaag ggtgttcgtg tcagtgtgg acgtcaatga caatgcccc  
420  
gaattcccct ttaagaccaa ggagataagg gtggaggagg acacgaaagt gaactccacc  
480  
gtcatccccg agacgcaact gcaggtgag gaccgagaca aggacgacat tctgttctac  
540  
accctccagg aaatgacagc aggtgccagt gactacttct ccctggtgag tgtaaaccgt  
600  
ccgcccctga ggctggaccg gccctggac ttctacgagc ggccgaacat gaccttctgg  
660  
ctgctggtgc gggacactcc gggggagaat gtggaacca gccacactgc caccgccaca  
720  
ctagtgtga acgtggtgcc cgcgacctg cggccccgt ggttcctgcc ctgcacctc  
780  
tcagatggct acgtctgcat tcaagctcag taccacgggg ctgtccccac ggggcacata  
840  
ctgccatctc ccctcgtcct gcgtcccga cccatctacg ctgaggacgg agaccgccc  
900  
atcaaccagc ccatcatcta cagcatcttt aggggaaacg tgaatggtac attcatcatc  
960  
caccagact cgggcaacct caccgtggcc aggagtgtcc ccagccccat gaccttctt  
1020  
ctgctggtga agggccaaca ggccgacctt gcccgctact cagtgacca ggtcaccgtg  
1080  
gagggtgtg gctgcgccg ggagcccgc ccgcttcccc cagagcctgt atcgtggcac  
1140  
cgtggcgctg ggcgtggag cgggcgttgt ggtcaaggat gcagctgccc cttttcagcc  
1200  
tctgaggatc c  
1211

&lt;210&gt; 750

&lt;211&gt; 385

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 750

Met Gly Ser Trp Ala Leu Leu Trp Pro Pro Leu Leu Phe Thr Gly Leu

```

1           5           10           15
Leu Val Arg Pro Pro Gly Thr Met Ala Gln Ala Gln Tyr Cys Ser Val
20           25           30
Asn Lys Asp Ile Phe Glu Val Glu Glu Asn Thr Asn Val Thr Glu Pro
35           40           45
Leu Val Asp Ile His Val Pro Glu Gly Gln Glu Val Thr Leu Gly Ala
50           55           60
Leu Ser Thr Pro Phe Ala Phe Arg Ile Gln Gly Asn Gln Leu Phe Leu
65           70           75           80
Asn Val Thr Pro Asp Tyr Glu Glu Lys Ser Leu Leu Glu Ala Gln Leu
85           90           95
Leu Cys Gln Ser Gly Gly Thr Leu Val Thr Gln Leu Arg Val Phe Val
100          105          110
Ser Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe Pro Phe Lys Thr
115          120          125
Lys Glu Ile Arg Val Glu Glu Asp Thr Lys Val Asn Ser Thr Val Ile
130          135          140
Pro Glu Thr Gln Leu Gln Ala Glu Asp Arg Asp Lys Asp Asp Ile Leu
145          150          155          160
Phe Tyr Thr Leu Gln Glu Met Thr Ala Gly Ala Ser Asp Tyr Phe Ser
165          170          175
Leu Val Ser Val Asn Arg Pro Ala Leu Arg Leu Asp Arg Pro Leu Asp
180          185          190
Phe Tyr Glu Arg Pro Asn Met Thr Phe Trp Leu Leu Val Arg Asp Thr
195          200          205
Pro Gly Glu Asn Val Glu Pro Ser His Thr Ala Thr Ala Thr Leu Val
210          215          220
Leu Asn Val Val Pro Ala Asp Leu Arg Pro Pro Trp Phe Leu Pro Cys
225          230          235          240
Thr Phe Ser Asp Gly Tyr Val Cys Ile Gln Ala Gln Tyr His Gly Ala
245          250          255
Val Pro Thr Gly His Ile Leu Pro Ser Pro Leu Val Leu Arg Pro Gly
260          265          270
Pro Ile Tyr Ala Glu Asp Gly Asp Arg Gly Ile Asn Gln Pro Ile Ile
275          280          285
Tyr Ser Ile Phe Arg Gly Asn Val Asn Gly Thr Phe Ile Ile His Pro
290          295          300
Asp Ser Gly Asn Leu Thr Val Ala Arg Ser Val Pro Ser Pro Met Thr
305          310          315          320
Phe Leu Leu Leu Val Lys Gly Gln Gln Ala Asp Leu Ala Arg Tyr Ser
325          330          335
Val Thr Gln Val Thr Val Glu Gly Cys Gly Cys Gly Arg Glu Pro Ala
340          345          350
Pro Leu Pro Pro Glu Pro Val Ser Trp His Arg Gly Ala Trp Arg Trp
355          360          365
Ser Gly Arg Cys Gly Gln Gly Cys Ser Cys Pro Phe Ser Ala Ser Glu
370          375          380
Asp
385

```

&lt;210&gt; 751

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 751

cgcgtcgcgg tcatacgtcaa cgacatgagc gaggtcaaca tcgacgcggc gctggtggcg  
 60  
 gcaggcggcg ggctgtcgcg caccgaggag aagctcgtcg agatgtcgaa cggctgcacg  
 120  
 tgctgcacgc tgcgcgacga cctgatgcag gaagtggcga gactggcggg cgaaggccgc  
 180  
 ttcgatgcgc tggatcatga gagcaccggc gtgtccgagc cgatgccggg cgcgcacacg  
 240  
 ttcgatttcc gtgaccagga cggcgtctcg ctgcgccgacg tcgcgcgggt ggataccatg  
 300  
 gtcaccgtcg tcgacgcgcg gtccttctcg cgcgactacg gctcg  
 345

&lt;210&gt; 752

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 752

Arg	Val	Ala	Val	Ile	Val	Asn	Asp	Met	Ser	Glu	Val	Asn	Ile	Asp	Ala
1				5					10					15	
Ala	Leu	Val	Ala	Ala	Gly	Gly	Gly	Leu	Ser	Arg	Thr	Glu	Glu	Lys	Leu
			20					25					30		
Val	Glu	Met	Ser	Asn	Gly	Cys	Ile	Cys	Cys	Thr	Leu	Arg	Asp	Asp	Leu
		35				40						45			
Met	Gln	Glu	Val	Ala	Arg	Leu	Ala	Gly	Glu	Gly	Arg	Phe	Asp	Ala	Leu
		50				55					60				
Val	Ile	Glu	Ser	Thr	Gly	Val	Ser	Glu	Pro	Met	Pro	Val	Ala	Ala	Thr
65					70					75				80	
Phe	Asp	Phe	Arg	Asp	Gln	Asp	Gly	Val	Ser	Leu	Ala	Asp	Val	Ala	Arg
			85					90					95		
Leu	Asp	Thr	Met	Val	Thr	Val	Val	Asp	Ala	Ala	Ser	Phe	Leu	Arg	Asp
			100					105					110		
Tyr	Gly	Ser													
			115												

&lt;210&gt; 753

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 753

gcgcgccagt acgccaagac cgtccgcaag gaccgcaagg gcgaacggcg gcgtcggggc  
 60  
 gcgtcggact agtccacgat gcatccgaac cgcgccttcc gctttgccga tgatgtctcg  
 120  
 atgctcgatt tcgcggccaa gcgagccttt gcgcacatct tcgtgagcac gcccgagggg  
 180  
 cctatggttag cgcattcccc ggttacgccc ttcgacggag ccttccgctt ccatgtcgcg  
 240  
 cgcggcaatc ggatcgcgcg gcacctggat ggcgcgacgc tgctgtctcag catcagcgcg  
 300

accgacggct atatcagccc gagctgggtac gccgacccgc agggaccaca gt  
352

<210> 754

<211> 91

<212> PRT

<213> Homo sapiens

<400> 754

Met	His	Pro	Asn	Arg	Ala	Phe	Arg	Phe	Ala	Asp	Asp	Val	Ser	Met	Leu
1				5					10					15	
Asp	Phe	Ala	Ala	Lys	Arg	Ala	Phe	Ala	His	Ile	Phe	Val	Ser	Thr	Pro
			20					25					30		
Glu	Gly	Pro	Met	Val	Ala	His	Ala	Pro	Val	Thr	Pro	Phe	Asp	Gly	Ala
		35					40					45			
Phe	Arg	Phe	His	Val	Ala	Arg	Gly	Asn	Arg	Ile	Ala	Arg	His	Leu	Asp
	50					55					60				
Gly	Ala	Thr	Leu	Leu	Leu	Ser	Ile	Ser	Ala	Thr	Asp	Gly	Tyr	Ile	Ser
65				70					75					80	
Pro	Ser	Trp	Tyr	Ala	Asp	Pro	Gln	Gly	Pro	Gln					
				85					90						

<210> 755

<211> 301

<212> DNA

<213> Homo sapiens

<400> 755

tgggatgcag ggtctttctt ctccaaggat ttcattcctg gagggagaaa agggccccag  
60  
ctgtctgccca tcaaaccggg ttgccgggct ggagctcctc ccaggcccgt gtgaggaaga  
120  
gcaaaggccg gcaggggctc gatgggacca gtcgctcgtc caggcccagg aaaaccacac  
180  
agctgggggc tgtcaggatt ggaccagggt caggccggcc aggcgatggc gggaaaagca  
240  
ggccactct gcagacctca atgtctcagg tgcactgcag ggcaacccc cctaccccgg  
300  
g  
301

<210> 756

<211> 99

<212> PRT

<213> Homo sapiens

<400> 756

Met	Gln	Gly	Leu	Ser	Ser	Pro	Arg	Ile	Ser	Phe	Leu	Glu	Gly	Glu	Lys
1				5					10					15	
Gly	Pro	Ser	Cys	Leu	Pro	Ser	Asn	Arg	Val	Ala	Gly	Leu	Glu	Leu	Leu
			20					25					30		
Pro	Gly	Pro	Cys	Glu	Glu	Glu	Gln	Arg	Pro	Ala	Gly	Ala	Arg	Trp	Asp
		35					40				45				
Gln	Ser	Leu	Ala	Gln	Ala	Gln	Glu	Asn	His	Thr	Ala	Gly	Gly	Cys	Gln

50                      55                      60  
 Asp Trp Thr Arg Val Arg Pro Ala Arg Arg Trp Arg Glu Lys Gln Ala  
 65                      70                      75                      80  
 His Ser Ala Asp Leu Asn Val Ser Gly Ala Leu Gln Gly Asn Pro Ala  
                     85                      90                      95  
 Tyr Pro Gly

<210> 757  
 <211> 311  
 <212> DNA  
 <213> Homo sapiens

<400> 757  
 actgaggcga tcgccagagg ggtgggctgt cgagggtgc tcaacatcca gttcgccctg  
 60  
 gtctccgatg ttctctacgt catcgaggcc aaccccaggg catcgcgcac agtccccctc  
 120  
 gtctcaaagg catccggcgt gcagctcgcc aaagcggcgg ccctcatcat gacaggggag  
 180  
 acgatgcct cgctcaggcg ctccggccac ctgcccaggg ccgacgccgc cgtcaccgat  
 240  
 cccgatgacc cgatcgccgt caaggaggcg gtcctaccct tcaaacgatt ccgcaccacc  
 300  
 gagggacgcg t  
 311

<210> 758  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 758  
 Thr Glu Ala Ile Ala Arg Gly Val Gly Val Arg Gly Leu Leu Asn Ile  
 1                      5                      10                      15  
 Gln Phe Ala Leu Val Ser Asp Val Leu Tyr Val Ile Glu Ala Asn Pro  
                     20                      25                      30  
 Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Ser Gly Val Gln  
                     35                      40                      45  
 Leu Ala Lys Ala Ala Ala Leu Ile Met Thr Gly Glu Thr Ile Ala Ser  
                     50                      55                      60  
 Leu Arg Arg Ser Gly His Leu Pro Glu Ala Asp Ala Ala Val Thr Asp  
 65                      70                      75                      80  
 Pro Asp Asp Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Lys Arg  
                     85                      90                      95  
 Phe Arg Thr Thr Glu Gly Arg  
                     100

<210> 759  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 759

gtgcacaccg gcaagctggt gtggaactgg gacagcggca acccggacga cactacgccg  
 60  
 attgccgagg gcaagaccta caccgcgaac tcgccgaaca tgtggtccat gttcgcgcgc  
 120  
 gacgaaaaac tcggcatgct ctacctgccg atgggcaacc agaccccgga ccagttcggg  
 180  
 ggctaccgca cgcctgcgct ggaactgcac gctgccggcc tgacagcgct ggatatcgac  
 240  
 actggtaaag tgcgctggca ctaccagttc acccaccatg acctgtggga catggacgtg  
 300  
 ggcggccagc cgagcctgat cgacatcaag accgccgccg gcgtgaaaca agccgtgatg  
 360  
 gcctcgacca agcaaggcag catctacgcg t  
 391

<210> 760  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 760  
 Val His Thr Gly Lys Leu Val Trp Asn Trp Asp Ser Gly Asn Pro Asp  
 1 5 10 15  
 Asp Thr Thr Pro Ile Ala Glu Gly Lys Thr Tyr Thr Arg Asn Ser Pro  
 20 25 30  
 Asn Met Trp Ser Met Phe Ala Val Asp Glu Lys Leu Gly Met Leu Tyr  
 35 40 45  
 Leu Pro Met Gly Asn Gln Thr Pro Asp Gln Phe Gly Gly Tyr Arg Thr  
 50 55 60  
 Pro Ala Ser Glu Leu His Ala Ala Gly Leu Thr Ala Leu Asp Ile Asp  
 65 70 75 80  
 Thr Gly Lys Val Arg Trp His Tyr Gln Phe Thr His His Asp Leu Trp  
 85 90 95  
 Asp Met Asp Val Gly Gly Gln Pro Ser Leu Ile Asp Ile Lys Thr Ala  
 100 105 110  
 Ala Gly Val Lys Gln Ala Val Met Ala Ser Thr Lys Gln Gly Ser Ile  
 115 120 125  
 Tyr Ala  
 130

<210> 761  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 761  
 cctaggtagg cccaaagggg cctaactttc ttgctgccct ggtggagcaa gaaatatctt  
 60  
 ctaggagagg ccaatccttc cctgccccac agtccttct ctgcaaagct cagggggcaa  
 120  
 tcaggtagct cctgccccag agggccccat ggttcctcgc ctaaggaagg cagggcgagg  
 180  
 cattgggagc cgttgacagc tgggctcagc tggggggagg ggtcagtttg ggagcaggtg  
 240



cagatttcag ggaggggggg gcctaaaggg aagtagggat cttggtaggc tgcaaaattt  
 300  
 tcctcccat ccccatcca caga  
 324

<210> 762  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 762  
 Met Gly Asp Gly Glu Glu Asn Phe Ala Ala Tyr Gln Asp Pro Tyr Phe  
 1 5 10 15  
 Pro Leu Gly Pro Pro Leu Pro Glu Ile Cys Thr Cys Ser Gln Thr Asp  
 20 25 30  
 Pro Ser Pro Gln Leu Ser Pro Ala Val Asn Gly Ser Gln Cys Pro Ala  
 35 40 45  
 Leu Pro Ser Leu Gly Glu Glu Pro Trp Gly Pro Leu Gly Gln Glu Val  
 50 55 60  
 Pro Asp Cys Pro Leu Ser Phe Ala Glu Lys Glu Leu Trp Gly Arg Glu  
 65 70 75 80  
 Gly Leu Ala Ser Pro Arg Arg Tyr Phe Leu Leu His Gln Gly Ser Lys  
 85 90 95  
 Lys Val Arg Pro Leu Trp Ala Tyr Leu  
 100 105

<210> 763  
 <211> 301  
 <212> DNA  
 <213> Homo sapiens

<400> 763  
 acgcgttatg ggcgccccgg atgggcgatg cgctatccca cacctcgatg atggcggaca  
 60  
 tcctcggcgg tgtgctggaa gtggcgccca atatcgcat tactcggggc ggcaccgctg  
 120  
 ccgcggtggc cgccaccggc tttaccgagg ccaccggcgg cctcggctgc ttctgctg  
 180  
 gcgctgcctt gggcaccatt gccggcctgg ccatgagcaa cattggcgcg gacacagggc  
 240  
 tgaccaagat atgcaatgcc tttaacaacg ccttatttgc gcccaccgtg catgcgaaca  
 300  
 t  
 301

<210> 764  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 764  
 Met Phe Ala Cys Thr Val Gly Ala Asn Lys Ala Leu Leu Lys Ala Leu  
 1 5 10 15  
 His Ile Leu Val Ser Pro Val Ser Ala Pro Met Leu Leu Met Ala Arg

```

      20      25      30
Pro Ala Met Val Pro Lys Ala Ala Pro Ser Arg Lys Gln Pro Arg Pro
      35      40      45
Pro Val Ala Ser Val Lys Pro Val Ala Ala Thr Ala Ala Val Ala
      50      55      60
Pro Ala Val Ile Ala Ile Leu Ala Ala Thr Ser Ser Thr Pro Pro Arg
65      70      75      80
Met Ser Ala Ile Ile Glu Val Trp Asp Ser Ala Ser Pro Ile Arg Ala
      85      90      95
Ala His Asn Ala
      100

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&lt;210&gt; 765

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 765

```

ngcacactcc agcctctgtt ctttctctcc ttgtgccttt gcccttacca cggttcctca
60
taacattggt gttcctgtat ttaaggccct ataaacaggg agatgcgcca cctcatcagt
120
agcctccaga atcacaatca ccagctgaaa ggggaggtcc tgagatataa gcggaaattg
180
agagaagccc agtctgacct gaacaagaca cgctgcgta gtggtagtgc cctcctgcag
240
tcccagtcta gtactgagga cccgaaggat gagcctgcgg agctaaaacc agattctggg
300
gacttatacct ccagtcctc agcttcaaag gcattctcagg aggatgccaa tgaaatcaag
360
tctaaacggg atgaagaaga acgagaacga gaaaggaggg agaaggagag ggaacgagaa
420
agagaacggg agaaggagaa ggagagagaa cgagagaagc agaagctaaa agagtcagaa
480
aaagagagag attctgctaa ggataaagag aaaggcaaac atgatgatgg acggaaaaag
540
gaagcagaaa ttatcaaaca attgaagatt gaactcaaga aggcacagga gagccaaaaa
600
gagatgaaac tattgctgga tatgtaccgt tctgccccaa aggaacagag agacaaagtt
660
cagctgatgg cagctgagaa gaagtctaag gcagagttgg aagatctaag gcaaagactc
720
aaggatctgg aagataaaga gaagaaagag aacaagaaaa tggctgatga ggatgccttg
780
aggaagatcc gggcagtgga ggagcagata gaatacctac agaagaagct a
831

```

&lt;210&gt; 766

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 766

Met Arg His Leu Ile Ser Ser Leu Gln Asn His Asn His Gln Leu Lys

1                    5                    10                    15  
 Gly Glu Val Leu Arg Tyr Lys Arg Lys Leu Arg Glu Ala Gln Ser Asp  
                   20                    25                    30  
 Leu Asn Lys Thr Arg Leu Arg Ser Gly Ser Ala Leu Leu Gln Ser Gln  
                   35                    40                    45  
 Ser Ser Thr Glu Asp Pro Lys Asp Glu Pro Ala Glu Leu Lys Pro Asp  
                   50                    55                    60  
 Ser Gly Asp Leu Ser Ser Gln Ser Ser Ala Ser Lys Ala Ser Gln Glu  
 65                    70                    75                    80  
 Asp Ala Asn Glu Ile Lys Ser Lys Arg Asp Glu Glu Glu Arg Glu Arg  
                   85                    90                    95  
 Glu Arg Arg Glu Lys Glu Arg Glu Arg Glu Arg Glu Arg Glu Lys Glu  
                   100                    105                    110  
 Lys Glu Arg Glu Arg Glu Lys Gln Lys Leu Lys Glu Ser Glu Lys Glu  
                   115                    120                    125  
 Arg Asp Ser Ala Lys Asp Lys Glu Lys Gly Lys His Asp Asp Gly Arg  
 130                    135                    140  
 Lys Lys Glu Ala Glu Ile Ile Lys Gln Leu Lys Ile Glu Leu Lys Lys  
 145                    150                    155                    160  
 Ala Gln Glu Ser Gln Lys Glu Met Lys Leu Leu Leu Asp Met Tyr Arg  
                   165                    170                    175  
 Ser Ala Pro Lys Glu Gln Arg Asp Lys Val Gln Leu Met Ala Ala Glu  
                   180                    185                    190  
 Lys Lys Ser Lys Ala Glu Leu Glu Asp Leu Arg Gln Arg Leu Lys Asp  
                   195                    200                    205  
 Leu Glu Asp Lys Glu Lys Lys Glu Asn Lys Lys Met Ala Asp Glu Asp  
 210                    215                    220  
 Ala Leu Arg Lys Ile Arg Ala Val Glu Glu Gln Ile Glu Tyr Leu Gln  
 225                    230                    235                    240  
 Lys Lys Leu

&lt;210&gt; 767

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 767

gctagctcgc tcgcactcat tctcgggagg cttccccgcg ccggccgcgt cccgcccgt  
 60  
 ccccgccacc agaagttcct ctgcgcgtcc gacggcgaca tgggcgtccc cacggccccg  
 120  
 gaggccggca gctggcgctg gggatccctg ctcttcgctc tcttctggtc tgcgtcccta  
 180  
 ggtcgggtgg cagccttcaa ggtcgccacg ccgtattccc tgtatgtctg tcccaggggg  
 240  
 cagaacgtca ccctcacctg caggtctctt ggccctgtgg acaaagggca cgatgtgacc  
 300  
 ttctacaaga cgtggtaccg cagctcgagg ggcgaggtgc agacctgctc agagcgccgg  
 360  
 cccatccgca acctcacgtt ccaggacctt cacctgcacc atggaggcca ccaggctgcc  
 420  
 aacaccagcc a  
 431

<210> 768  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 768  
 Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly Ser  
 1 5 10 15  
 Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala  
 20 25 30  
 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln  
 35 40 45  
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His  
 50 55 60  
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val  
 65 70 75 80  
 Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp  
 85 90 95  
 Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser  
 100 105 110

<210> 769  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<400> 769  
 tgtacacctc gtaatacatg atcgcgatac cgcccgcgat gaccctaagc aactcattct  
 60  
 cgacttcgaa ctccatcaag tgatttttgc ggtcgacgaa tctggtttcc gtatgaaaga  
 120  
 acggtatgtt ttgtatgtcg cgccctgcc actcaaacct caccgtgtca cccacctcaa  
 180  
 aaaaatcccg ggtcggccca caaataaatc aattgcgccg ctctccgag ttcttccatg  
 240  
 tcaacgatct cccctggctg ctcaagccaa ggccctcgcg gccgtgggac tccaagggtg  
 300  
 acgttgaccc gactgatttc ggaccagttg gcgtcggtat tgggggcagg gtagttaccg  
 360  
 cccatgtcga tgatctacat cgccaccggc agcgtgtctt cgtagtcgtc atgcctgatc  
 420  
 an  
 422

<210> 770  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 770  
 Met Phe Cys Met Ser Arg Pro Cys His Ser Asn Leu Thr Val Ser Pro  
 1 5 10 15  
 Thr Ser Lys Lys Ser Arg Val Gly Pro Gln Ile Asn Gln Leu Arg Arg

```

      20      25      30
Ser Ser Glu Phe Phe His Val Asn Asp Leu Pro Trp Leu Leu Lys Pro
      35      40      45
Arg Pro Ser Arg Pro Trp Asp Ser Lys Val Asp Val Asp Pro Thr Asp
      50      55      60
Phe Gly Pro Val Gly Val Gly Ile Gly Gly Arg Val Val Thr Ala His
      65      70      75      80
Val Asp Asp Leu His Arg His Arg Gln Arg Val Phe Val Val Val Met
      85      90      95
Pro Asp Xaa

```

<210> 771  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

```

<400> 771
gcctacgcgc aattcctcgc gggatatggcg tttaacaatg cgtctctcgg gtatgtgcat
60
gcaatggcgc atcagctggg cggtttttac gatctgccgc acggcgtgtg caatgcgata
120
ctgttgccac acgtgcagac gtttaactgc aaagtggcgg cctcgcgcct gcgtgattgc
180
gcccaggcca tgggtgtcga tgtcagtcaa atgacagcag aacagggcgc acaggcgtgt
240
atcgcagaga ttcgctctct ggcacgtcag gtgaatatcc cgggtgggatt gcgtgacctc
300
aacgtgaagg aagcggactt cccgattctg gcgaccaacg cgctaaaaga ccctgtgggt
360
ttgattaat
369

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<210> 772  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

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<400> 772
Ala Tyr Ala Gln Phe Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu
1      5      10      15
Gly Tyr Val His Ala Met Ala His Gln Leu Gly Gly Phe Tyr Asp Leu
      20      25      30
Pro His Gly Val Cys Asn Ala Ile Leu Leu Pro His Val Gln Thr Phe
      35      40      45
Asn Cys Lys Val Ala Ala Ser Arg Leu Arg Asp Cys Ala Gln Ala Met
      50      55      60
Gly Val Asp Val Ser Gln Met Thr Ala Glu Gln Gly Ala Gln Ala Cys
      65      70      75      80
Ile Ala Glu Ile Arg Ser Leu Ala Arg Gln Val Asn Ile Pro Val Gly
      85      90      95
Leu Arg Asp Leu Asn Val Lys Glu Ala Asp Phe Pro Ile Leu Ala Thr
      100     105     110
Asn Ala Leu Lys Asp Pro Val Gly Leu Ile Asn

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115

120

<210> 773  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<400> 773  
 ccgccgttgc cggcgttga ttttctggta ggcttgaatc agcgccctggc tgccgacatc  
 60  
 ggttacttga tccgcgttga gccgggcgta caaactccgg aattcacctt ggaaaacgcc  
 120  
 tccggttctt gccgggattc ggcgtggttg ctggtgcaac tgctgcgcaa cctgggcctg  
 180  
 gcggcgcgat ttgtgtctgg ctatctgata caactgaccg ccgacgtcaa agccctcgac  
 240  
 ggcccgtccg gcaccgaggt ggatttcacc gacctgcatg cctggtgcga agtgtatttg  
 300  
 cccggcgccc  
 309

<210> 774  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 774  
 Pro Pro Leu Pro Ala Val Asp Phe Leu Val Gly Leu Asn Gln Arg Leu  
 1 5 10 15  
 Ala Ala Asp Ile Gly Tyr Leu Ile Arg Val Glu Pro Gly Val Gln Thr  
 20 25 30  
 Pro Glu Phe Thr Leu Glu Asn Ala Ser Gly Ser Cys Arg Asp Ser Ala  
 35 40 45  
 Trp Leu Leu Val Gln Leu Leu Arg Asn Leu Gly Leu Ala Ala Arg Phe  
 50 55 60  
 Val Ser Gly Tyr Leu Ile Gln Leu Thr Ala Asp Val Lys Ala Leu Asp  
 65 70 75 80  
 Gly Pro Ser Gly Thr Glu Val Asp Phe Thr Asp Leu His Ala Trp Cys  
 85 90 95  
 Glu Val Tyr Leu Pro Gly Ala  
 100

<210> 775  
 <211> 4125  
 <212> DNA  
 <213> Homo sapiens

<400> 775  
 nncaggatgg gcgcgaacaa tggcaaacag tacggcagtg agggcaaagg cagctcgagc  
 60  
 atctcatctg acgtgagttc aagtacagat cacacgccc ctaaagccc gaagaatgtg  
 120  
 gctaccagcg aagactccga cctgagcatg cgcacactga gcacgcccag cccagccctg  
 180

atatgtccac cgaatctccc aggatttcag aatggaaggg gctcgtccac ctccctcgccc  
240  
tccatcaccg gggagacggt ggccatggtg cactccccgc ccccgaccgc cctcacacac  
300  
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&lt;210&gt; 776

&lt;211&gt; 483

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 776

Tyr	Gly	Ser	Glu	Gly	Lys	Gly	Ser	Ser	Ser	Ile	Ser	Ser	Asp	Val	Ser
1				5					10					15	
Ser	Ser	Thr	Asp	His	Thr	Pro	Thr	Lys	Ala	Gln	Lys	Asn	Val	Ala	Thr
			20					25					30		
Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro
		35					40					45			
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly
	50					55					60				
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val
65					70				75					80	
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala
			85					90					95		
Ser	Arg	Pro	Gln	Lys	Asp	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His
		100					105					110			
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg
	115					120					125				
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg
	130				135						140				
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg
145				150					155					160	
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val
			165				170							175	
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr

```

      180      185      190
Asp Arg Gly Leu Tyr Thr Ile Ala Gln Cys Cys Pro Glu Leu Arg Arg
      195      200      205
Leu Glu Val Ser Gly Cys Tyr Asn Ile Ser Asn Glu Ala Val Phe Asp
      210      215      220
Val Val Ser Leu Cys Pro Asn Leu Glu His Leu Asp Val Ser Gly Cys
      225      230      235      240
Ser Lys Val Thr Cys Ile Ser Leu Thr Arg Glu Ala Ser Ile Lys Leu
      245      250      255
Ser Pro Leu His Gly Lys Gln Ile Ser Ile Arg Tyr Leu Asp Met Thr
      260      265      270
Asp Cys Phe Val Leu Glu Asp Glu Gly Leu His Thr Ile Ala Ala His
      275      280      285
Cys Thr Gln Leu Thr His Leu Tyr Leu Arg Arg Cys Val Arg Leu Thr
      290      295      300
Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu
      305      310      315      320
Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu
      325      330      335
Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
      340      345      350
Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
      355      360      365
Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
      370      375      380
Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
      385      390      395      400
Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
      405      410      415
Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
      420      425      430
Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
      435      440      445
Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
      450      455      460
Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
      465      470      475      480
Ala Phe Phe

```

&lt;210&gt; 777

&lt;211&gt; 705

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 777

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caccaatctg ctctttaatg ccagactgat ggctctaaca atccttatta actccttttt
120
gtggcttcaa ggaaaaacaa aaacctcttc tctcattcac cacctctagg ccaggagaaa
180
ttatTTTTTgg ttcaggcttt cacagtgggg gtctgaaagt gaccagtcta gaaaaggatg
240

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actcagcaaa aggagagctc tgaagggtccc tgaggcggca cgggtccagca ttattaggtc  
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 420  
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 480  
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 aacactttct ttttcctttt ggcgttaaag tctgccttct ccgcgccgcc gtcccagtgg  
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 705

<210> 778  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 778  
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 Gly Gly Ala Glu Lys Ala Asp Phe Asn Ala Lys Arg Lys Lys Lys Val  
 20 25 30  
 Leu Glu Ile His Gln Ala Leu Asn Ser Asp Pro Thr Asp Val Ala Ala  
 35 40 45  
 Leu Arg Arg Met Ala Ile Ser Glu Gly Gly Leu Leu Thr Asp Glu Ile  
 50 55 60  
 Arg Arg Lys Val Trp Pro Lys Leu Leu Asn Val Asn Ala Asn Asp Pro  
 65 70 75 80  
 Pro Pro Ile Ser Gly Lys Asn Leu Arg Gln Met Ser Lys Asp Tyr Gln  
 85 90 95  
 Gln Val Leu Leu Asp Val Arg Arg Ser Leu Arg Arg Phe Pro Pro Gly  
 100 105 110  
 Glu Lys Leu Ser Arg Ser Cys His Ile Trp Glu Glu Arg Ile Cys Phe  
 115 120 125  
 Arg Ser Tyr His Val Thr  
 130

<210> 779  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

<400> 779  
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 120  
 cgccttgctt ttgaaggaac ccagtgggaa ggctagacca agtaaataatg aatcaccaaa  
 180

cgccagcaac ttcacgtca ggcattgtggc aactggcaaa gagggcactg atgatgagta  
 240  
 tgctaactca aactactact actcgatgtc tgccaatcga ctaggagacg aggaaacgga  
 300  
 ggaaatgata ggtttggtta cc  
 322

<210> 780

<211> 105

<212> PRT

<213> Homo sapiens

<400> 780

Met	Cys	Lys	Gln	Phe	Asn	Asp	Val	Val	Arg	Arg	His	Gly	Val	His	His
1				5					10					15	
Ser	Val	Thr	Val	Ser	Asp	Ser	Glu	Asp	Thr	Val	Ala	Pro	Ser	Gln	Leu
			20					25					30		
Val	Arg	Ser	Pro	Arg	Asn	Ala	Leu	Pro	Leu	Lys	Glu	Pro	Ser	Gly	Lys
			35				40					45			
Ala	Arg	Pro	Ser	Lys	Tyr	Glu	Ser	Pro	Asn	Ala	Ser	Asn	Phe	Ile	Val
			50				55					60			
Arg	His	Val	Ala	Thr	Gly	Lys	Glu	Gly	Thr	Asp	Asp	Glu	Tyr	Ala	Asn
65					70				75					80	
Ser	Asn	Tyr	Tyr	Tyr	Ser	Met	Ser	Ala	Asn	Arg	Leu	Gly	Asp	Glu	Glu
			85						90					95	
Thr	Glu	Glu	Met	Ile	Gly	Leu	Ala	Thr							
			100					105							

<210> 781

<211> 297

<212> DNA

<213> Homo sapiens

<400> 781

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 gtgtgtatgn gaatatgtgt gtgtatngaa atgtgtgtgt gtgtttggaa tgtgtgtatg  
 120  
 gaatgtgtgt ctgtgtatgg aatatgtgtg agtatngaa tgtgtgtgtg tgtttggaat  
 180  
 gtatcgaatg tgtgtctgtg tgtaaggaat gtgtgtgtat ggaatgtgtt tacgtgcatg  
 240  
 tgtctggaat gtgtgtgtat ggaatgtgtg tgtatgtgta tgngaattgt tgtgtgt  
 297

<210> 782

<211> 99

<212> PRT

<213> Homo sapiens

<400> 782

Xaa	Arg	Val	Pro	Gly	Met	Cys	Val	Cys	Val	Cys	Val	Cys	Met	Tyr	Val
1					5				10					15	
Cys	Met	Glu	Cys	Val	Cys	Met	Xaa	Ile	Cys	Val	Cys	Met	Xaa	Met	Cys

```

      20      25      30
Val Cys Val Trp Asn Val Cys Met Glu Cys Val Ser Val Tyr Gly Ile
      35      40      45
Cys Val Ser Met Xaa Met Cys Val Cys Val Trp Asn Val Ser Asn Val
      50      55      60
Cys Leu Cys Val Arg Asn Val Cys Val Trp Asn Val Phe Thr Cys Met
      65      70      75      80
Cys Leu Glu Cys Val Cys Met Glu Cys Val Cys Met Cys Met Xaa Met
      85      90      95
Cys Val Cys

```

<210> 783  
 <211> 612  
 <212> DNA  
 <213> Homo sapiens

```

<400> 783
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120
ttgttgagc acgtcgatga cgggcaactt caaggaaatc caggtgcgga cttgcgcggt
180
ccgcacaaaa atcggtctggg tgctgatcaa ctgcgggttg ccaatcgagc aatttgcgcg
240
gttcgatgac acgtgtcttc accgtgatat tcagcagccc cagtacgtcc accggcaact
300
cgacggccac cgcgctggct ttgttggaaca gctgcacaaa gccctgaatc aggttgaaca
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420
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480
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600
tggccgacgc gt
612

```

<210> 784  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

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<400> 784
Met Ser Ile Cys Val Pro Gly Thr Gly Ser Ser Glu Leu Pro Ser Ser
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Lys Pro Thr Thr Ser Val Thr Arg Pro Ile Thr Leu Leu Ser Thr Ser
20      25      30
Met Thr Gly Asn Phe Lys Glu Ile Gln Val Arg Thr Cys Ala Val Arg
35      40      45
Thr Lys Ile Gly Trp Val Ser Ile Asn Cys Gly Leu Pro Ile Ala Glu

```

```

      50              55              60
Phe Ala Arg Phe Asp Asp Thr Cys Leu His Arg Asp Ile Gln Gln Pro
65              70              75              80
Gln Tyr Val His Arg Gln Leu Asp Gly His Arg Ala Gly Phe Val Gly
      85              90              95
Gln Leu His Lys Ala Leu Asn Gln Val Glu Gln Leu Gln Val Asp Val
      100             105             110
Gln Gly Ala Leu Val Arg Ala Val Leu Tyr Ile Asp Gln Val Ala Gln
      115             120             125
Val Gln Asp Leu Arg Ala Trp Gly Asn Gln Leu Asp Cys Phe Glu Val
      130             135             140
Ile Asp His His Leu Asp Arg Ile Thr Ala Gln Leu Glu His Ile Asp
145             150             155             160
Gly Gly Leu Asp Gln Leu Ala Asp Gly Arg Val Gly Leu Glu Gln Leu
      165             170             175
Val Val Val Ala Gly Ala Asp Val Glu Ala Asp Gly Arg Arg
      180             185             190

```

&lt;210&gt; 785

&lt;211&gt; 408

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 785

```

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60
cttcaggccg cccacgctcg tggctgtgca gtactgctcg acgggggtgg caaccacgtc
120
tcgctgctgca accgcatcgt gcaggatgcg cagagtgtcg ggccagattc agacgccggc
180
cgtatgggttc gctgggtgtga ggggcgcctc gacgttttcg aggggtcatag tgacctggtc
240
gcactcaacc acgacaaccc cgcagtgcgg gaacatgtca cccggatcat gaactattgg
300
tgcggtcgcg gtgttgacgg ctggcggtcg gacgccgcta ttccgtcaat cctgagttct
360
gggctgcggg gctgcctccg gtgcgagaga agcgccctga cgtgagga
408

```

&lt;210&gt; 786

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 786

```

Thr Leu Asp Tyr Phe Thr Ile Asp Pro Arg Leu Gly Asp Asp Asp Asp
1      5      10      15
Phe Asp His Leu Leu Gln Ala Ala His Ala Arg Gly Leu Ser Val Leu
      20      25      30
Leu Asp Gly Val Val Asn His Val Ser Arg Arg Asn Arg Ile Val Gln
      35      40      45
Asp Ala Gln Ser Ala Gly Pro Asp Ser Asp Ala Gly Arg Met Val Arg
      50      55      60
Trp Cys Glu Gly Arg Leu Asp Val Phe Glu Gly His Ser Asp Leu Val

```

```

65           70           75           80
Ala Leu Asn His Asp Asn Pro Ala Val Arg Glu His Val Thr Arg Ile
           85           90           95
Met Asn Tyr Trp Cys Gly Arg Gly Val Asp Gly Trp Arg Leu Asp Ala
           100          105          110
Ala Ile Pro Ser Ile Leu Ser Ser Gly Leu Arg Cys Cys Leu Arg Cys
           115          120          125
Glu Arg Ser Ala Leu Thr
           130

```

<210> 787  
 <211> 310  
 <212> DNA  
 <213> Homo sapiens

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<400> 787
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120
ccttggtctc tcctcattgc tgccgtcact gtgtgctggg catgccctgc agttacccca
180
aagctttatg tcacaacatt gaggctggcg gagaaagacc ggcccccttca cccacctta
240
gacttcctgg aagggccgcc cgggtccaca acctggcccg ttaactccct gggcagctgc
300
tggggggagaa
310

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<210> 788  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

```

<400> 788
Met Met Leu Val Ala Asp Thr Val Gly Thr Thr Asp Asp Ala Thr Leu
1           5           10           15
Val Ser Ala Val Arg His Trp Pro Thr Trp Arg Pro Trp Ser Leu Leu
           20           25           30
Ile Ala Ala Val Thr Val Cys Trp Ala Cys Pro Ala Val Thr Pro Lys
           35           40           45
Leu Tyr Val Thr Thr Leu Arg Leu Ala Glu Lys Asp Arg Pro Leu His
           50           55           60
Pro Thr Leu Asp Phe Leu Glu Gly Pro Pro Gly Ser Thr Thr Trp Pro
65           70           75           80
Val Asn Ser Leu Gly Ser Cys Trp Gly Arg
           85           90

```

<210> 789  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

<400> 789

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 tctgccagac agcagcgctg ggacctctcc cctccccagc aggatgggccc ggctctggaa  
 120  
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 180  
 gcccttgctg gtttgcttgc ttgctttttt ctttttttgc ctgcacaga tatcgctagg  
 240  
 gcagagtatt gacatttcgt tttctttttg ttatgggtga taaagcacgg tgtttcttgt  
 300  
 gagtgatgc ctgtatttcc ctgcagagct gattgccagt ccattttctt ctatcccatc  
 360  
 cccattttc  
 369

<210> 790

<211> 114

<212> PRT

<213> Homo sapiens

<400> 790

Met	Asp	Trp	Gln	Ser	Ala	Leu	Gln	Gly	Asn	Thr	Gly	Ile	His	Ser	Gln
1				5				10					15		
Glu	Thr	Pro	Cys	Phe	Ile	Thr	His	Asn	Lys	Lys	Lys	Thr	Lys	Cys	Gln
		20						25					30		
Tyr	Ser	Ala	Leu	Ala	Ile	Ser	Val	Arg	Gly	Lys	Lys	Arg	Lys	Lys	Gln
		35					40					45			
Ala	Ser	Lys	Pro	Ala	Arg	Ala	Leu	Ala	Phe	Gly	Asn	Asn	Tyr	Leu	Thr
		50				55					60				
Ala	Ala	Cys	Leu	His	Phe	Gly	Thr	Pro	Arg	Ala	Ser	Arg	Ala	Gly	Pro
65					70				75					80	
Ser	Cys	Trp	Gly	Gly	Glu	Arg	Ser	Gln	Arg	Cys	Cys	Leu	Ala	Asp	Leu
			85					90					95		
Gly	Phe	Gly	Gly	His	Gln	Lys	Arg	Gly	Arg	Leu	Leu	Ala	Ala	Ala	Thr
			100					105					110		
Ser	Arg														

<210> 791

<211> 420

<212> DNA

<213> Homo sapiens

<400> 791

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 120  
 agaatcaaaa tggaagaggt gggtaatgtg tggttactgg aaatttctaa cattcaaaaa  
 180  
 ggagaagggg gagagtacat gtgtcatgct gtaaacaatca taggggaagc aaagagcttt  
 240  
 gcaaagttag acataatgcc ccaggaagaa agagtgggtg cactaccacc tccagtaaca  
 300



catcagcatg tcattggagtt tgatttggaa cacaccacat catcaagaac accttctcct  
 360  
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 420

<210> 792

<211> 138

<212> PRT

<213> Homo sapiens

<400> 792

Thr	Lys	Arg	Lys	Val	Tyr	Glu	Asn	Thr	Thr	Leu	Gly	Phe	Ile	Val	Glu
1				5					10					15	
Val	Glu	Gly	Leu	Pro	Val	Pro	Gly	Val	Lys	Trp	Tyr	Arg	Asn	Lys	Ser
			20					25					30		
Leu	Leu	Glu	Pro	Asp	Glu	Arg	Ile	Lys	Met	Glu	Arg	Val	Gly	Asn	Val
			35				40					45			
Cys	Ser	Leu	Glu	Ile	Ser	Asn	Ile	Gln	Lys	Gly	Glu	Gly	Gly	Glu	Tyr
	50					55					60				
Met	Cys	His	Ala	Val	Asn	Ile	Ile	Gly	Glu	Ala	Lys	Ser	Phe	Ala	Asn
	65				70				75					80	
Val	Asp	Ile	Met	Pro	Gln	Glu	Glu	Arg	Val	Val	Ala	Leu	Pro	Pro	Pro
				85					90					95	
Val	Thr	His	Gln	His	Val	Met	Glu	Phe	Asp	Leu	Glu	His	Thr	Thr	Ser
			100					105					110		
Ser	Arg	Thr	Pro	Ser	Pro	Gln	Glu	Ile	Val	Leu	Glu	Val	Glu	Leu	Ser
		115				120						125			
Glu	Lys	Asp	Val	Lys	Glu	Phe	Glu	Lys	Gln						
	130						135								

<210> 793

<211> 479

<212> DNA

<213> Homo sapiens

<400> 793

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 120  
 aagccaaagt ctacaggtca ctggggcaga ggccgcccga aaccagcttc ccctcccggc  
 180  
 ctaggcgcgc caggtccccg cccagccggg gcgatacttt ggtcggacag tgaggttggg  
 240  
 agcccaccgc acccaagtcc gccgcacca cccggcgagc gcgacccccg acgggcagcc  
 300  
 gctcaccttc tcctggcccc ggcttcagga aaactgcctg gaggtggccg gggttcccta  
 360  
 gcggaggctg ggcgggcggc ttgcgcctg cctcagtcct cccatccgtg gcccggggga  
 420  
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 479

<210> 794

<211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 794  
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 Glu Met Leu Arg Pro Arg Thr Val Leu Arg Glu Pro Lys Arg Ser Phe  
 20 25 30  
 Leu Thr Pro Asp Val Pro Glu Pro Lys Pro Lys Ser Thr Gly His Trp  
 35 40 45  
 Gly Arg Gly Arg Pro Lys Pro Ala Ser Pro Pro Gly Leu Gly Ala Pro  
 50 55 60  
 Gly Pro Arg Pro Ala Gly Ala Ile Leu Trp Ser Asp Ser Glu Val Gly  
 65 70 75 80  
 Ser Pro Pro His Pro Ser Pro Pro His Pro Pro Gly Ala Gly Asp Pro  
 85 90 95  
 Arg Arg Ala Ala Ala His Leu Leu Leu Ala Pro Ala Ser Gly Lys Leu  
 100 105 110  
 Pro Gly Gly Gly Arg Gly Ser Leu Ala Glu Ala Gly Arg Arg Ala Ser  
 115 120 125  
 Arg Leu Pro Gln Ser Pro His Pro Trp Pro Gly Gly Trp Ser Pro Leu  
 130 135 140  
 Arg Ala Glu Ala Ala Ala Gly Pro Ser Gln Val Pro Trp Asn Val  
 145 150 155

<210> 795  
 <211> 1418  
 <212> DNA  
 <213> Homo sapiens

<400> 795  
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 120  
 gtggcagga tccctggagca ctgcgtgatg taccctcatg actgcgtcaa gaccgggatg  
 180  
 cagagtctac agcctgaccc agctgcccgc tatcgcaatg tgttggaggc cctctggagg  
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 300  
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 420  
 acattacttc atgatgcagc catgaaccct gcggaaggct gatctgctga cttggggctc  
 480  
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 720  
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 780  
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 840  
 aacacccagg agtccttggc tttgaactca cacattacag gacatatcac aggcattggct  
 900  
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 960  
 gccagagtaa ttaccagat cccctccaca gccatcgcat ggtctgtgta tgagttcttc  
 1020  
 aaatacctaa tcactaaaag gcaagaagag tggagggctg gcaagtgaag tagcactgaa  
 1080  
 cgaagccagg gggtcagatg aactgtctgc atcctgggtca cattctctgt ctctggaat  
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 1200  
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 1320  
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 1380  
 agcctttaaa ttaaaaaaaaa aaaaaaaaaa aaaaaaaaa  
 1418

&lt;210&gt; 796

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 796

Met	Ala	Leu	Leu	Val	Val	Lys	Gln	Arg	Met	Gln	Met	Tyr	Asn	Ser	Pro
1				5					10					15	
Tyr	His	Arg	Val	Thr	Asp	Cys	Val	Arg	Ala	Val	Trp	Gln	Asn	Glu	Gly
			20					25					30		
Ala	Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr	Gln	Leu	Thr	Met	Asn	Val
		35					40					45			
Pro	Phe	Gln	Ala	Ile	His	Phe	Met	Thr	Tyr	Glu	Phe	Leu	Gln	Glu	His
	50					55				60					
Phe	Asn	Pro	Gln	Arg	Arg	Tyr	Asn	Pro	Ser	Ser	His	Val	Leu	Ser	Gly
65				70					75					80	
Ala	Cys	Ala	Gly	Ala	Val	Ala	Ala	Ala	Ala	Thr	Thr	Pro	Leu	Asp	Val
			85					90						95	
Cys	Lys	Thr	Leu	Leu	Asn	Thr	Gln	Glu	Ser	Leu	Ala	Leu	Asn	Ser	His
			100				105						110		
Ile	Thr	Gly	His	Ile	Thr	Gly	Met	Ala	Ser	Ala	Phe	Arg	Thr	Val	Tyr
		115				120					125				
Gln	Val	Gly	Gly	Val	Thr	Ala	Tyr	Phe	Arg	Gly	Val	Gln	Ala	Arg	Val
	130					135					140				
Ile	Tyr	Gln	Ile	Pro	Ser	Thr	Ala	Ile	Ala	Trp	Ser	Val	Tyr	Glu	Phe
145				150						155				160	
Phe	Lys	Tyr	Leu	Ile	Thr	Lys	Arg	Gln	Glu	Glu	Trp	Arg	Ala	Gly	Lys

165

170

175

&lt;210&gt; 797

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 797

```

aaattttaccg gcggcaaaac ccacgtcacc gactacacca acgcctcgcg caccatgctc
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ttcaacatcc acacgctgga gtgggatgcg aagatgctgg agattctcga cgtgccgcgc
120
gagatgctgc cggaagttaa gtcgtcttca gaaatctacg gccgcaccaa aagcggatc
180
gctatcgggcgc gcatcgcggg cgaccaacag gctgctctgt tcggccagat gtgcgtggaa
240
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300
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360
gtggcttatg cgctggaagg cgcggtgttc aacggtgggt cccccgtgca gtggctgcgt
420
gatgagctga agatcatcgc ggacgccacc gacaccgaat acttcgccgg caaggtcaag
480
gacagcaacg gcgtctacct ggtgccggcc ttaccggcc tgggcgctcc gtactgggac
540
ccgtatgccg gtggcgcttt gtttggcctg actcgtggcg tacgc
585

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&lt;210&gt; 798

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 798

```

Lys Phe Thr Gly Gly Lys Thr His Val Thr Asp Tyr Thr Asn Ala Ser
1           5           10           15
Arg Thr Met Leu Phe Asn Ile His Thr Leu Glu Trp Asp Ala Lys Met
20           25           30
Leu Glu Ile Leu Asp Val Pro Arg Glu Met Leu Pro Glu Val Lys Ser
35           40           45
Ser Ser Glu Ile Tyr Gly Arg Thr Lys Ser Gly Ile Ala Ile Gly Gly
50           55           60
Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Met Cys Val Glu
65           70           75           80
Ala Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Leu Leu Met
85           90           95
Asn Thr Gly Asp Lys Ala Val Lys Ser Lys His Gly Met Leu Thr Thr
100          105          110
Ile Ala Cys Gly Pro Arg Gly Glu Val Ala Tyr Ala Leu Glu Gly Ala
115          120          125
Val Phe Asn Gly Gly Ser Pro Val Gln Trp Leu Arg Asp Glu Leu Lys
130          135          140
Ile Ile Ala Asp Ala Thr Asp Thr Glu Tyr Phe Ala Gly Lys Val Lys

```

145		150		155		160									
Asp	Ser	Asn	Gly	Val	Tyr	Leu	Val	Pro	Ala	Phe	Thr	Gly	Leu	Gly	Ala
			165						170					175	
Pro	Tyr	Trp	Asp	Pro	Tyr	Ala	Arg	Gly	Ala	Leu	Phe	Gly	Leu	Thr	Arg
			180					185					190		
Gly	Val	Arg													
		195													

&lt;210&gt; 799

&lt;211&gt; 2152

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 799

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caagtgtccc agcagcatga ctgaacatca ctacttccc ctacttgatc tacaaggcca
120
acgccgagag cccagaccag gattccaaac aactgacag agaattattgt ggatccgctg
180
tcaggtaagt gtccgtcact gaccagacg ctgttacgtg gcacatgact gtacagtgcc
240
acgtaacagc actgtacttt tctcccataa acagttacct gccatgtatc tacatgattc
300
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360
ctttgatgtt gtaacgacaa catagcatca ctttacgaca gaatcatctg gaaaaacaga
420
acaacgaata catacatctt aaaaaatgct ggggtggggc aggcacagct caccgctgta
480
atcccagcac tttgggaggg tgaggcgggt ggatcacgta atcccagcac tttgaggggc
540
agaggtggac agatcatgag gtcaagagat caagaccatc ctggtcaaaa tggtgaaacc
600
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660
ctacttggga ggctgaggca ggagaatcgc ttgaaccag gagacacagg ctgcagtgc
720
tcgagatcac gccactgcac tccagcctgg cgacagagcg agactccatc tcaaaaaaaaa
780
aaaccaacaa aaaaactggg gtgaaaatct aacggataat tcagcattgc cgcatagaaa
840
cctccgcaaa accggccaaa caaacgcgga caggcggccc tggcgtcagc gcacgacagt
900
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960
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1080
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1140
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1200

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 1320  
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 1380  
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 1440  
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 1500  
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 1980  
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 2040  
 ggcgatgtc gggctgagtt ctgcgaggca gttgtcagca gccgccagtt cactgagcag  
 2100  
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 2152

&lt;210&gt; 800

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 800

Cys	Cys	Asn	Asp	Asn	Ile	Ala	Ser	Leu	Tyr	Asp	Arg	Ile	Ile	Trp	Lys
1				5					10					15	
Asn	Arg	Thr	Thr	Asn	Thr	Tyr	Ile	Leu	Lys	Asn	Ala	Gly	Val	Gly	Gln
		20						25					30		
Ala	Gln	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Glu	Ala	Glu	Ala	Gly
		35					40				45				
Gly	Ser	Arg	Asn	Pro	Ser	Thr	Leu	Arg	Gly	Arg	Gly	Gly	Gln	Ile	Met
	50					55				60					
Arg	Ser	Arg	Asp	Gln	Asp	His	Pro	Gly	Gln	Asn	Gly	Glu	Thr	Pro	Ser
65				70				75					80		
Leu	Leu	Lys	Ile	Gln	Lys	Leu	Ala	Glu	Leu	Ser	Gly	Thr	His	Leu	
				85				90					95		

&lt;210&gt; 801

&lt;211&gt; 424

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 801

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nntcatgaat cggtataaac acaatgggta gtgtatatca tatctatagg agatactatg
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120
gtaacatttc ctaccaataa aataacagcc ataattggac cgaatggatg tggtaagtct
180
accctactta gccatctata tcgacttcac tcaacaaaaa acaaaatcac attaaacgga
240
aaaccttttag agtcttataa aggtcgcgaa tttgctcaat tggtagcagt cttaacacaa
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420
atgn
424

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&lt;210&gt; 802

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 802

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Met Tyr Gln Ile Asn Gln Leu Ser Phe Ser Tyr Glu Thr Lys Glu Val
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Leu Lys Asn Ile Ser Val Thr Phe Pro Thr Asn Lys Ile Thr Ala Ile
20          25          30
Ile Gly Pro Asn Gly Cys Gly Lys Ser Thr Leu Leu Ser His Leu Tyr
35          40          45
Arg Leu His Ser Thr Lys Asn Lys Ile Thr Leu Asn Gly Lys Pro Leu
50          55          60
Glu Ser Tyr Lys Gly Arg Glu Phe Ala Gln Leu Val Ala Val Leu Thr
65          70          75          80
Gln Ser Arg Asp Ala Met Ile Asp Asp Phe Leu Val Lys Asp Ile Val
85          90          95
Leu Met Gly Arg Asp Pro Tyr Lys Gln His Phe Gly Thr Tyr Ser Ser
100         105         110
Glu Asp Val Lys Ile Ala Glu His Tyr Met
115         120

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&lt;210&gt; 803

&lt;211&gt; 6863

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 803

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120

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180  
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240  
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tactgcaagg gaaacaaggg caagcttggg gtcctcgttt ctgcctacat gcactacagc  
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cccatgctgc cagcctttga acctggcaca ggcttcagc ccttccttaa aatctaccag  
960  
tccatgcagc ttgtctacac atctggagtc tatcacattg caggccctgg tccccagcag  
1020  
ctttgcatca gcctggagcc agccctctc ctcaaaggcg atgtcatggt aacatgttat  
1080  
cacaagggtg gccggggcac agaccggacc ctcgtgttcc gagtccagtt ccacacctgc  
1140  
accatccacg gaccacagct cactttcccc aaggaccagc ttgacgaggc ctggactgat  
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1740



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<211> 1400

<212> PRT

<213> Homo sapiens

<400> 804

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863

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 Arg Phe His Thr Gln Arg Glu Asp Ser Pro Thr Gln Thr Leu Lys Arg  
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Gln Glu Arg Ser Asp Gly Leu Arg Gln Leu Gln Thr Leu Ile Thr Glu
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&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 809

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&lt;210&gt; 810

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 810

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Arg Arg Ser Val Pro Pro Leu Pro His Asp Pro Asp Gly Pro Glu Ile
      50      55      60
Pro Asp Asp Val Thr Thr Leu Ala Gln Gln Val Met Gly Leu Pro Arg
      65      70      75      80
His Leu Gly Ile His Ser Ala Gly Met Val Leu Thr Arg Glu Pro Val
      85      90      95
Gly Arg Ile Cys Pro Ile Glu Pro Ala Arg Met Phe Gly Arg Thr Gly
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 Pro Cys His Leu Val Phe Pro Val Ile Phe Asn Pro Ile Leu Cys Ala  
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 Val Thr Gly Ser Ser Ala Leu Tyr His Ser  
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 <211> 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 813

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480
gcgtcgacct gttcgccgaa ccgccggcg gcgcagaagg cgaggcggaa gaatttgagc
540
ttgttggcgg atacgcgt
558

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&lt;210&gt; 814

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 814

```

Met Thr Phe Ser Ala Gly Ser Leu Thr Ser Thr Gly Pro Pro Gly Trp
1          5          10          15
Ala Gly Lys Pro Trp Asn Lys Gly Ser Gly Gly Gly Ala Arg Gly Asp
20          25          30
Ala Phe Gly Pro Leu Ala Phe Gly Gln Arg Ala Ala Gln Phe Gly Val
35          40          45
Glu Asp Asp Pro Arg Pro Phe Asp Leu Asp His Asp Leu Gln Leu Pro
50          55          60
Ala Ile Val Phe Ala Ala Asp Ile Gln Arg Ala Ala Ala His Gln Arg
65          70          75          80
Leu Ala Gly Asp Gln Gly Glu Val Gln His His Leu Gln Arg Gly Leu
85          90          95
Gly Gln Arg Leu Arg Phe His Pro Pro Val Glu Leu Arg Ala Leu Ile
100         105         110
Val Gly Asn Gln Pro Leu Val Arg Gly Phe Arg Phe Ala Arg Val Asp
115         120         125
Leu Phe Ala Glu Pro Ala Gly Gly Ala Glu Gly Glu Ala Glu Glu Phe
130         135         140
Glu Leu Val Gly Gly Tyr Ala
145         150

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&lt;210&gt; 815

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 815

acgcgttgag actgtcaciaa ggctaggcta acttcatata gctatgccat cagatctgcc  
60  
caaagtggac gatgagaaaag ctcacgacgc gcctcacacg gatgggtcgg agcctggaca  
120  
agctagcgca ggagaaagcc gagacctcac gtccgaagcg gattcagcaa gtgcacaacc  
180  
ttctaccac gctgaggttt ccagtgaagt tactgctacg tccagtatag atgagcaggt  
240  
agacctcatt gctgcaccgt taagcgaaga gtccaatgtc agcaagctcg ggccgtcccc  
300  
tgaggccgat acatc  
315

&lt;210&gt; 816

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 816

Met	Pro	Ser	Asp	Leu	Pro	Lys	Val	Asp	Asp	Glu	Lys	Ala	His	Asp	Ala
1				5				10					15		
Pro	His	Thr	Asp	Gly	Ser	Glu	Pro	Gly	Gln	Ala	Ser	Ala	Gly	Glu	Ser
			20					25					30		
Arg	Asp	Leu	Thr	Ser	Glu	Ala	Asp	Ser	Ala	Ser	Ala	Gln	Pro	Ser	Thr
		35					40					45			
His	Ala	Glu	Val	Ser	Ser	Glu	Val	Thr	Ala	Thr	Ser	Ser	Ile	Asp	Glu
	50					55				60					
Gln	Val	Asp	Leu	Ile	Ala	Ala	Pro	Leu	Ser	Glu	Glu	Ser	Asn	Val	Ser
65				70						75				80	
Lys	Leu	Gly	Pro	Ser	Pro	Glu	Ala	Asp	Thr						
				85					90						

&lt;210&gt; 817

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 817

gaattcaaag agaaatatct gcctagacct tatgtgatta atctaattgga cgaactgacc  
60  
ctgaaaggaa tcacacaata ttatgctttt gttgaagagg ggcagaaggt tcattgcctg  
120  
aatacacttt tctcaaagct tcaaattaat caatccatta tattctgcaa ctctgttaat  
180  
agtgttgagc tgctggctaa aaaaataact gaactcgggtt attcatgctt ctacattcat  
240  
gctaagatgt tgcaagacca cagaaatcga gtattccatg attgtcgtaa tgggtgcttg  
300  
agaaaccttg tgtgcacaga t  
321

<210> 818  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 818  
 Glu Phe Lys Glu Lys Tyr Leu Pro Arg Pro Tyr Val Ile Asn Leu Met  
 1 5 10 15  
 Asp Glu Leu Thr Leu Lys Gly Ile Thr Gln Tyr Tyr Ala Phe Val Glu  
 20 25 30  
 Glu Gly Gln Lys Val His Cys Leu Asn Thr Leu Phe Ser Lys Leu Gln  
 35 40 45  
 Ile Asn Gln Ser Ile Ile Phe Cys Asn Ser Val Asn Ser Val Glu Leu  
 50 55 60  
 Leu Ala Lys Lys Ile Thr Glu Leu Gly Tyr Ser Cys Phe Tyr Ile His  
 65 70 75 80  
 Ala Lys Met Leu Gln Asp His Arg Asn Arg Val Phe His Asp Cys Arg  
 85 90 95  
 Asn Gly Ala Cys Arg Asn Leu Val Cys Thr Asp  
 100 105

<210> 819  
 <211> 3422  
 <212> DNA  
 <213> Homo sapiens

<400> 819  
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 120  
 gcagggggccc atggactctc caaaggcccc ctggagaagc ggccctatct tggccccggt  
 180  
 ctgccccctga ctccccgaga cagggccagt ggacacacaag gggccagtga ggacaactct  
 240  
 ggtggaggag gcaagaagcc aaagatggag gagctgggcc tggcctccca cccccggag  
 300  
 ggcaggccct gccagcccca gacaaggcca cagaaacagc caggccacac caactacagc  
 360  
 agctattcca agcggaagcg cctcactcgg ggccgggcca agaaccacac ctcttcaccc  
 420  
 tgtaaggggc gtgccaagcg acgacgacag cagcaggtgc tgcccctgga tcccgagag  
 480  
 cctgaaatcc gcctcaagta catttcctct tgcaagcggc tgaggtcaga cagccggacc  
 540  
 cccgccttct cacccttcgt gcgggtggag aagcgagacg cgttcaccac catatgcact  
 600  
 gttgtcaact cccttgaga tgcgccaag cccacagga agccttcctc ctctgectcc  
 660  
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 720  
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gggcctgtgg tttccaaggc cctgagtacc tcttgccctg tttgctgcct ctgccaaaac  
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900  
cccaaaaaga agccaaaact caaggagaag gtgcgccag aaggcacctg tgaggaggcc  
960  
tcgctgccgc ttgagagaac actcaaaggt cccgagtgtg cagctgccgc cactgccggg  
1020  
aagcccccca ggcctgacgg cccagctgac ccggccaagc agggccact ggcaccagt  
1080  
gcccggggcc tgtcccgag gctgcagagc tgctactgct gtgatggccg ggaggatggg  
1140  
ggcgaggagg cagccccagc cgacaagggt cgcaaacatg agtgacgaa ggaggctccg  
1200  
gcagagcccg gcggggaggc ccaggagcac tgggtgcatg aggcctgtgc cgtgtggacc  
1260  
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1320  
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1380  
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1440  
gagaactttt ctttgaaatg tcccaaact aagaggctgc cgtagtaatc caccacaacg  
1500  
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1560  
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1620  
tcccggatcg tggatccggc cgcctagggc tcagacttgc ggccccgggt tgggagga  
1680  
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1740  
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1800  
ctccggcgag ggtgggagac ggctttgtcc tggggacact ttcctctgg aatctcaaga  
1860  
cgacgtggca cacattccac gtgggtgctg ccgccacccc agtcggtcgt ggcgtgcagc  
1920  
tgggagccct gggcttgggg gtgggggtcg aaacagtact ggaagaggcg gaggcggt  
1980  
cctagctccg tggactaggc gggggagaaa ggaagcctt ctgagagcgg gctaggccgg  
2040  
cactggagag gccggagcct ttggaacaaa ccgtgcgaa cgcgtccagg ggccttccc  
2100  
cccagcctt gccagatctc tcgtgcggtt cgggcaaagc cggggtagac ctgggctatg  
2160  
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gtttgtcccc tttccagtcc tccacccac ccctggagcc cagcctggga gcgcaaaacc  
2280  
caagaagcgg ccagaacgca cctccggctc cggcgagcgc gcgaccgtt tgcaccacca  
2340  
gggaccgccg cgcctactct gcacgggagc agggacagcg ctagatttcg tgtacaaaac  
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ctgtgtaccc ctctatatat atgttacata gaatgtatat atgttgggaa catgctcgt  
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 2700  
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 2820  
 ttgcttcaca ctgaagattg tgtgtatcga gctgtttcta aaagatgttt attttcctta  
 2880  
 agagtaaaaa acagtcattg cattcagaaa aaaaaaaaaa aagtcaataa agatacaacg  
 2940  
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 3360  
 atccatcagc tgaagacaca aaaccagat tataaataat ttcattttta attctctgta  
 3420  
 ca  
 3422

&lt;210&gt; 820

&lt;211&gt; 494

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 820

Met	Asn	Ser	Lys	Lys	Leu	Ser	Ser	Thr	Asp	Cys	Phe	Lys	Thr	Glu	Ala
1				5					10					15	
Phe	Thr	Ser	Pro	Glu	Ala	Leu	Gln	Pro	Gly	Gly	Thr	Ala	Leu	Ala	Pro
			20					25					30		
Lys	Lys	Arg	Ser	Arg	Lys	Gly	Arg	Ala	Gly	Ala	His	Gly	Leu	Ser	Lys
		35				40					45				
Gly	Pro	Leu	Glu	Lys	Arg	Pro	Tyr	Leu	Gly	Pro	Ala	Leu	Pro	Leu	Thr
	50				55					60					
Pro	Arg	Asp	Arg	Ala	Ser	Gly	Thr	Gln	Gly	Ala	Ser	Glu	Asp	Asn	Ser
65				70					75					80	
Gly	Gly	Gly	Gly	Lys	Lys	Pro	Lys	Met	Glu	Glu	Leu	Gly	Leu	Ala	Ser

```

      85              90              95
His Pro Pro Glu Gly Arg Pro Cys Gln Pro Gln Thr Arg Ala Gln Lys
      100              105              110
Gln Pro Gly His Thr Asn Tyr Ser Ser Tyr Ser Lys Arg Lys Arg Leu
      115              120              125
Thr Arg Gly Arg Ala Lys Asn Thr Thr Ser Ser Pro Cys Lys Gly Arg
      130              135              140
Ala Lys Arg Arg Arg Gln Gln Gln Val Leu Pro Leu Asp Pro Ala Glu
      145              150              155              160
Pro Glu Ile Arg Leu Lys Tyr Ile Ser Ser Cys Lys Arg Leu Arg Ser
      165              170              175
Asp Ser Arg Thr Pro Ala Phe Ser Pro Phe Val Arg Val Glu Lys Arg
      180              185              190
Asp Ala Phe Thr Thr Ile Cys Thr Val Val Asn Ser Pro Gly Asp Ala
      195              200              205
Pro Lys Pro His Arg Lys Pro Ser Ser Ser Ala Ser Ser Ser Ser
      210              215              220
Ser Ser Ser Phe Ser Leu Asp Ala Ala Gly Ala Ser Leu Ala Thr Leu
      225              230              235              240
Pro Gly Gly Ser Ile Leu Gln Pro Arg Pro Ser Leu Pro Leu Ser Ser
      245              250              255
Thr Met His Leu Gly Pro Val Val Ser Lys Ala Leu Ser Thr Ser Cys
      260              265              270
Leu Val Cys Cys Leu Cys Gln Asn Pro Ala Asn Phe Lys Asp Leu Gly
      275              280              285
Asp Leu Cys Gly Pro Tyr Tyr Pro Glu His Cys Leu Pro Lys Lys Lys
      290              295              300
Pro Lys Leu Lys Glu Lys Val Arg Pro Glu Gly Thr Cys Glu Glu Ala
      305              310              315              320
Ser Leu Pro Leu Glu Arg Thr Leu Lys Gly Pro Glu Cys Ala Ala Ala
      325              330              335
Ala Thr Ala Gly Lys Pro Pro Arg Pro Asp Gly Pro Ala Asp Pro Ala
      340              345              350
Lys Gln Gly Pro Leu Arg Thr Ser Ala Arg Gly Leu Ser Arg Arg Leu
      355              360              365
Gln Ser Cys Tyr Cys Cys Asp Gly Arg Glu Asp Gly Gly Glu Glu Ala
      370              375              380
Ala Pro Ala Asp Lys Gly Arg Lys His Glu Cys Ser Lys Glu Ala Pro
      385              390              395              400
Ala Glu Pro Gly Gly Glu Ala Gln Glu His Trp Val His Glu Ala Cys
      405              410              415
Ala Val Trp Thr Gly Gly Val Tyr Leu Val Ala Gly Lys Leu Phe Gly
      420              425              430
Leu Gln Glu Ala Met Lys Val Ala Val Asp Met Met Cys Ser Ser Cys
      435              440              445
Gln Glu Ala Gly Ala Thr Ile Gly Cys Cys His Lys Gly Cys Leu His
      450              455              460
Thr Tyr His Tyr Pro Cys Ala Ser Asp Ala Gly Cys Ile Phe Ile Glu
      465              470              475              480
Glu Asn Phe Ser Leu Lys Cys Pro Lys His Lys Arg Leu Pro
      485              490

```

&lt;210&gt; 821

&lt;211&gt; 420



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 821

```

acgcgtcccg tcacctgcgg tatggaccaa gtgagttgtg tgctcgacaa tgggttcgcc
60
gccatcatgg atgtgccggg tttcaactat cgcgcccatc gttacaccga agcctatcgg
120
cgtttgccgc aaaatgtggt gctaggttcg gaaacgacct cgacggtgag cagccgtggg
180
gtctacaagt ttctgttgt gctgaagtcc gatgccatct atcccgacca tcagtcgtca
240
ggctacgaca cagagtattg ttcgtggtcg aacacccccg atgtcgattt cgcctcggc
300
gaagactatc cctggacgat ggggcagttt gtctggacgg gcttcgacta cctcggtgaa
360
ccttcgcctt acgacaccga tgctggccc tctcacgcct ccctcttcgg cattgtcgac
420

```

&lt;210&gt; 822

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 822

```

Met Asp Gln Val Ser Cys Val Leu Asp Asn Gly Phe Ala Ala Ile Met
 1          5          10          15
Asp Val Pro Gly Phe Asn Tyr Arg Ala His Arg Tyr Thr Glu Ala Tyr
 20          25          30
Arg Arg Leu Pro Gln Asn Val Val Leu Gly Ser Glu Thr Thr Ser Thr
 35          40          45
Val Ser Ser Arg Gly Val Tyr Lys Phe Pro Val Val Leu Lys Ser Asp
 50          55          60
Ala Ile Tyr Pro Asp His Gln Ser Ser Gly Tyr Asp Thr Glu Tyr Cys
 65          70          75          80
Ser Trp Ser Asn Thr Pro Asp Val Asp Phe Ala Leu Ala Glu Asp Tyr
 85          90          95
Pro Trp Thr Met Gly Gln Phe Val Trp Thr Gly Phe Asp Tyr Leu Gly
100          105          110
Glu Pro Ser Pro Tyr Asp Thr Asp Ala Trp Pro Ser His Ala Ser Leu
115          120          125
Phe Gly Ile Val Asp
130

```

&lt;210&gt; 823

&lt;211&gt; 550

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 823

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tctagattct tgggcagccg agcccccttt gaattcctca gcctaccatc atgatcaaca
60
cctcccatgt tccgtccatg aatgaccgca ctgacagcac tggagagatt taatgggtca
120

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ccaattgagg cagtgaaggc actcatggca ctcagagctg gaatggggct gatctgagtt  
 180  
 gtactgttga ctgcagtggg gatgacaacc tgcattcctt tgctggctgc atcgacaact  
 240  
 gctttgtaaa tggcatctac ggaagcatca cctgggccac ccacaacgag gccatccttc  
 300  
 acctgttgac caagagatgg gtcaatcctc ggttgcaact cacaagggtg atcttgaaaa  
 360  
 ggtggaagtg tagtgtttgg attctcagga agtgctgtga gcccaggctg agtgcttatt  
 420  
 cttttgttta ggagagctgc atcttcctgc attctcacct gaaagttctg aaacagacaa  
 480  
 gccatggggg tattgttagc tgggcaagga attgtggact gtccttgga cgcctggaga  
 540  
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<210> 824

<211> 161

<212> PRT

<213> Homo sapiens

<400> 824

Met	Ala	Cys	Leu	Phe	Gln	Asn	Phe	Gln	Val	Arg	Met	Gln	Glu	Asp	Ala
1				5					10					15	
Ala	Leu	Leu	Asn	Lys	Arg	Ile	Ser	Thr	Gln	Pro	Gly	Leu	Thr	Ala	Leu
			20					25					30		
Pro	Glu	Asn	Pro	Asn	Thr	Thr	Leu	Pro	Pro	Phe	Gln	Asp	Thr	Pro	Cys
		35					40					45			
Glu	Leu	Gln	Pro	Arg	Ile	Asp	Pro	Ser	Leu	Gly	Gln	Gln	Val	Lys	Asp
	50					55					60				
Gly	Leu	Val	Val	Gly	Gly	Pro	Gly	Asp	Ala	Ser	Val	Asp	Ala	Ile	Tyr
65					70				75					80	
Lys	Ala	Val	Val	Asp	Ala	Ala	Ser	Lys	Gly	Met	Gln	Val	Val	Ile	Thr
			85					90						95	
Thr	Ala	Val	Asn	Ser	Thr	Thr	Gln	Ile	Ser	Pro	Ile	Pro	Ala	Leu	Ser
		100					105					110			
Ala	Met	Ser	Ala	Phe	Thr	Ala	Ser	Ile	Gly	Asp	Pro	Leu	Asn	Leu	Ser
		115					120					125			
Ser	Ala	Val	Ser	Ala	Val	Ile	His	Gly	Arg	Asn	Met	Gly	Gly	Val	Asp
	130						135				140				
His	Asp	Gly	Arg	Leu	Arg	Asn	Ser	Arg	Gly	Ala	Arg	Leu	Pro	Lys	Asn
145					150					155				160	
Leu															

<210> 825

<211> 327

<212> DNA

<213> Homo sapiens

<400> 825

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 120  
 aaccgcgata tcctcacctc ttcgggtggcg gcgggtatcg cctccatcat cggtacgatt  
 180  
 gcgcagattc tttcgtttgg cgcgatgttc ggtggatcca accgcgatgg tgaacgttcc  
 240  
 aaccccctcg ccatgttcgt ggttgctatg ctggctccca ttgctactca ggtcatccag  
 300  
 atggctatta gccgcacccg tgaattc  
 327

<210> 826

<211> 109

<212> PRT

<213> Homo sapiens

<400> 826

Ala	Phe	Ala	Thr	Gly	Arg	Asn	Pro	Gln	Asn	Ala	Ala	Val	Cys	Cys	Thr
1				5					10				15		
Glu	Gly	Ile	Leu	Gln	Leu	Leu	Asp	Glu	Arg	Glu	Met	Arg	Gly	Val	Leu
			20				25					30			
Gly	His	Glu	Leu	Met	His	Val	Tyr	Asn	Arg	Asp	Ile	Leu	Thr	Ser	Ser
	35					40					45				
Val	Ala	Ala	Gly	Ile	Ala	Ser	Ile	Ile	Gly	Thr	Ile	Ala	Gln	Ile	Leu
	50				55					60					
Ser	Phe	Gly	Ala	Met	Phe	Gly	Gly	Ser	Asn	Arg	Asp	Gly	Glu	Arg	Ser
65				70				75				80			
Asn	Pro	Leu	Ala	Met	Phe	Val	Val	Ala	Met	Leu	Ala	Pro	Ile	Ala	Thr
			85					90				95			
Gln	Val	Ile	Gln	Met	Ala	Ile	Ser	Arg	Thr	Arg	Glu	Phe			
			100					105							

<210> 827

<211> 534

<212> DNA

<213> Homo sapiens

<400> 827

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 120  
 cccgacccat cgatcaccca cccgacggcc gttacgagga ttatcttgtg ctctggcaag  
 180  
 gcgcgggtggg agctgggtcaa gcaacgtaag gccgccagtc ttgacggaca gctcgccatc  
 240  
 atcccgatgg agcgtctcta cccgctacca gtcgacgagt tggtgaggt ttttgcgcct  
 300  
 tacaccaacg tcacggatgt ccgctgggtc caagaagagc cagagaacca gggcgccctg  
 360  
 tactacatgc tgaccacact gcccaggcc atgtcggaga agctgccagg attctttgat  
 420  
 gggttagtcg gcatcaccgg cccaccgtcc tcagctccgt cgggtgggaca gcacagcgtc  
 480

cacatccgtg aagagcagga gttactcgag aaggctatag cctgagcgac ctga  
534

<210> 828

<211> 174

<212> PRT

<213> Homo sapiens

<400> 828

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Ser Met Leu Arg Asn Lys Met Ala Thr Ser Asp Pro Glu Glu Phe Thr  
20 25 30  
Thr Gly Arg Trp Arg Pro Val Leu Pro Asp Pro Ser Ile Thr Asp Pro  
35 40 45  
Thr Ala Val Thr Arg Ile Ile Leu Cys Ser Gly Lys Ala Arg Trp Glu  
50 55 60  
Leu Val Lys Gln Arg Lys Ala Ala Ser Leu Asp Gly Gln Leu Ala Ile  
65 70 75 80  
Ile Pro Met Glu Arg Leu Tyr Pro Leu Pro Val Asp Glu Leu Ala Glu  
85 90 95  
Val Phe Ala Pro Tyr Thr Asn Val Thr Asp Val Arg Trp Val Gln Glu  
100 105 110  
Glu Pro Glu Asn Gln Gly Ala Trp Tyr Tyr Met Leu Thr His Leu Pro  
115 120 125  
Gln Ala Met Ser Glu Lys Leu Pro Gly Phe Phe Asp Gly Leu Val Gly  
130 135 140  
Ile Thr Arg Pro Pro Ser Ser Ala Pro Ser Val Gly Gln His Ser Val  
145 150 155 160  
His Ile Arg Glu Glu Gln Glu Leu Leu Glu Lys Ala Ile Ala  
165 170

<210> 829

<211> 492

<212> DNA

<213> Homo sapiens

<400> 829

nagtggccgg gtggccggcg ggtgccagcc gccatggagg ccgtgccccg catgccccatg  
60  
atctggctgg acctgaagga ggccggtgac ttccacttcc agccagctgt gaagaagttt  
120  
gtcctgaaga attatggaga gaaccagaa gcctacaatg aagaactgaa gaagctggag  
180  
ttgctcagac agaatgctgt ccgtgtccca cgagactttg agggctgtag tgtcctccgc  
240  
aagtacctcg gccagcttca ttacctgcag agtcgggtcc ccatggggctc gggccaggag  
300  
gccgctgtcc ctgtcacatg gacagagatc ttctcaggca agtctgtggc ccatgaggac  
360  
atcaagtacg agcaggcctg tattttctcc aacnttgag cgctgcactc catgctgggg  
420  
gccatggaca agcgggtgtc tgaggagggc atgaaggctc cctgtaccca tttccagtgc  
480

gcagccggcg cc  
492

<210> 830  
<211> 164  
<212> PRT  
<213> Homo sapiens

<400> 830  
Xaa Trp Pro Gly Gly Arg Arg Val Pro Ala Ala Met Glu Ala Val Pro  
1 5 10 15  
Arg Met Pro Met Ile Trp Leu Asp Leu Lys Glu Ala Gly Asp Phe His  
20 25 30  
Phe Gln Pro Ala Val Lys Lys Phe Val Leu Lys Asn Tyr Gly Glu Asn  
35 40 45  
Pro Glu Ala Tyr Asn Glu Glu Leu Lys Lys Leu Glu Leu Leu Arg Gln  
50 55 60  
Asn Ala Val Arg Val Pro Arg Asp Phe Glu Gly Cys Ser Val Leu Arg  
65 70 75 80  
Lys Tyr Leu Gly Gln Leu His Tyr Leu Gln Ser Arg Val Pro Met Gly  
85 90 95  
Ser Gly Gln Glu Ala Ala Val Pro Val Thr Trp Thr Glu Ile Phe Ser  
100 105 110  
Gly Lys Ser Val Ala His Glu Asp Ile Lys Tyr Glu Gln Ala Cys Ile  
115 120 125  
Phe Ser Asn Xaa Gly Ala Leu His Ser Met Leu Gly Ala Met Asp Lys  
130 135 140  
Arg Val Ser Glu Glu Gly Met Lys Val Ser Cys Thr His Phe Gln Cys  
145 150 155 160  
Ala Ala Gly Ala

<210> 831  
<211> 303  
<212> DNA  
<213> Homo sapiens

<400> 831  
gcgttgctgc ggcgtggcga gaccatgacg gcggagaatc agcgtgccaa tgtgcgcatc  
60  
gccgcaaacc acatcaagga ggttgcggtc gatcacgagg tcgttgtagc ccatggtaat  
120  
ggcccccagg taggtctgtt ggctctgcaa tcgacagcct acgaggaagt cggtatctat  
180  
ccgctggatg tcctgggagc agagtcacag gccatgatcg gctacatgat cgagcaggaa  
240  
ctcggaatg tgatgcctca ggatcagcag atcgtcacca tgatcacgat gacagtcgctc  
300  
gac  
303

<210> 832  
<211> 101  
<212> PRT

<213> Homo sapiens

<400> 832

```

Ala Leu Leu Arg Arg Gly Glu Thr Met Thr Ala Glu Asn Gln Arg Ala
 1           5           10           15
Asn Val Arg Ile Ala Ala Asn His Ile Lys Glu Val Ala Val Asp His
      20           25           30
Glu Val Val Val Ala His Gly Asn Gly Pro Gln Val Gly Leu Leu Ala
      35           40           45
Leu Gln Ser Thr Ala Tyr Glu Glu Val Gly Ile Tyr Pro Leu Asp Val
      50           55           60
Leu Gly Ala Glu Ser Gln Ala Met Ile Gly Tyr Met Ile Glu Gln Glu
      65           70           75           80
Leu Gly Asn Val Met Pro Gln Asp Gln Gln Ile Val Thr Met Ile Thr
      85           90           95
Met Thr Val Val Asp
      100

```

<210> 833

<211> 466

<212> DNA

<213> Homo sapiens

<400> 833

```

nngatccgcg cgatcgacga ggcgggtgcg tgatgttgac agcgaaaatg cgcagccggc
60
catttgacga gggctgaaaa cgtcttctac cggctctgctg tgccgcctgg tgtcagcaaa
120
cgacgccatg atcgctccagt gggatcgcg ttgttctgcg gcgctggggg attcagttgc
180
ggattccacc aggccgggtg gcatgttgcg gcggcggttg agcacgacgt gtcggcgctc
240
ctgacctatg tcatgaatct cgctcgcccc ggctcaaga ttcacatcga ccccgagcac
300
ccggagctgg gcccagacc accgcgaacc aagaagaaga gcggcgggcg agtgccgttc
360
gatgcgcgcatg tcggaactgg gtggatcgcc agcgagcccc cgcagcatcc cggctgcgaa
420
cacttctacg tgtacgacgt caagaacctc agcggcgagc ggatcc
466

```

<210> 834

<211> 142

<212> PRT

<213> Homo sapiens

<400> 834

```

Gln Arg Lys Cys Ala Ala Gly His Leu Thr Arg Ala Glu Asn Val Phe
 1           5           10           15
Tyr Arg Ser Ala Val Pro Pro Gly Val Ser Lys Arg Arg His Asp Arg
      20           25           30
Pro Val Gly Ile Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser Cys Gly
      35           40           45
Phe His Gln Ala Gly Trp His Val Ala Ala Ala Val Glu His Asp Val

```

50                      55                      60  
 Ser Ala Ser Leu Thr Tyr Val Met Asn Leu Ala Arg Pro Gly Val Lys  
 65                      70                      75                      80  
 Ile His Ile Asp Pro Glu His Pro Glu Leu Gly Pro Arg Pro Pro Arg  
                     85                      90                      95  
 Thr Lys Lys Lys Ser Gly Gly Ala Val Pro Phe Asp Ala His Val Gly  
                     100                      105                      110  
 Thr Gly Trp Ile Ala Ser Glu Pro Ala Asp Asp Pro Gly Cys Glu His  
                     115                      120                      125  
 Phe Tyr Val Tyr Asp Val Lys Asn Leu Ser Gly Glu Arg Ile  
                     130                      135                      140

<210> 835  
 <211> 482  
 <212> DNA  
 <213> Homo sapiens

<400> 835  
 acgcgtgaag ggattttgat caccagaac aaccacctgt ctttttagat caagaagcag  
 60  
 aagctcagag caaagaacat cacaccacgt ccctcagtga ttgaagcagt gattgagtca  
 120  
 cagaataaat ctggaactca ggtcttctga tctttgctcc agatggtaga gacaaaacta  
 180  
 aaagtaaat accaagtga atcaaagcat cagcattgag cccagaacat gaaaaagaac  
 240  
 ttcttgcccc acttgagaaa ctgttaaacc ggacatacct ttggggactt cttcccttct  
 300  
 ctggaataag attgatgttt ccatgctgtg aaagacgatg atgttccttc tcccagattc  
 360  
 ctgctgtctt caaaaggcct agcaaaaacc actgctgctg ggtgcagttg agaaagggaa  
 420  
 tgaagaacaa tcccatggcc atgcaggcac tctcccttc cacctctctg cctttcacgc  
 480  
 gt  
 482

<210> 836  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 836  
 Met Ala Met Gly Leu Phe Phe Ile Pro Phe Leu Asn Cys Thr Gln Gln  
 1                      5                      10                      15  
 Gln Trp Phe Leu Leu Gly Leu Leu Lys Thr Ala Gly Ile Trp Glu Lys  
                     20                      25                      30  
 Glu His His Arg Leu Ser Gln His Gly Asn Ile Asn Leu Ile Pro Glu  
                     35                      40                      45  
 Lys Gly Arg Ser Pro Gln Arg Tyr Val Arg Phe Asn Ser Phe Ser Ser  
                     50                      55                      60  
 Gly Pro Gly Ser Ser Phe Ser Cys Ser Gly Leu Asn Arg Asp Ala Leu  
 65                      70                      75                      80  
 Ile Ser Leu Gly Ile Leu Leu Leu Val Leu Ser Leu Thr Ser Gly Ala

WO 00/58473

85 90 95  
 Lys Ile Arg Arg Pro Glu Phe Gln Ile Tyr Ser Val Thr Gln Ser Leu  
 100 105 110  
 Leu Gln Ser Leu Arg Asp Val Val  
 115 120

<210> 837  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<400> 837  
 acgcgtggac ccccggttctg ccgcctttg cagtcacgc cctccctgaa gtcaccgctg  
 60  
 cagaaatacg caggcactga cctgggggta cagccaggca agggagagac gaggggctca  
 120  
 ctctgcacca gccaaaggcct gtgtcctggc atggctcccc caggaagcga ggatggcggg  
 180  
 gcctggcggg cgagcccctc ttatcctggg gaatgctggg gggcggttct gagcagacct  
 240  
 gcctgctgcc cctgctggct ggactgccc ctccccggg gaaagggttg gtggtcccc  
 300  
 caggggaact caaagcaggg gagcccctgg aggccccaag tccctggaat atcttgccgc  
 360  
 tcagatggcc cccctcgaac accctcacac gggggggccg cgcggtggga ggtgaccag  
 420  
 cagccactct tacttgccga agacttttct cccaatgcga gcgcgggttg taccagcctg  
 480  
 agccttcagg ttggtgaggc tgggggtacc  
 509

<210> 838  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 838  
 Met Ala Pro Pro Gly Ser Glu Asp Gly Gly Ala Trp Arg Ser Ser Pro  
 1 5 10 15  
 Ser Tyr Pro Gly Glu Cys Trp Gly Ala Phe Leu Ser Arg Pro Ala Cys  
 20 25 30  
 Cys Pro Cys Trp Leu Ala Leu Pro Leu Pro Arg Gly Lys Val Gly Trp  
 35 40 45  
 Ser Pro Gln Gly Asn Ser Lys Gln Gly Ser Pro Trp Arg Pro Gln Val  
 50 55 60  
 Pro Gly Ile Ser Trp Arg Ser Asp Gly Pro Pro Arg Thr Pro Ser His  
 65 70 75 80  
 Gly Gly Ala Ala Arg Trp Glu Val Thr Gln Gln Pro Leu Leu Leu Gly  
 85 90 95  
 Glu Asp Phe Ser Pro Asn Ala Ser Ala Gly Gly Ile Ser Leu Ser Leu  
 100 105 110  
 Gln Val Gly Glu Ala Gly Val  
 115



<210> 839  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens

<400> 839  
 acgcgtctcg tgttcgtgcg gcacggcagg acggcggttca atgtggaggg tcggctccag  
 60  
 ggccgtctcg acatgccgtt ggatgaggtg gggcgccgtc aggcactcac agtggctcaa  
 120  
 gtcacgcgag agatggaacc tgacgcgac atggcctctc cgctacaacg tgcgcgcgac  
 180  
 acagctcagg caatcggtgc ttgtgctgga ttgggcgtac agctggatga tcgactcatc  
 240  
 gagatcgatg tcggacgttg gtcggggacaa cgggctgcgg acctgcgtcg caacgatcct  
 300  
 gagtacgcag caagtgtggt cagccctatc gattaccggg tcggagn  
 347

<210> 840  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 840  
 Thr Arg Leu Val Phe Val Arg His Gly Arg Thr Ala Phe Asn Val Glu  
 1 5 10 15  
 Gly Arg Leu Gln Gly Arg Leu Asp Met Pro Leu Asp Glu Val Gly Arg  
 20 25 30  
 Arg Gln Ala Leu Thr Val Ala Gln Val Ile Ala Glu Met Glu Pro Asp  
 35 40 45  
 Ala Ile Met Ala Ser Pro Leu Gln Arg Ala Arg Asp Thr Ala Gln Ala  
 50 55 60  
 Ile Gly Ala Cys Ala Gly Leu Gly Val Gln Leu Asp Asp Arg Leu Ile  
 65 70 75 80  
 Glu Ile Asp Val Gly Arg Trp Ser Gly Gln Arg Ala Ala Asp Leu Arg  
 85 90 95  
 Arg Asn Asp Pro Glu Tyr Ala Ala Ser Val Val Ser Pro Ile Asp Tyr  
 100 105 110  
 Arg Val Gly  
 115

<210> 841  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 841  
 tccggaactc accccgacgc cgtcattatg gacgtcatga tgccgcgtct agatggcttg  
 60  
 gaagccaccc ggatgctgcg cagcaatggc aacgacgtcc cgatcctcgt cctcaccgcc  
 120  
 cgcgatgctg tcgacgatcg cggtgacggc ctgcacgctg gcgccgatga ctacatggtc  
 180

aagcccttcg cctcgcgca actcctcgct cgcctacgag cctcactcg tcgttcccg  
 240  
 cccgagccag agcaaaacga ggccctgaa caactctcct tcgctgacct cacccttgat  
 300  
 ccaggcaccg gcgagatcac ccgcgggaac cgtcgcatca gtttgacgag t  
 351

<210> 842

<211> 117

<212> PRT

<213> Homo sapiens

<400> 842

Ser	Gly	Thr	His	Pro	Asp	Ala	Val	Ile	Met	Asp	Val	Met	Met	Pro	Arg
1				5				10						15	
Leu	Asp	Gly	Leu	Glu	Ala	Thr	Arg	Met	Leu	Arg	Ser	Asn	Gly	Asn	Asp
	20						25						30		
Val	Pro	Ile	Leu	Val	Leu	Thr	Ala	Arg	Asp	Ala	Val	Asp	Asp	Arg	Val
	35						40					45			
Asp	Gly	Leu	Asp	Ala	Gly	Ala	Asp	Asp	Tyr	Met	Val	Lys	Pro	Phe	Ala
	50					55					60				
Leu	Asp	Glu	Leu	Leu	Ala	Arg	Leu	Arg	Ala	Leu	Thr	Arg	Arg	Ser	Arg
65					70				75					80	
Pro	Glu	Pro	Glu	Gln	Asn	Glu	Ala	Pro	Glu	Gln	Leu	Ser	Phe	Ala	Asp
				85				90					95		
Leu	Thr	Leu	Asp	Pro	Gly	Thr	Arg	Glu	Ile	Thr	Arg	Gly	Asn	Arg	Arg
			100					105					110		
Ile	Ser	Leu	Thr	Arg											
			115												

<210> 843

<211> 393

<212> DNA

<213> Homo sapiens

<400> 843

ctagcccagg ctctcgcca cgaggggctg cgcgctgtgg cctctggggc aaaccgggtc  
 60  
 ggccctcaagc gcggtatcga gaaggctgtc gacgccgttg tggaggagct ccgctctatc  
 120  
 tcgcgcgcca tcgacaccac ctcgacatg gccagcgttg ccaccatctc cagccgtgac  
 180  
 gagaccatcg gcgccctcat cgctgaggcc ttcgacaagg ttggttaagga cgggggttatc  
 240  
 accgtcgacg agtcgcagac cttcggcact gagcttgact tcaccgaggg catgcagttc  
 300  
 gacaagggtt acctgtcgcc ctacatggtc accgaccagg ttcgcatgga ggctgtgatc  
 360  
 gaggatcctt acatcctcat tcaactccgc aag  
 393

<210> 844

<211> 131

<212> PRT

<213> Homo sapiens

<400> 844

```

Leu Ala Gln Ala Leu Val His Glu Gly Leu Arg Ala Val Ala Ser Gly
 1           5           10           15
Ala Asn Pro Val Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Ala
          20           25           30
Val Val Glu Glu Leu Arg Ser Ile Ser Arg Ala Ile Asp Thr Thr Ser
          35           40           45
Asp Met Ala Ser Val Ala Thr Ile Ser Ser Arg Asp Glu Thr Ile Gly
          50           55           60
Ala Leu Ile Ala Glu Ala Phe Asp Lys Val Gly Lys Asp Gly Val Ile
65           70           75           80
Thr Val Asp Glu Ser Gln Thr Phe Gly Thr Glu Leu Asp Phe Thr Glu
          85           90           95
Gly Met Gln Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Met Val Thr Asp
          100          105          110
Gln Val Arg Met Glu Ala Val Ile Glu Asp Pro Tyr Ile Leu Ile His
          115          120          125
Ser Arg Lys
          130

```

<210> 845

<211> 505

<212> DNA

<213> Homo sapiens

<400> 845

```

gccacctgcc caaggctgga tgacgggcct agggcacatc taaggaacaa ggacaggaca
60
gaagcaaagc cacagctgct ggggcagggt gggggccggt atgtctggcc agcagcatca
120
cccctgcccc cggcggggct ccaggaccgg gagactcatc agccggaagc tcttgaggga
180
ggcggtgcc gtgaagacag gcaccttgc tcctgagagg ggcacccaga gaaccaagac
240
tcagcagagg gaacacaggg ctacgcccag gccccaggcc tgatatccag agtctaaatc
300
ccacctcagc ccagggggga gccttgagag gagctatgtc cctcatggac cccagtttcc
360
tctgcatacg ggctccgagc cctgcactgc ctccagggtg gttcccaagg tcttttccca
420
ttacctcta cgtgagcact cagtaaacca atacacatac acaagggtga cattaattcc
480
agccacagaa tcccaggcca cgcgt
505

```

<210> 846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 846

```

Met Gly Lys Asp Leu Gly Asn Tyr Pro Gly Gly Ser Ala Gly Leu Gly

```

```

      1             5             10             15
Ala Arg Met Gln Arg Lys Leu Gly Ser Met Arg Asp Ile Ala Pro Leu
      20             25             30
Lys Ala Pro Pro Trp Ala Glu Val Gly Phe Arg Leu Trp Ile Ser Gly
      35             40             45
Leu Gly Pro Gly Arg Ser Pro Val Phe Pro Leu Leu Ser Leu Gly Ser
      50             55             60
Leu Gly Ala Pro Leu Arg Ser Lys Gly Ala Cys Leu His Gly Ser Arg
      65             70             75             80
Leu Leu Gln Glu Leu Pro Ala Asp Glu Ser Pro Gly Pro Gly Ala Pro
      85             90             95
Pro Gly Ala Gly Val Met Leu Leu Ala Arg His Thr Gly Pro His Pro
      100            105            110
Ala Pro Ala Ala Val Ala Leu Leu Leu Ser Cys Pro Cys Ser Leu Asp
      115            120            125
Val Pro
      130

```

&lt;210&gt; 847

&lt;211&gt; 448

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 847

```

aagcttttaa aggagcaaga aaacatgaaa gagctagtag tcaaccttct ccgcatgact
60
caaatcaaaa ttgatgaaaa ggaacaaaag tccaaggatt tcctgaaagc tcagcaaaaa
120
tacaccaaca ttgttaaaga aatgaaagca aaggatcttg aaatcaggat acacaagaag
180
aaaaaatgtg aaatttatcg gagactgaga gagcttgcta aactgtatga caccattcga
240
aatgaaagaa acaaatttgt taacttactc cacaaagctc atcagaaagt aaatgaaata
300
aaagaaaggc ataaaatgtc attaaatgaa cttgaaattc tgagaaatag tgccgtagt
360
caagaaagaa agctacaaaa ttccatgctg aaacacgcca acaatgttac catcagagag
420
agcatgcaaa acgatgtgcg caaaattt
448

```

&lt;210&gt; 848

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 848

```

Lys Leu Leu Lys Glu Gln Glu Asn Met Lys Glu Leu Val Val Asn Leu
      1             5             10             15
Leu Arg Met Thr Gln Ile Lys Ile Asp Glu Lys Glu Gln Lys Ser Lys
      20             25             30
Asp Phe Leu Lys Ala Gln Gln Lys Tyr Thr Asn Ile Val Lys Glu Met
      35             40             45
Lys Ala Lys Asp Leu Glu Ile Arg Ile His Lys Lys Lys Lys Cys Glu

```

```

      50              55              60
Ile Tyr Arg Arg Leu Arg Glu Leu Ala Lys Leu Tyr Asp Thr Ile Arg
65              70              75              80
Asn Glu Arg Asn Lys Phe Val Asn Leu Leu His Lys Ala His Gln Lys
      85              90              95
Val Asn Glu Ile Lys Glu Arg His Lys Met Ser Leu Asn Glu Leu Glu
      100             105             110
Ile Leu Arg Asn Ser Ala Val Ser Gln Glu Arg Lys Leu Gln Asn Ser
      115             120             125
Met Leu Lys His Ala Asn Asn Val Thr Ile Arg Glu Ser Met Gln Asn
      130             135             140
Asp Val Arg Lys Ile
145

```

<210> 849  
 <211> 463  
 <212> DNA  
 <213> Homo sapiens

```

<400> 849
nnacgcgtga ttgttggggc caaggaatgc catgtggaga gtgcaggtga agtgataagt
60
cttttggaga tggggaatgc agccagacat acaggtacca ctcaaataaa tgagcactcc
120
agcagatcac atgcaatttt tacaatcagc atttgtcaag ttcataaaaa tatggaggca
180
gctgaagatg gatcatggta ttcccctcgg catattgtct caaagttcca ctttgtggat
240
ttggcaggat cagaaagagt aacaaaaacy gggaataactg gtgaacggtt caaagaatcc
300
attcaaataca atagtggatt gctggcttta ggaaatgtaa taagcgctct tggggaccca
360
cgaggaaga gttcacatat tccatatagg gatgctaaaa ttaccgggt tctgaaagat
420
tctctgggag gcagtgctaa gactgtcatg atcacatgtg tca
463

```

<210> 850  
 <211> 154  
 <212> PRT  
 <213> Homo sapiens

```

<400> 850
Xaa Arg Val Ile Val Gly Ala Lys Glu Cys His Val Glu Ser Ala Gly
1              5              10              15
Glu Val Ile Ser Leu Leu Glu Met Gly Asn Ala Ala Arg His Thr Gly
      20              25              30
Thr Thr Gln Met Asn Glu His Ser Ser Arg Ser His Ala Ile Phe Thr
      35              40              45
Ile Ser Ile Cys Gln Val His Lys Asn Met Glu Ala Ala Glu Asp Gly
      50              55              60
Ser Trp Tyr Ser Pro Arg His Ile Val Ser Lys Phe His Phe Val Asp
65              70              75              80
Leu Ala Gly Ser Glu Arg Val Thr Lys Thr Gly Asn Thr Gly Glu Arg

```

```

      85          90          95
Phe Lys Glu Ser Ile Gln Ile Asn Ser Gly Leu Leu Ala Leu Gly Asn
      100      105      110
Val Ile Ser Ala Leu Gly Asp Pro Arg Arg Lys Ser Ser His Ile Pro
      115      120      125
Tyr Arg Asp Ala Lys Ile Thr Arg Leu Leu Lys Asp Ser Leu Gly Gly
      130      135      140
Ser Ala Lys Thr Val Met Ile Thr Cys Val
145          150

```

<210> 851  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

```

<400> 851
aaatttcctg tttctgatcg acgaaataaa gtttagcgtg atgagtgagc tgcttatgca
60
gttcctccat tcgcttataa acagttttat ttctcatttc gaaaactctc gatgcagaat
120
aaaggctaga gtctggggac caagtcccca gctccgttta cgcgacttcc ttgacctgtg
180
ttgttatgct gataagggtta ttcagcttga cgatttggtc gtggtctttc aaccgttttg
240
cagctgggtcg acgatattcc tggtaggaac tacgatagaa gaccagcatc ggaagaactt
300
tgtagatgct gaacaaacac ccaccgatca cttcagcctc gaagtaaggg ttatactgct
360
taacccacgc gt
372

```

<210> 852  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

```

<400> 852
Met Ser Glu Leu Leu Met Gln Phe Leu His Ser Leu Ile Asn Ser Phe
1      5      10      15
Ile Ser His Phe Glu Asn Ser Arg Cys Arg Ile Lys Ala Arg Val Trp
      20      25      30
Gly Pro Ser Pro Gln Leu Arg Leu Arg Asp Phe Leu Asp Leu Val Cys
      35      40      45
Tyr Ala Asp Lys Val Ile Gln Leu Asp Asp Leu Phe Val Val Phe Gln
      50      55      60
Pro Phe Cys Ser Trp Ser Thr Ile Phe Leu Val Gly Thr Thr Ile Glu
65      70      75      80
Asp Gln His Arg Lys Asn Phe Val Asp Ala Glu Gln Thr Pro Thr Asp
      85      90      95
His Phe Ser Leu Glu Val Arg Val Ile Leu Ser Asn Pro Arg
      100      105      110

```

<210> 853  
 <211> 423

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 853

acgcgttcag aaacttatgg tgaaatggcc gaactagaaa acctagtcga cgaatattac  
 60  
 caagctatgg gcatggatgt gcgtcgagaa acctggctgc gcgagcagat actcaagaaa  
 120  
 gtccaagaaa cgcatttggt agaagagctt gcaggcatag aatcaggtga tgatggcgca  
 180  
 gtgggtggaag agagcgtatt agaaggcctc gatacctatt tatgtgagat aaaagaagca  
 240  
 cagattcgtc atggattgca tcgtcttgga gaattaccag aagacgataa attggccgat  
 300  
 accttggctc ccttattgcg tttaccccggt ggcagtgaca ttaccagcaa gggaattttg  
 360  
 catgccttaa tggcagattt agagttagaa caagacgatt ttgaccaat gcaaagcacg  
 420  
 cgt  
 423

&lt;210&gt; 854

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 854

Thr	Arg	Ser	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Glu	Leu	Glu	Asn	Leu	Val
1				5					10					15	
Asp	Glu	Tyr	Tyr	Gln	Ala	Met	Gly	Met	Asp	Val	Arg	Arg	Glu	Thr	Trp
		20					25						30		
Leu	Arg	Glu	Gln	Ile	Leu	Lys	Lys	Val	Gln	Glu	Thr	His	Leu	Leu	Glu
	35					40						45			
Glu	Leu	Ala	Gly	Ile	Glu	Ser	Gly	Asp	Asp	Gly	Ala	Val	Val	Glu	Glu
	50					55				60					
Ser	Val	Leu	Glu	Gly	Leu	Asp	Thr	Tyr	Leu	Cys	Glu	Ile	Lys	Glu	Ala
65				70						75				80	
Gln	Ile	Arg	His	Gly	Leu	His	Arg	Leu	Gly	Glu	Leu	Pro	Glu	Asp	Asp
			85					90					95		
Lys	Leu	Ala	Asp	Thr	Leu	Val	Ala	Leu	Leu	Arg	Leu	Pro	Arg	Gly	Ser
		100					105					110			
Asp	Ile	Thr	Ser	Lys	Gly	Ile	Leu	His	Ala	Leu	Met	Ala	Asp	Leu	Glu
		115					120					125			
Leu	Glu	Gln	Asp	Asp	Phe	Asp	Pro	Met	Gln	Ser	Thr	Arg			
	130					135						140			

&lt;210&gt; 855

&lt;211&gt; 338

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 855

acgcgtgaag ggggagctca aagtagatgg acctctgact agatggagct ctgagtaaga  
 60

tgaatgtctg tgcggatgtt gctcacagca agatagtgtt tggagcgatt ggcacttcga  
 120  
 acaagatgga gcatggagca gatggagctc tgagcaagat ggagcgtgga gtagatagag  
 180  
 cttggagcaa gaaggagctc caagcaagat ggagcttgca gcaggtgctt ctcaagtgtaa  
 240  
 gatggagctc agagaagatg atgctcagag taagattgag ctcggtgatt ggcactccaa  
 300  
 acattgtctt gagcccattg gagnctctga gcagaaag  
 338

<210> 856

<211> 93

<212> PRT

<213> Homo sapiens

<400> 856

Met	Asn	Val	Cys	Ala	Asp	Val	Ala	His	Ser	Lys	Ile	Val	Leu	Gly	Ala
1				5					10				15		
Ile	Gly	Thr	Ser	Asn	Lys	Met	Glu	His	Gly	Ala	Asp	Gly	Ala	Leu	Ser
			20					25				30			
Lys	Met	Glu	Arg	Gly	Val	Asp	Arg	Ala	Trp	Ser	Lys	Lys	Glu	Leu	Gln
		35				40				45					
Ala	Arg	Trp	Ser	Leu	Gln	Gln	Val	Leu	Leu	Ser	Val	Arg	Trp	Ser	Ser
	50				55				60						
Glu	Lys	Met	Met	Leu	Arg	Val	Arg	Leu	Ser	Ser	Val	Ile	Gly	Thr	Pro
65				70					75				80		
Asn	Ile	Ala	Leu	Ser	Pro	Leu	Glu	Xaa	Leu	Ser	Arg	Lys			
			85						90						

<210> 857

<211> 435

<212> DNA

<213> Homo sapiens

<400> 857

ccggacagtg ggccaccagt gtttgccccc agcaatcatg tcagtgaagc ccaacctcgg  
 60  
 gagacacccc ggcccctcat gcctcctacc aagcctttcc tagcacctga gaccaccagc  
 120  
 cctggtgaca ggggtggagac ccctgtgggg gagagagccc caaccctgt ctcagcaagc  
 180  
 tctgaggtct cccctgagag ccaagaggac tcagagaccc cagcagagga ggacagtggc  
 240  
 tctgagcagc ctcccaacag cgtcctgcct gacaaactga aggtgagctg ggagaacccc  
 300  
 agccccaggg agggccctgc tgcagagagt gcagaaccgt cccaggcacc ctgttctgag  
 360  
 acttctgagg ctgccccag ggagggtggg aagcccccta caccaccacc caagatctta  
 420  
 tcagagaaac tgaaa  
 435

<210> 858



<211> 145  
 <212> PRT  
 <213> Homo sapiens

<400> 858  
 Pro Asp Ser Gly Pro Pro Val Phe Ala Pro Ser Asn His Val Ser Glu  
 1 5 10 15  
 Ala Gln Pro Arg Glu Thr Pro Arg Pro Leu Met Pro Pro Thr Lys Pro  
 20 25 30  
 Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly Asp Arg Val Glu Thr Pro  
 35 40 45  
 Val Gly Glu Arg Ala Pro Thr Pro Val Ser Ala Ser Ser Glu Val Ser  
 50 55 60  
 Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro Ala Glu Glu Asp Ser Gly  
 65 70 75 80  
 Ser Glu Gln Pro Pro Asn Ser Val Leu Pro Asp Lys Leu Lys Val Ser  
 85 90 95  
 Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro Ala Ala Glu Ser Ala Glu  
 100 105 110  
 Pro Ser Gln Ala Pro Cys Ser Glu Thr Ser Glu Ala Ala Pro Arg Glu  
 115 120 125  
 Gly Gly Lys Pro Pro Thr Pro Pro Pro Lys Ile Leu Ser Glu Lys Leu  
 130 135 140  
 Lys  
 145

<210> 859  
 <211> 561  
 <212> DNA  
 <213> Homo sapiens

<400> 859  
 nacgcgtgggt gtggtaatcc ggtttctgggt ggcgacggct gccacccctc gtggcaagac  
 60  
 atgccgttgc gtgccgatat gccatacgaa gcttggccta gtgcgaaaag ctgctggaa  
 120  
 ccctcgaaga ggcagggtcg gcaggttacc gtggtcgggtg tacgcctcgt ttcgacgatg  
 180  
 aaccccatc tgggagcaga tatgacgacg taccagtacc tcattgtcgg tggcgggatg  
 240  
 gccgctgatt ctgccgcccg cggatatcgc gacatcgaca agaaagggtc gatcgccatc  
 300  
 ctcagcgctg acgtcgacgc cccgtatcct cggccagcgc tgagcaagaa gctgtggact  
 360  
 gaccctgagt tcacctggga ccaggctcgc cttgctactg tcgctgacac cggcgcgga  
 420  
 ttgcggctcg gcaactgaggt gctcagcatt gaccgtgacg gcaagaccgt cctgaccgt  
 480  
 tccggccagg tattcggcta ccagaagttg ctgctcgta cggccttac cccgtcgcgc  
 540  
 attgacgacg acggcgatgc c  
 561

<210> 860

<211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 860  
 Xaa Ala Trp Cys Gly Asn Pro Val Ser Gly Gly Asp Gly Cys His Pro  
 1 5 10 15  
 Ser Trp Gln Asp Met Pro Leu Arg Ala Asp Met Pro Tyr Glu Ala Trp  
 20 25 30  
 Pro Ser Ala Lys Ser Ser Leu Glu Pro Ser Lys Arg Gln Gly Arg Gln  
 35 40 45  
 Val Thr Val Val Gly Val Arg Ile Val Ser Thr Met Asn Pro Ile Leu  
 50 55 60  
 Gly Ala Asp Met Thr Thr Tyr Gln Tyr Leu Ile Val Gly Gly Gly Met  
 65 70 75 80  
 Ala Ala Asp Ser Ala Ala Arg Gly Ile Arg Asp Ile Asp Lys Lys Gly  
 85 90 95  
 Ser Ile Ala Ile Leu Ser Ala Asp Val Asp Ala Pro Tyr Pro Arg Pro  
 100 105 110  
 Ala Leu Ser Lys Lys Leu Trp Thr Asp Pro Glu Phe Thr Trp Asp Gln  
 115 120 125  
 Val Asp Leu Ala Thr Val Ala Asp Thr Gly Ala Glu Leu Arg Leu Gly  
 130 135 140  
 Thr Glu Val Leu Ser Ile Asp Arg Asp Gly Lys Thr Val Leu Thr Ala  
 145 150 155 160  
 Ser Gly Gln Val Phe Gly Tyr Gln Lys Leu Leu Leu Val Thr Gly Leu  
 165 170 175  
 Thr Pro Ser Arg Ile Asp Asp Asp Gly Asp Ala  
 180 185

<210> 861  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

<400> 861  
 ccattgggttt ctatgctctg aggtttcatc tgtggggaac agtattgact tacttacaaa  
 60  
 gagataatgg tcatacccta tggctactca ccatagtctg gcggtacatg gacttctcag  
 120  
 cccagtaag atctgtatcc acaggacact taaagtcacc ttacagaggg ctatccag  
 180  
 gcctgaggcc tattagaggc gtctcttttc agccatcagt gttagaggcc atctgcatgg  
 240  
 gatcccagag cctgcctcgg gaatggcaga agctggctgg tgcttgccgt gggctttg  
 300  
 tgtttctactg ctttcaggga ggcctgccac aggggagaaa ctgggggggg ga  
 352

<210> 862  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 862

```

Met Gly Phe Tyr Ala Leu Arg Phe His Leu Trp Gly Thr Val Leu Thr
 1           5           10           15
Tyr Leu Gln Arg Asp Asn Gly His Thr Leu Trp Ser Leu Thr Ile Val
          20           25           30
Trp Arg Tyr Met Asp Phe Ser Ala Pro Val Arg Ser Val Ser Thr Gly
          35           40           45
His Leu Lys Ser Pro Tyr Arg Gly Leu Ser Gln Cys Leu Arg Pro Ile
          50           55           60
Arg Gly Val Ser Phe Gln Pro Ser Val Leu Glu Ala Ile Cys Met Gly
65           70           75           80
Ser Gln Ser Leu Pro Arg Glu Trp Gln Lys Leu Ala Gly Ala Trp Arg
          85           90           95
Gly Leu Cys Leu Phe His Cys Phe Gln Gly Gly Leu Pro Gln Gly Arg
          100          105          110
Asn Trp Gly Gly
          115

```

&lt;210&gt; 863

&lt;211&gt; 327

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 863

```

tccggatcga cccggacgaa ttccacggtc cagccattga ctccaaatg ctctttgaca
60
tacgccgtga catgttcaat gtccaactta cgcattgtcca cccgctcacc ggtctcattg
120
agtttgagct gcgagtagac gttgcggtag ttctcgttga ccgactgttc atacgagatg
180
tgcagaagca tcggtttgcg gccatcctcg gacggcattg gcttggttga catggccgct
240
tggcggaaca tggtcagggt aaagcccgac ttgaagttgt gcgacagggc agaaacacac
300
agcatttctg accggcgatg acccatn
327

```

&lt;210&gt; 864

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 864

```

Met Gly His Arg Arg Ser Glu Met Leu Cys Val Ser Ala Leu Ser His
 1           5           10           15
Asn Phe Lys Ser Gly Phe Thr Leu Asn Met Phe Arg Gln Ala Ala Met
          20           25           30
Tyr Asn Lys Pro Met Pro Ser Glu Asp Gly Arg Lys Pro Met Leu Leu
          35           40           45
His Ile Ser Tyr Glu Gln Ser Val Asn Glu Asn Tyr Arg Asn Val Tyr
          50           55           60
Ser Gln Leu Lys Leu Asn Glu Thr Gly Glu Arg Val Asp Met Arg Lys
65           70           75           80
Leu Asp Ile Glu His Val Thr Ala Tyr Val Lys Glu His Leu Glu Val

```

85 90 95  
 Asn Gly Trp Thr Val Glu Phe Val Arg Val Asp Pro  
 100 105

<210> 865  
 <211> 729  
 <212> DNA  
 <213> Homo sapiens

<400> 865  
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 60  
 agctctcggt ctggtctctg agcatgccca cggcgctctg cacacagctt ctcagcagcc  
 120  
 tgggtggtgtc caggatcgac acatcactgc ctccgagttc agaggtttcc tttccaccc  
 180  
 tctcagaact ttctgtttcc atggcctcct ctgccacctc tgccacctcc cctgatgtgc  
 240  
 tggcctccgt ctccatcgcc tctcatggc cgtcttcgc cgggtgttcc aagcccagct  
 300  
 caggcaagtc tccgggcgcg aacagctggc tgatggtgac atgctgcagc ctggtcacat  
 360  
 cagaaacccat gaggggtgat ctccggaggt catcgatgtg gacagactgc cacagccctc  
 420  
 cgtggaagcc cacataggct gttcctcttc ccacccggga cagttttgtg atgaaataga  
 480  
 cgaagatacg gtctcattt tctcgattt tgttgattt atttataaca gaatacttag  
 540  
 ctgaggcaat gagctgggcg ctacggattc catcttcaaa atctgtctga aaaatgagga  
 600  
 ttttacattt ggctgtattc gttaaacagt ttcggacttc tttgaggaat gagtactcgg  
 660  
 tgtcaaactg ctgcagccac aggagtgtgg gtttcggagc cctgcctgtg acctctgatt  
 720  
 ctaaaattt  
 729

<210> 866  
 <211> 83  
 <212> PRT  
 <213> Homo sapiens

<400> 866  
 Ala Cys Pro Arg Arg Ser Ala His Ser Phe Ser Ala Ala Trp Trp Cys  
 1 5 10 15  
 Pro Gly Ser Thr His His Cys Leu Arg Val Gln Arg Phe Pro Phe Pro  
 20 25 30  
 Pro Ser Gln Asn Phe Leu Phe Pro Trp Pro Pro Leu Pro Pro Leu Pro  
 35 40 45  
 Pro Pro Leu Met Cys Trp Pro Pro Ser Pro Ser Pro Pro His Gly Arg  
 50 55 60  
 Leu Pro Pro Gly Val Pro Ser Pro Ala Gln Ala Ser Leu Arg Ala Arg  
 65 70 75 80  
 Thr Ala Gly

<210> 867  
 <211> 640  
 <212> DNA  
 <213> Homo sapiens

<400> 867  
 nntccggaac atcaagatcc aggcgcagaa gaccgtcaga agctgcactg gccacctcct  
 60  
 tcagggtggac tctcgttggt ggccggcgctc gctggccccc tcgcaccccg tcccgtgtca  
 120  
 catgctccag ggcgcagctc ttgtccacct ttacctcatc gaaagccttg tttttgcctc  
 180  
 ggtaaatccc ttcattgagg gctttgatcc aggattcctt ctctccccc gtgggtgcct  
 240  
 ggaatttgat gtcgctgacc ttgttccttg gggatcgcag caggataaag cgggtgtttc  
 300  
 gcttgaggag ggcacgaagg tcttggcact tctcatagct gccagctcc acagtctcca  
 360  
 cacacttctg atcatcctca ttctcataga ccagcagctg ggcttggcag aggagcagat  
 420  
 atcggctctt ccagaaaccc aggaggcccc cactgctctt cttgatccag ccagccttgt  
 480  
 ccaccatctg tgetccccga ggcttctcac cggcttctct cacaccctcc tctccatgg  
 540  
 cgagtcgcgc gaggtcccg cgtccgcca ctcgcttcca gcgcgcgcg ggctctgcca  
 600  
 ccgcgtctac gcccggccag gcggcgactc tccgcgttct  
 640

<210> 868  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 868  
 Gly Gly His Glu Gly Pro Gly Thr Ser His Ser Cys Pro Ala Pro Gln  
 1 5 10 15  
 Ser Pro His Thr Ser Asp His Pro His Ser His Arg Pro Ala Ala Gly  
 20 25 30  
 Pro Gly Arg Gly Ala Asp Ile Gly Leu Ser Arg Asn Pro Gly Gly Pro  
 35 40 45  
 His Cys Ser Ser  
 50

<210> 869  
 <211> 321  
 <212> DNA  
 <213> Homo sapiens

<400> 869  
 ngggtgatgc tgctcgcggc attgagcatc tttgtgctca gcgcgctgtt tategacaac  
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ttctgtcgcg cgctgaatat gcgcgggctg ggccctggcga tttcgacggt gggcatcgct  
 120  
 gcgtgcacca tgctgttctg cctggcgctg gggcatttcg acttgctcgtt gggctcgggtg  
 180  
 atcgctgtg cgggtgtggt cgcggggatt gtgattcgtg acaccgatag cgtggcactc  
 240  
 ggcgtgtccg ctgcgttggc catgggcctg gtagtggggc tgatcaacgg catcgtgatc  
 300  
 gccaaagctgc gcatcaacgc g  
 321

<210> 870

<211> 107

<212> PRT

<213> Homo sapiens

<400> 870

Xaa	Val	Met	Leu	Leu	Ala	Ala	Leu	Ser	Ile	Phe	Val	Leu	Ser	Ala	Leu
1				5					10					15	
Phe	Ile	Asp	Asn	Phe	Leu	Ser	Pro	Leu	Asn	Met	Arg	Gly	Leu	Gly	Leu
		20					25					30			
Ala	Ile	Ser	Thr	Val	Gly	Ile	Ala	Ala	Cys	Thr	Met	Leu	Phe	Cys	Leu
		35				40					45				
Ala	Ser	Gly	His	Phe	Asp	Leu	Ser	Val	Gly	Ser	Val	Ile	Ala	Cys	Ala
	50				55				60						
Gly	Val	Val	Ala	Gly	Ile	Val	Ile	Arg	Asp	Thr	Asp	Ser	Val	Ala	Leu
65			70					75						80	
Gly	Val	Ser	Ala	Ala	Leu	Ala	Met	Gly	Leu	Val	Val	Gly	Leu	Ile	Asn
		85					90						95		
Gly	Ile	Val	Ile	Ala	Lys	Leu	Arg	Ile	Asn	Ala					
		100					105								

<210> 871

<211> 320

<212> DNA

<213> Homo sapiens

<400> 871

agatcttcag agtcctcgtc ttttaaattgg gggtaacagc agcaagtcct cagaggtgtc  
 60  
 ctgagcctca aaacacatcc tggtttgtaa cgtcgcgagc ctcagcaggg gctaggcaca  
 120  
 gaacaagcat tcaggacctg gaaggtagca gcgacacctg gtcctccctt cccaggcaca  
 180  
 aggcagcccc tctccattca agctctgccc cagcccagca aagagagggg tcctcagcca  
 240  
 ctgccccac cactaccaca atcataactca cctctcctgg tccatacgtg acaaaggacc  
 300  
 tgccacggcc agggagacaa  
 320

<210> 872

<211> 98

<212> PRT

<213> Homo sapiens

<400> 872

```

Met Gly Val Thr Ala Ala Ser Pro Gln Arg Cys Pro Glu Pro Gln Asn
 1           5           10           15
Thr Ser Trp Phe Val Thr Ser Ala Ala Ser Ala Gly Ala Arg His Arg
      20           25           30
Thr Ser Ile Gln Asp Leu Glu Gly Thr Ser Asp Thr Trp Ser Ser Leu
      35           40           45
Pro Arg His Lys Ala Ala Pro Leu His Ser Ser Ser Ala Pro Ala Gln
      50           55           60
Gln Arg Glu Gly Ser Ser Ala Thr Ala Pro Thr Thr Thr Thr Ile Ile
65           70           75           80
Leu Thr Ser Pro Gly Pro Tyr Val Thr Lys Asp Leu Pro Arg Pro Gly
      85           90           95
Arg Gln

```

<210> 873

<211> 363

<212> DNA

<213> Homo sapiens

<400> 873

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nttgtttagc atcgtttttt acgggtgtat cagcgcgttt agcagcgttt ttagcggatg
60
catcagcatg ttttgcgtca cgttttacaa ctgtgctacc gtgttttagca tcatttttga
120
cggaggtatc aatacgttta gcatcgtttt taacagatgt atcaacacgg ggttcacccg
180
cttttagcaga atccccagct ctagtagcca ctttagatac ttcagatttt atatgagtcg
240
cagttgtttc agcgtgagcc atgctgaatg tagaaccaag ggccaatgta attgctaaag
300
acaaagataa tttatttagt ttcatgttcg gagagaagtg tgccaattcg gcgatacagt
360
cag
363

```

<210> 874

<211> 108

<212> PRT

<213> Homo sapiens

<400> 874

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Met Lys Leu Asn Lys Leu Ser Leu Ser Leu Ala Ile Thr Leu Ala Leu
 1           5           10           15
Gly Ser Thr Phe Ser Met Ala His Ala Glu Thr Thr Ala Thr His Ile
      20           25           30
Lys Ser Glu Val Ser Lys Val Ala Thr Arg Ala Gly Asp Ser Ala Lys
      35           40           45
Ala Asp Glu Pro Arg Val Asp Thr Ser Val Lys Asn Asp Ala Lys Arg
      50           55           60
Ile Asp Thr Ser Val Lys Asn Asp Ala Lys His Gly Ser Thr Val Val

```





caatccacct atgctaaacg tggtcagcaa gggtatctca cacgagaatt ctttggtttg  
 120  
 ttggccaata ccatgggaga tcaaatcctt ttagtacagg cgtacagaga aggcgaagcg  
 180  
 atcgccgcgt cgtggtgttt ctttgatgat cattcactat atgggcgtta ttggggctgt  
 240  
 atggaagaag tggattgcct gcattttgaa gcttggttatt accaaggaat cgagttttgt  
 300  
 ctcgaaaaag gggtacagca ttctgatccg ggtacacaag gggaacacaa gattgcgcgc  
 360  
 ggctttgaac ctgttttttag ccacagcgtg cattacattg ctcacaaagg ttttcgtgaa  
 420  
 gcgattggga atttctgtga ggaagaagcg caagctgtgc gcgagtatca tcaagatacc  
 480  
 cacgcgt  
 487

&lt;210&gt; 878

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 878

Thr	Arg	Thr	Leu	Gly	Asn	Glu	Leu	Thr	Thr	Ala	Glu	Ile	Asp	Cys	Leu
1				5					10					15	
Tyr	Leu	Cys	Tyr	Gln	Ser	Thr	Tyr	Ala	Lys	Arg	Gly	Gln	Gln	Gly	Tyr
			20					25					30		
Leu	Thr	Arg	Glu	Phe	Phe	Gly	Leu	Leu	Ala	Asn	Thr	Met	Gly	Asp	Gln
			35				40					45			
Ile	Leu	Leu	Val	Gln	Ala	Tyr	Arg	Glu	Gly	Glu	Ala	Ile	Ala	Ala	Ser
			50			55				60					
Trp	Cys	Phe	Phe	Asp	Asp	His	Ser	Leu	Tyr	Gly	Arg	Tyr	Trp	Gly	Cys
65					70					75				80	
Met	Glu	Glu	Val	Asp	Cys	Leu	His	Phe	Glu	Ala	Cys	Tyr	Tyr	Gln	Gly
				85					90					95	
Ile	Glu	Phe	Cys	Leu	Glu	Lys	Gly	Leu	Gln	His	Phe	Asp	Pro	Gly	Thr
			100				105						110		
Gln	Gly	Glu	His	Lys	Ile	Ala	Arg	Gly	Phe	Glu	Pro	Val	Phe	Ser	His
			115				120					125			
Ser	Val	His	Tyr	Ile	Ala	His	Gln	Gly	Phe	Arg	Glu	Ala	Ile	Gly	Asn
			130			135				140					
Phe	Cys	Glu	Glu	Glu	Ala	Gln	Ala	Val	Arg	Glu	Tyr	His	Gln	Asp	Thr
145					150					155				160	
His	Ala														

&lt;210&gt; 879

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 879

nncttagcat ttaagccaac gaggcagcta atgtcctctg aacagcaaag gaaattcagc  
 60

agccagtcga gtagggctct gaccctctt tcctacagta ctgctaaaaa ttcattggga  
 120  
 tcaagatcca gtgaatcctt tgggaagtac acatcgccag taatgagtga gcatggggac  
 180  
 gagcacaggc agctcctctc tcacccaatg caaggccctg gactccgtgc agctacctca  
 240  
 tccaaccact ctgtggacga gcaactgaag aatactgaca cgcacctcat cgacctggta  
 300  
 accaatgaga ttatcaccca aggacctcca gtggactgga atgacattgc tggctctcgac  
 360  
 ctgggtgaagg ctgtcattaa agaggagggt ttatggccag tgttgaggtc agacgcgttc  
 420  
 agtggactga cggccttacc tcggagcacc cttttatttg gacctcgggg gacaggcaaa  
 480  
 acattatttg gcagatgcat cgctagtcag ctggggggcca catttttcaa aattgccggg  
 540  
 tctggactag tcgccaaggg gttaggagaa gcagagaaaa ttatccatgc ctcttttctt  
 600  
 gtggccagggt gtcgccagcc ctcggtgatt tttgttagtg acattgacat gcttctctcc  
 660  
 tctcaagtga atgaggaaca tagtccagtc agtcggatga gaaccgaatt tctgatgcaa  
 720  
 ctggacactg tactaacttc ggctgaggac caaatcgtag taatttgtgc caccagtaaa  
 780  
 ccagaagaaa tagatgaatc ctttcggagg tacttcatga aacgactttt aatcccactt  
 840  
 cctgacagca cagcgaggca ccagataata gtacaactgc tctcacagca caattactgt  
 900  
 ctcaatgaca aggagtttgc actgctcgtc cagcgcacag aaggcttttc tggactagat  
 960  
 gtggctcatt tgtgtcagga agcagtgggt ggc  
 993

&lt;210&gt; 880

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 880

Xaa	Leu	Ala	Phe	Lys	Pro	Thr	Arg	Gln	Leu	Met	Ser	Ser	Glu	Gln	Gln
1				5				10					15		
Arg	Lys	Phe	Ser	Ser	Gln	Ser	Ser	Arg	Ala	Leu	Thr	Pro	Pro	Ser	Tyr
			20					25					30		
Ser	Thr	Ala	Lys	Asn	Ser	Leu	Gly	Ser	Arg	Ser	Ser	Glu	Ser	Phe	Gly
			35				40					45			
Lys	Tyr	Thr	Ser	Pro	Val	Met	Ser	Glu	His	Gly	Asp	Glu	His	Arg	Gln
			50				55				60				
Leu	Leu	Ser	His	Pro	Met	Gln	Gly	Pro	Gly	Leu	Arg	Ala	Ala	Thr	Ser
65					70					75				80	
Ser	Asn	His	Ser	Val	Asp	Glu	Gln	Leu	Lys	Asn	Thr	Asp	Thr	His	Leu
				85					90					95	
Ile	Asp	Leu	Val	Thr	Asn	Glu	Ile	Ile	Thr	Gln	Gly	Pro	Pro	Val	Asp
			100				105						110		
Trp	Asn	Asp	Ile	Ala	Gly	Leu	Asp	Leu	Val	Lys	Ala	Val	Ile	Lys	Glu

```

      115      120      125
Glu Val Leu Trp Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr
      130      135      140
Ala Leu Pro Arg Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys
145      150      155      160
Thr Leu Leu Gly Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe
      165      170      175
Lys Ile Ala Gly Ser Gly Leu Val Ala Lys Gly Leu Gly Glu Ala Glu
      180      185      190
Lys Ile Ile His Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser
      195      200      205
Val Ile Phe Val Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn
      210      215      220
Glu Glu His Ser Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln
225      230      235      240
Leu Asp Thr Val Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys
      245      250      255
Ala Thr Ser Lys Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe
      260      265      270
Met Lys Arg Leu Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln
      275      280      285
Ile Ile Val Gln Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys
      290      295      300
Glu Phe Ala Leu Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp
305      310      315      320
Val Ala His Leu Cys Gln Glu Ala Val Val Gly
      325      330

```

<210> 881  
 <211> 313  
 <212> DNA  
 <213> Homo sapiens

```

<400> 881
cgcgtagagcg tgcacaatgc tccaggaacc ggtgtgtatg aggccgggga ttctaccggt
60
cgtgggtttgc agggcatgcg tgagcgcgcc cgtatccatg gcggcaccgc gcgctggggc
120
gactcgagcgt attatgaagg cggtttcaac gtcacggtgg agattccaac atgagcgggc
180
aaaggatgaa catggacacg acgcgccccca atcacggtcg gggcttgccg acgatcagcc
240
ggctgggtgc gcaccggttt tgccatggtg ctggattcgc aggacgacat cacggtggcc
300
tggcaagccg acn
313

```

<210> 882  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

```

<400> 882
Arg Val Ser Val Asp Asn Ala Pro Gly Thr Gly Val Tyr Glu Ala Gly

```

```

      1           5           10           15
Asp Ser Thr Gly Arg Gly Leu Gln Gly Met Arg Glu Arg Ala Arg Ile
      20           25           30
His Gly Gly Thr Ala Arg Trp Gly Asp Ser Gln Tyr Tyr Glu Gly Gly
      35           40           45
Phe Asn Val Thr Val Glu Ile Pro Thr
      50           55

```

&lt;210&gt; 883

&lt;211&gt; 576

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 883

```

naattaagat ctgggggtccc agtgtcattg gtgaaggcct tgggattcga ggcagctgag
60
tcctcactga ccaaggcaag ccattgcttct gattgcttga ggccaccgaa atgaacaaat
120
ggaaaacact cccatctttt tcaagcctac cttttagcag aagaggcaga tacacaagcc
180
ctaaagatgt aacatcaggc tgagtggagg aaggctgaga agaaaaataa agcaggctca
240
ggaggagaga gtgatgtcag gatgcccttg tgcttactcc agcctccttg tgaaaaccca
300
gctctcctgt ctcccagtga agacttgat ggagccatc aggggaaggct gggccccage
360
tgaggagtatg ggtgtgagct ctatagacca tcctctcttg caatcaataa aacttgctt
420
gtgaaagagg cccaagccac catccgcatt gacaccagtg caagtggccc caccgcctg
480
gtcctcagtg actgtgccac cagccatggg agcctgcgca tccaactgct gcataagctc
540
tccttccttg tgaacgcctt agctaagcag gtcattg
576

```

&lt;210&gt; 884

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 884

```

Met Pro Leu Cys Leu Leu Gln Pro Pro Cys Glu Asn Pro Ala Leu Leu
      1           5           10           15
Ser Pro Ser Glu Asp Leu Asp Gly Ser His Gln Gly Arg Leu Gly Pro
      20           25           30
Ser Trp Glu Tyr Gly Cys Glu Leu Tyr Arg Pro Ser Leu Ser Ala Ile
      35           40           45
Asn Lys His Leu Pro Val Lys Glu Ala Gln Ala Thr Ile Arg Met Asp
      50           55           60
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
      65           70           75           80
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
      85           90           95
Val Asn Ala Leu Ala Lys Gln Val Met

```

100

105

<210> 885  
 <211> 370  
 <212> DNA  
 <213> Homo sapiens

<400> 885  
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 60  
 ggtgaggcga tgctgacgaa cgacacaccg gtgacttggg atggcgggaa agtacggggc  
 120  
 aggcgggtgt cgcgcctcgg tgcgatcgag ttgtcgtcga ccccggtccg ccagatccg  
 180  
 gtacgggctc gccacgtggc gctggaagca gtgaggtctg ggggacttga cgtagcgagc  
 240  
 ctgacgaaga acggtgaatc tttgcgacgc cgtcttgccc tggcccatcg ggtgtttggt  
 300  
 gatccctggc ccgatgtcag cgatgaggct ctgctagcct gcgccgagga gtggcttgac  
 360  
 ctcgacgcgt  
 370

<210> 886  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 886  
 Thr Ser Gly Ala Leu Ile Arg Ala Ala Val Pro Leu Ser Glu Ser Ala  
 1 5 10 15  
 Ala Leu Glu Ser Gly Glu Ala Met Leu Thr Asn Asp Thr Pro Val Thr  
 20 25 30  
 Trp Asp Gly Gly Lys Val Arg Gly Arg Arg Val Ser Arg Leu Gly Ala  
 35 40 45  
 Ile Glu Leu Ser Ser Thr Pro Val Arg Pro Asp Pro Val Arg Ala Arg  
 50 55 60  
 His Val Ala Leu Glu Ala Val Arg Ser Gly Gly Leu Asp Val Ala Ser  
 65 70 75 80  
 Leu Thr Lys Asn Gly Glu Ser Leu Arg Arg Arg Leu Ala Leu Ala His  
 85 90 95  
 Arg Val Phe Gly Asp Pro Trp Pro Asp Val Ser Asp Glu Ala Leu Leu  
 100 105 110  
 Ala Cys Ala Glu Glu Trp Leu Asp Leu Asp Ala  
 115 120

<210> 887  
 <211> 447  
 <212> DNA  
 <213> Homo sapiens

<400> 887  
 cagggcggtg cgctcggctg cgtgctgccg atggtcacgc tcggaggctt aaccgccatc  
 60

attatctccg gctgcctgaa ccagcttggt aaacgctatc cgcattctgac cggcgaaggc  
 120  
 caactgatgc caaacctgac taatgctgat accacggctt cccaaccggc gttctccggt  
 180  
 aaagcggacg tgaccaccat tgcctccggc gcgttgctgg ccgtgctgct ttacatgggt  
 240  
 ggtaggttgg ttcacaagtt gattggcctg cctgctccgg ttggcatgtc gtttgtggcg  
 300  
 gtgctgggtca aactgtgcaa cggcgtttct cccgcctgac tcgaaggctc gcaggtgggt  
 360  
 tacaaattct tccagacctc cgtaacctat ccgattctgt tcgccgttgg cgtggcgatt  
 420  
 acgccgtggc aggaactggc caacgcg  
 447

<210> 888

<211> 149

<212> PRT

<213> Homo sapiens

<400> 888

Gln Gly Val Ala Leu Gly Arg Val Leu Pro Met Val Met Leu Gly Gly  
 1 5 10 15  
 Leu Thr Ala Ile Ile Ile Ser Gly Cys Leu Asn Gln Leu Gly Lys Arg  
 20 25 30  
 Tyr Pro His Leu Thr Gly Glu Gly Gln Leu Met Pro Asn Arg Ala Asn  
 35 40 45  
 Ala Asp Thr Thr Ala Ser Gln Pro Ala Phe Ser Gly Lys Ala Asp Val  
 50 55 60  
 Thr Thr Ile Ala Ser Gly Ala Leu Leu Ala Val Leu Leu Tyr Met Val  
 65 70 75 80  
 Gly Arg Leu Val His Lys Leu Ile Gly Leu Pro Ala Pro Val Gly Met  
 85 90 95  
 Leu Phe Val Ala Val Leu Val Lys Leu Cys Asn Gly Ala Ser Pro Arg  
 100 105 110  
 Leu Leu Glu Gly Ser Gln Val Val Tyr Lys Phe Phe Gln Thr Ser Val  
 115 120 125  
 Thr Tyr Pro Ile Leu Phe Ala Val Gly Val Ala Ile Thr Pro Trp Gln  
 130 135 140  
 Glu Leu Val Asn Ala  
 145

<210> 889

<211> 450

<212> DNA

<213> Homo sapiens

<400> 889

ggtaccaccc cacacctgac aagaggtggc cagggaggaa gggagggttc ttacctcccc  
 60  
 atctcccctc agtaaaattc aggatgccca gtgaagtttg aatgtcagat aaacaatttg  
 120  
 ttagtataag gatgtacctc gcattgaaat gatgccttgt aatttactaa atctgcaact  
 180

atgcagcctt atttcatggc gggcagtggc ggtgatccca ggtttcaggg gcggggaagg  
 240  
 gtgctgggga gatcctgagg tcaggaaccc gtacacctct gcttctgccc tctcttcct  
 300  
 gtgccggcca caaggcaatg actcctgtgt ggggtgcagag gcagaaatgg gtctggaagg  
 360  
 ggattcccag tgtctggcaa gttctggtaa attctgcatt ggaggttctc tctgtagtaa  
 420  
 ggggagttgg cctggccgcc cttcacgcgt  
 450

<210> 890

<211> 100

<212> PRT

<213> Homo sapiens

<400> 890

Met	Met	Pro	Cys	Asn	Leu	Leu	Asn	Leu	Gln	Leu	Cys	Ser	Leu	Ile	Ser
1				5					10					15	
Trp	Arg	Ala	Val	Ala	Val	Ile	Pro	Gly	Phe	Arg	Gly	Gly	Glu	Gly	Cys
			20					25					30		
Trp	Gly	Asp	Pro	Glu	Val	Arg	Asn	Pro	Tyr	Thr	Ser	Ala	Ser	Ala	Leu
		35					40					45			
Ser	Ser	Leu	Cys	Arg	Pro	Gln	Gly	Asn	Asp	Ser	Cys	Val	Gly	Ala	Glu
		50				55					60				
Ala	Glu	Met	Gly	Leu	Glu	Gly	Asp	Ser	Gln	Cys	Leu	Ala	Ser	Ser	Gly
65					70					75				80	
Lys	Phe	Cys	Ile	Gly	Gly	Ser	Leu	Cys	Ser	Lys	Gly	Ser	Trp	Pro	Gly
			85						90					95	
Arg	Pro	Ser	Arg												
															100

<210> 891

<211> 318

<212> DNA

<213> Homo sapiens

<400> 891

nncaccgtcc ccgtactgga tccgcgcgag gatttcgccg actgcatgca cattgacgta  
 60  
 ctggatccct tccacactga caacaccagt gagcacagtg acctggccac agatggccag  
 120  
 actaacggcc cggctgatag cgggactggc acccactctg agcagggaaa ctccgacata  
 180  
 tctagccccg tcagctctag tgacgtgct aacaccaccg acagcactgc tggcaatacc  
 240  
 ggtgaaggta ctgccgcgaa tatgcctggg gacatggctc attcttcgac ggctaccac  
 300  
 ccctatgcaa gcaccggt  
 318

<210> 892

<211> 106

<212> PRT

<213> Homo sapiens

<400> 892

```

Xaa Thr Val Pro Val Leu Asp Pro Arg Glu Asp Phe Ala Asp Cys Met
 1           5           10           15
His Ile Asp Val Leu Asp Pro Phe His Thr Asp Asn Thr Ser Glu His
      20           25           30
Ser Asp Leu Ala Thr Asp Gly Gln Thr Asn Gly Pro Ala Asp Ser Gly
      35           40           45
Thr Gly Thr His Ser Glu Gln Gly Asn Ser Asp Ile Ser Ser Pro Val
      50           55           60
Ser Ser Ser Asp Ala Ala Asn Thr Thr Asp Ser Thr Ala Gly Asn Thr
65           70           75           80
Gly Glu Gly Thr Ala Ala Asn Met Pro Gly Asp Met Ala His Ser Ser
      85           90           95
Thr Ala Thr His Pro Tyr Ala Ser Thr Gly
      100           105

```

<210> 893

<211> 510

<212> DNA

<213> Homo sapiens

<400> 893

```

nnggataccta tccctgaatc taagggttggt gacacatgtg tttgggatag caaggtagag
60
aagtcacaga aaaagcctgt ggaaaacagg atgaaggagg acaaaagcag catcagggaa
120
gcaatcagca aagccaagag tacagcaaata ataaagacag aacaggaagg tgaggcatct
180
gagaagagct tgcattctgag cccacagcat atcacacacc agactatgcc tataggacag
240
agaggcagtg agcaaggcaa acgtgtggag aacattaatg gaacctccta ccctagtcta
300
cagcagaaaa ccaatgctgt taagaaatta cataaatgtg atgaatgtgg gaaatccttc
360
aaatataatt cccgccttgt tcaacataaa attatgcaca ctggggaaaa gcgctatgaa
420
tgtgatgact gtggaggggac tttccggagc agctcgagcc ttcgggtcca caaacggatc
480
cacactgggt acggagagaa gacaacgcgt
510

```

<210> 894

<211> 170

<212> PRT

<213> Homo sapiens

<400> 894

```

Xaa Asp Pro Ile Pro Glu Ser Lys Val Gly Asp Thr Cys Val Trp Asp
 1           5           10           15
Ser Lys Val Glu Lys Ser Gln Lys Lys Pro Val Glu Asn Arg Met Lys
      20           25           30
Glu Asp Lys Ser Ser Ile Arg Glu Ala Ile Ser Lys Ala Lys Ser Thr

```



35	40	45
Ala Asn Ile Lys Thr Glu Gln Glu Gly Glu Ala Ser Glu Lys Ser Leu		
50	55	60
His Leu Ser Pro Gln His Ile Thr His Gln Thr Met Pro Ile Gly Gln		
65	70	75
Arg Gly Ser Glu Gln Gly Lys Arg Val Glu Asn Ile Asn Gly Thr Ser		
85	90	95
Tyr Pro Ser Leu Gln Gln Lys Thr Asn Ala Val Lys Lys Leu His Lys		
100	105	110
Cys Asp Glu Cys Gly Lys Ser Phe Lys Tyr Asn Ser Arg Leu Val Gln		
115	120	125
His Lys Ile Met His Thr Gly Glu Lys Arg Tyr Glu Cys Asp Asp Cys		
130	135	140
Gly Gly Thr Phe Arg Ser Ser Ser Ser Leu Arg Val His Lys Arg Ile		
145	150	155
His Thr Gly Tyr Gly Glu Lys Thr Thr Arg		160
165	170	

&lt;210&gt; 895

&lt;211&gt; 1119

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 895

cgccgcgaga attgggtcgg gcatttccag atgttcccgt ggttgattcg tccggcaatc  
 60  
 acgttcggga gagggtcgat tcaactcccc gattaatcgt tgccacccca agggccgaac  
 120  
 ccgcaccgga atcgggcttt tcctggggct gccttcctaa atgcggtgtc ctccttgctg  
 180  
 aggcctggcc tggcggcggt ggagcagacc gtcgatcggg ggatggcaat cctggccttg  
 240  
 gtccgatcag tgcgggatgg gggccgggca gttatcgtcg ggccttcgga ggacgccgcc  
 300  
 ttgcaggcca tgggtcgaaa tgatccagtc ggggtgggca cacgtgaact cgccgatcgt  
 360  
 cgggaggcac atttcccgcc cgcggtgccg tgcggaattg tgcacggtga cccgaaagcg  
 420  
 gtggctacag cggcacagcg actacgcgag tgggtcggaa ccgaccttga gatgcttggc  
 480  
 ccagctccac aaccacgccg tgccagcgaa tcggaacggg atcgaattat cgtgcgtcct  
 540  
 cgtagcacga tgcctctcgc cgagctttcc cagggtctat ttcggctacg ttccaaacac  
 600  
 actatgagcc gcgaaccagg aagcttacgc gtggtcatcg acccggccaa cttgttgtga  
 660  
 ggtcggtagg cttgcggtgt gagacttctt ttgctggta ccccgagcgt ggccgtccca  
 720  
 acgcttaccg ccttggttagc cgatccccgt cacgaggtag ctgccgtcct gacgcgtccg  
 780  
 gatgcagcag taggacggca ccgtactcca cgtccatgcc cggtcgcca gggtgccgag  
 840  
 gaactcggtg tccccgcat taaggcgacc agcgtgaagt ccggcgaggg tcaatgatgcc  
 900

gtcacttccc tcgatgtcga cgtagccgtc gtcgtagcct acggaggtct cattccccgcc  
 960  
 gatctgctgg cagtaccacg acacggctgg attaacttac actttttctct cctaccgcga  
 1020  
 tggcgcgggcg ctgctcccat acaacggggc atcatggcgg gggatgagga gacgggcgct  
 1080  
 tgtgtctttc agctagttga aagcctcgat gccggaccg  
 1119

<210> 896

<211> 147

<212> PRT

<213> Homo sapiens

<400> 896

Val	Arg	Leu	Leu	Phe	Ala	Gly	Thr	Pro	Asp	Val	Ala	Val	Pro	Thr	Leu
1				5					10					15	
Thr	Ala	Leu	Val	Ala	Asp	Pro	Arg	His	Glu	Val	Ala	Ala	Val	Leu	Thr
			20					25					30		
Arg	Pro	Asp	Ala	Ala	Val	Gly	Arg	His	Arg	Thr	Pro	Arg	Pro	Cys	Pro
		35					40					45			
Val	Ala	Lys	Ala	Ala	Glu	Glu	Leu	Gly	Ile	Pro	Ala	Ile	Lys	Ala	Thr
	50					55				60					
Ser	Val	Lys	Ser	Gly	Glu	Gly	His	Asp	Ala	Val	Thr	Ser	Leu	Asp	Val
65					70				75					80	
Asp	Val	Ala	Val	Val	Val	Ala	Tyr	Gly	Gly	Leu	Ile	Pro	Ala	Asp	Leu
				85					90					95	
Leu	Ala	Val	Pro	Arg	His	Gly	Trp	Ile	Asn	Leu	His	Phe	Ser	Leu	Leu
			100					105					110		
Pro	Arg	Trp	Arg	Gly	Ala	Ala	Pro	Ile	Gln	Arg	Ala	Ile	Met	Ala	Gly
		115				120						125			
Asp	Glu	Thr	Gly	Ala	Cys	Val	Phe	Gln	Leu	Val	Glu	Ser	Leu	Asp	
	130				135					140					
Ala	Gly	Pro													
145															

<210> 897

<211> 384

<212> DNA

<213> Homo sapiens

<400> 897

gagctcgagg ctggcaagcc ggaagtgccg ctgttcccga cggccgacgg catgtcgctc  
 60  
 gacgactacc tcgtccagct gtcgaaggaa gggctcgaga cccgtctcgc gcagctgtat  
 120  
 ccggctcgaag cccgacgcga cgcgcagcgc gacacctact acaagcgcc cgaattcgag  
 180  
 tgcggggacca tcacgaagat gggctttccc ggctacttcc tgatcgctgc ggacttcac  
 240  
 aactgggcaa agaacaacgg cgtgccggtc ggcccgggcc gcggctcggg cgccgggttcg  
 300  
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 360

gagcgccttcc tgaaccgga acgc  
384

<210> 898  
<211> 128  
<212> PRT  
<213> Homo sapiens

<400> 898  
Glu Leu Glu Ala Gly Lys Pro Glu Val Pro Leu Phe Pro Thr Pro Asp  
1 5 10 15  
Gly Met Ser Leu Asp Asp Tyr Leu Val Gln Leu Ser Lys Glu Gly Leu  
20 25 30  
Glu Thr Arg Leu Ala Gln Leu Tyr Pro Val Glu Ala Arg Arg Asp Ala  
35 40 45  
Gln Arg Asp Thr Tyr Tyr Lys Arg Leu Glu Phe Glu Cys Gly Thr Ile  
50 55 60  
Thr Lys Met Gly Phe Pro Gly Tyr Phe Leu Ile Val Ala Asp Phe Ile  
65 70 75 80  
Asn Trp Ala Lys Asn Asn Gly Val Pro Val Gly Pro Gly Arg Gly Ser  
85 90 95  
Gly Ala Gly Ser Leu Val Ala Tyr Ala Leu Gly Ile Thr Asp Leu Glu  
100 105 110  
Val Leu Arg Tyr Asp Leu Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg  
115 120 125

<210> 899  
<211> 6171  
<212> DNA  
<213> Homo sapiens

<400> 899  
ttctccaagg ccttaaatct cagatacttg aatgcatctg caaatagtct ggagtcttta  
60  
ccatccgcct gcactggaga ggagagtttg agtatgctgc agctgcttta tctgaccaac  
120  
aatctcctga cggatcagtg catacctgtc ctggtagggc acctgcacct gcgaatcttg  
180  
caccttgcaa acaatcagtt acagaccttt cctgcaagca aactaaataa attggagcaa  
240  
ttggaggaac tgaacctaa tggaacaag cttaaaacca tccccacaac catagcaaac  
300  
tgtaaaaggc tgcacaccct tggtgcacac tccaacaaca tcagcatttt cccagaaata  
360  
ctgcagttgc ctcagatcca gttttagtagac ctaagttgca acgacttgac agaaatcctg  
420  
attccagagg ctttgctgac tacattacaa gaccttgacc tgactggaaa tacaatctg  
480  
gttctggaac acaagacact ggacatattt agccatatca caaccctgaa aattgatcag  
540  
aaacctttgc caaccacaga ttctacagtt acgtcaacct tctggagcca tggactggct  
600  
gagatggcag ggcagagaaa taagctgtgt gtctcagcac ttgctatgga tagctttgca  
660

gagggggtgg gagctgtgta tggcatgttt gatggagacc gaaatgagga gctcccgcgc  
720  
ctgctgcagt gtacgatggc agatgtgctt ttagaagagg tacagcagtc aactaatgac  
780  
acagttttca tggctaacac cttcttggtta tctcacagga aattaggaat ggctggccag  
840  
aagttgggct cctccgctct cctgtgctac atccgccctg aactgcccga tccagcaagt  
900  
agcttttagct tgactgtagc caatgttggc acgtgccaaag cagtccctgtg ccgaggtggg  
960  
aagccagtgc ccctctctaa agtcttcagc ctggagcagg acccagagga ggctcaaagg  
1020  
gtgaaggacc aaaaagccat catcacagag gacaacaaag tgaatggggg aacctgctgt  
1080  
acccggatgc tgggctgtac atacctctac ccttggatcc tccccaagcc ccacatatct  
1140  
tccactccgc tgaccattca agatgagttg ctgattctgg gaaacaaagc attgtgggaa  
1200  
cacttgctct acacagaagc tgtcaatgct gtacgtcacg tacaagacct attagcagct  
1260  
gctaagaagc tgtgcacatt agcgcagagc tatggctgtc aggacagtgt aggggcgatg  
1320  
gtagtttatt tgaatattgg tgaggaaggc tgcacttgtg aaatgaatgg gctcaccctc  
1380  
ccaggtcctg tgggatttgc ttcaaccacc actatcaagg atgcccctaa gccagccact  
1440  
ccatcctcta gcagtgggat tgctctgag ttcagcagtg agatgtccac ctgagaggtg  
1500  
agcagtgaag tggggtccac tgcttctgat gagcataatg ctgggggcct ggacactgcc  
1560  
ttgcttccga ggccagagcg gcgctgcagc ctccacccaa caccacctc tgggctgttt  
1620  
cagcgccagc cttcttctgc taccttctcc agtaaccagt ctgacaacgg cctggacagt  
1680  
gatgatgacc agcccgttga gggggtcata accaatggca gcaaggtaga ggtggaagta  
1740  
gacatccact gctgcagggg gagggatctg gagaactcac cccctctcat agagagttct  
1800  
cctaccctgt gttctgagga acatgctaga gggtcgtgtt ttgggatccg aagacagaac  
1860  
agtgtgaata gtggcatgct cctgccaatg agcaaggaca ggatggagtt acagaagtct  
1920  
ccctccacct cctgcctcta tgggaagaaa ctctccaatg gctctattgt gcccttagag  
1980  
gacagcctga acctcattga agtggccaca gaagtgccca agaggaaaac tggctatttt  
2040  
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<211> 734

<212> PRT

<213> Homo sapiens

<400> 900

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Thr	Ile	Ala	Asn	Cys	Lys	Arg	Leu	His	Thr	Leu	Val	Ala	His	Ser	Asn
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			115				120					125			
Val	Asp	Leu	Ser	Cys	Asn	Asp	Leu	Thr	Glu	Ile	Leu	Ile	Pro	Glu	Ala
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Val	Leu	Glu	His	Lys	Thr	Leu	Asp	Ile	Phe	Ser	His	Ile	Thr	Thr	Leu
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Lys	Ile	Asp	Gln	Lys	Pro	Leu	Pro	Thr	Thr	Asp	Ser	Thr	Val	Thr	Ser
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Lys	Val	Asn	Gly	Val	Thr	Cys	Cys	Thr	Arg	Met	Leu	Gly	Cys	Thr	Tyr
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His	Leu	Ser	Tyr	Thr	Glu	Ala	Val	Asn	Ala	Val	Arg	His	Val	Gln	Asp
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Cys	Gln	Asp	Ser	Val	Gly	Ala	Met	Val	Val	Tyr	Leu	Asn	Ile	Gly	Glu
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Gly	Phe	Ala	Ser	Thr	Thr	Thr	Ile	Lys	Asp	Ala	Pro	Lys	Pro	Ala	Thr
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Pro	Ser	Ser	Ser	Ser	Gly	Ile	Ala	Ser	Glu	Phe	Ser	Ser	Glu	Met	Ser
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Thr	Ser	Glu	Val	Ser	Ser	Glu	Val	Gly	Ser	Thr	Ala	Ser	Asp	Glu	His
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Asn	Ala	Gly	Gly	Leu	Asp	Thr	Ala	Leu	Leu	Pro	Arg	Pro	Glu	Arg	Arg
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Cys	Ser	Leu	His	Pro	Thr	Pro	Thr	Ser	Gly	Leu	Phe	Gln	Arg	Gln	Pro
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 Pro Lys Arg Lys Thr Gly Tyr Phe Ala Ala Pro Thr Gln Met Glu Pro  
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 Gln Met Lys Gln His Gln Asp Ser Arg Leu Glu Pro Glu Pro His Glu  
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                                 20                      25                      30  
 Ile Arg Leu Pro Ser Val Ser Val Val Ser Ser Asp Gly His Leu Trp  
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 Ser Phe Gln Arg Leu Met His Trp Val Thr Arg His Cys Lys Arg Pro  
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 Gln Ile Ala Gln His His Leu Thr Phe Thr Pro His His Ile Asn Ile  
 65                      70                      75                      80  
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 Pro Cys His Pro Arg Asp Cys Ser Pro Ile Leu Tyr His His Glu Val  
 50 55 60  
 Gln Lys Ile Pro Ser Cys Glu Phe Ser Phe Lys Trp Pro Trp Ser Pro  
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 <212> DNA  
 <213> Homo sapiens

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<210> 906

<211> 125

<212> PRT

<213> Homo sapiens

<400> 906

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			20					25					30		
Asp	Ala	Val	Ile	Ser	Val	Ser	Gln	Gly	Leu	Cys	Asp	Arg	Leu	Ala	Gly
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His	Gly	Val	Thr	Ser	Thr	Val	Val	Pro	Asn	Ile	Val	Asp	Val	Glu	Leu
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<211> 332

<212> DNA

<213> Homo sapiens

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<210> 908

<211> 106

<212> PRT

<213> Homo sapiens

&lt;400&gt; 908

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Val Pro Gln Gly Thr Phe Ala Glu Arg Ile Arg Ala Gly Ala Ala Gly
      35           40           45
Ile Ala Ala Phe Phe Thr Pro Thr Gly Tyr Gly Thr Ala Val Gln Lys
      50           55           60
Gly Glu Leu Val Leu Lys Tyr Glu Lys Lys Asp Gly Lys Ala Val Pro
65           70           75           80
Val Met Thr Ser Lys Pro Arg Glu Val Arg Ser Phe Asp Gly Arg Asp
      85           90           95
Tyr Ile Ile Glu Glu Val Ile Lys Asp Glu
      100           105

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&lt;210&gt; 909

&lt;211&gt; 318

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 909

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318

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&lt;210&gt; 910

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 910

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      35           40           45
Arg Glu Ser Arg Gly Cys Val Thr Pro Leu Phe Phe Pro Pro Gln His
      50           55           60
Arg Thr Gly Gly Pro Trp Leu Arg Ile Arg Thr Pro Phe Ala Pro Ala
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 <212> DNA  
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<210> 912  
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 <212> PRT  
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 Pro Gly Trp Trp Lys Ala Asp Leu Arg Thr Leu Asp Phe Phe Phe Phe  
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 Gly Gln Gly Val Pro Gln Gly Leu Leu Gln Arg Pro Gly Cys Ser Val  
 65 70 75 80  
 Val Pro Gly Pro Ser Arg Leu Arg Phe His Pro Leu Ala His Ser Ser  
 85 90 95  
 His Gly Arg Thr Pro Ala Pro Val Pro Thr Pro Glu Val Ser Arg Pro  
 100 105 110  
 Ala Thr Lys Pro Asp Met His Phe Thr Pro Thr Ser His Ala Ala Ser  
 115 120 125  
 Arg

<210> 913  
 <211> 339

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 913

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 tttttcgttc gcgagaacgg taaaaccctc gcaacctcga tgttcacggg ttgtgtcgcc  
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 180  
 aacgaggggg accttatacct taccgctaac gtctttgctc tcatggggctt gcgtcagttg  
 240  
 tatttcctta ttggaagcct gttggaacgt ctgggtgtact tgtcgtcggg actgggtcgtg  
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 339

&lt;210&gt; 914

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 914

Arg Phe Met Ala Trp Phe Arg Arg Thr Val Pro Ala Thr Gly Asp Tyr  
 1 5 10 15  
 Arg Gly Thr Lys Phe Phe Val Arg Glu Asn Gly Lys Thr Leu Ala Thr  
 20 25 30  
 Ser Met Phe Met Val Cys Val Ala Leu Gly Ala Thr Asp Leu Leu Phe  
 35 40 45  
 Ala Leu Asp Ser Ile Pro Ala Ser Tyr Gly Phe Thr Asn Glu Gly Tyr  
 50 55 60  
 Leu Ile Leu Thr Ala Asn Val Phe Ala Leu Met Gly Leu Arg Gln Leu  
 65 70 75 80  
 Tyr Phe Leu Ile Gly Ser Leu Leu Glu Arg Leu Val Tyr Leu Ser Leu  
 85 90 95  
 Gly Leu Val Val Ile Leu Gly Phe Ile Ala Leu Lys Leu Ile Gly His  
 100 105 110  
 Ala

&lt;210&gt; 915

&lt;211&gt; 663

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 915

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 gacagtgaag atcctgttgt ggacattgtt gctgctaccc ctgtcatcaa tggacagtca  
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 180  
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 240

gcaagtgagc agagagtatc catggcatcg tcaggcagct cccagcctga actagtgact  
 300  
 atcccccttga ttaagggccc taaaggggtt gggtttgcaa ttgctgacag ccctactgga  
 360  
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 420  
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 480  
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 660  
 tcc  
 663

&lt;210&gt; 916

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 916

Xaa	Val	Pro	Val	Asn	Gln	Tyr	Val	Asn	Leu	Thr	Leu	Cys	Arg	Gly	Tyr
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Pro	Leu	Pro	Asp	Asp	Ser	Glu	Asp	Pro	Val	Val	Asp	Ile	Val	Ala	Ala
			20					25					30		
Thr	Pro	Val	Ile	Asn	Gly	Gln	Ser	Leu	Thr	Lys	Gly	Glu	Thr	Cys	Met
		35					40					45			
Asn	Pro	Gln	Asp	Phe	Lys	Pro	Gly	Ala	Met	Val	Leu	Glu	Gln	Asn	Gly
	50					55					60				
Lys	Ser	Gly	His	Thr	Leu	Thr	Gly	Asp	Gly	Leu	Asn	Gly	Pro	Ser	Asp
65					70					75				80	
Ala	Ser	Glu	Gln	Arg	Val	Ser	Met	Ala	Ser	Ser	Gly	Ser	Ser	Gln	Pro
			85					90						95	
Glu	Leu	Val	Thr	Ile	Pro	Leu	Ile	Lys	Gly	Pro	Lys	Gly	Phe	Gly	Phe
		100						105					110		
Ala	Ile	Ala	Asp	Ser	Pro	Thr	Gly	Gln	Lys	Val	Lys	Met	Ile	Leu	Asp
		115					120					125			
Ser	Gln	Trp	Cys	Gln	Gly	Leu	Gln	Lys	Gly	Asp	Ile	Ile	Lys	Glu	Ile
	130					135					140				
Tyr	His	Gln	Asn	Val	Gln	Asn	Leu	Thr	His	Leu	Gln	Val	Val	Glu	Val
145				150					155					160	
Leu	Lys	Gln	Phe	Pro	Val	Gly	Ala	Asp	Val	Pro	Leu	Leu	Ile	Leu	Arg
			165					170						175	
Gly	Gly	Pro	Pro	Ser	Pro	Thr	Lys	Ser	Ala	Lys	Met	Lys	Thr	Asp	Lys
		180					185					190			
Lys	Glu	Asn	Ala	Gly	Ser	Leu	Glu	Ala	Ile	Asn	Glu	Pro	Ile	Pro	Gln
		195				200						205			
Pro	Met	Pro	Phe	Pro	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Ser			
	210					215					220				

&lt;210&gt; 917

&lt;211&gt; 615

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 917

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 180  
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 240  
 ggggagatgc tcttcggcct agtgcgccag ggcctcaagt gcgatggctg cgggctgaac  
 300  
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 420  
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 480  
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 615

&lt;210&gt; 918

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 918

Ile Val Asp Gln Lys Phe Pro Glu Cys Gly Phe Tyr Gly Leu Tyr Asp  
 1 5 10 15  
 Lys Ile Leu Leu Phe Lys His Asp Pro Thr Ser Ala Asn Leu Leu Gln  
 20 25 30  
 Leu Val Arg Ser Ser Gly Asp Ile Gln Glu Gly Asp Leu Val Glu Val  
 35 40 45  
 Val Leu Ser Ala Ser Ala Thr Phe Glu Asp Phe Gln Ile Arg Pro His  
 50 55 60  
 Ala Leu Thr Val His Ser Tyr Arg Ala Pro Ala Phe Cys Asp His Cys  
 65 70 75 80  
 Gly Glu Met Leu Phe Gly Leu Val Arg Gln Gly Leu Lys Cys Asp Gly  
 85 90 95  
 Cys Gly Leu Asn Tyr His Lys Arg Cys Ala Phe Ser Ile Pro Asn Asn  
 100 105 110  
 Cys Ser Gly Ala Arg Lys Arg Arg Leu Ser Ser Thr Ser Leu Ala Ser  
 115 120 125  
 Gly His Ser Val Arg Leu Gly Thr Ser Glu Ser Leu Pro Cys Thr Ala  
 130 135 140  
 Glu Glu Glu Pro  
 145



<210> 919  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<400> 919  
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 acaaatgcga tcttgctcga tagcgagcgc ggtgagtacc tcgccaagat gggcccgcgcg  
 120  
 gaagaagact tcatttcgaa cgcgacccat cgtggcgatc acctgaccgc acagcgcgcc  
 180  
 accttcgcca acccgacctt gctcaacgag atggccgtag tcgatgggtga agtgaagaaa  
 240  
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 294

<210> 920  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 920  
 Thr Gly Met Arg Pro Leu Ala Val Leu Gly Asp Asn Ile Thr Thr Asp  
 1 5 10 15  
 His Leu Ser Pro Thr Asn Ala Ile Leu Leu Asp Ser Ala Ala Gly Glu  
 20 25 30  
 Tyr Leu Ala Lys Met Gly Pro Pro Glu Glu Asp Phe Ile Ser Asn Ala  
 35 40 45  
 Thr His Arg Gly Asp His Leu Thr Ala Gln Arg Ala Thr Phe Ala Asn  
 50 55 60  
 Pro Thr Leu Leu Asn Glu Met Ala Val Val Asp Gly Glu Val Lys Lys  
 65 70 75 80  
 Gly Ser Leu Ala Arg Val Glu Pro Glu Gly His Val Met Arg Met Trp  
 85 90 95  
 Glu Ala

<210> 921  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<400> 921  
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 aaccaggacg tgctgttggt catcgacaac atcttccggt tctcccaggc tggttctgag  
 120  
 gtttcaaccc tgctaggtcg tatgccctcg gcggtgggct accagcccaa cttggccgac  
 180  
 gagatgggccc aattgcagga gcgaatcacc tcgacccgtg gtcactccat cacctcgatg  
 240  
 caggccgtct acgtccccgc tgacgattac accgacccgg ctccggcgac gaccttcgcc  
 300

cacctggatg ccaccacgga gctttctcgt gagattgcct ctcgtggcct gtacccggcc  
 360  
 gtggatccgc tggcgtcg  
 378

<210> 922  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 922  
 Thr Arg Leu Arg Ile Ala Leu Thr Gly Leu Thr Met Ala Glu Tyr Phe  
 1 5 10 15  
 Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe  
 20 25 30  
 Arg Phe Ser Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met  
 35 40 45  
 Pro Ser Ala Val Gly Tyr Gln Pro Asn Leu Ala Asp Glu Met Gly Gln  
 50 55 60  
 Leu Gln Glu Arg Ile Thr Ser Thr Arg Gly His Ser Ile Thr Ser Met  
 65 70 75 80  
 Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala  
 85 90 95  
 Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Ser Arg Glu Ile  
 100 105 110  
 Ala Ser Arg Gly Leu Tyr Pro Ala Val Asp Pro Leu Ala Ser  
 115 120 125

<210> 923  
 <211> 571  
 <212> DNA  
 <213> Homo sapiens

<400> 923  
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 caacgcaaga atgtcgaaga agaagacatc ttcgccgccc accttgcgct attggaagac  
 180  
 cccacgctgc tggacgccgc cactggtgcc atcgaacacg gcagcgccgc caccacgcc  
 240  
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<210> 924  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

<400> 924  
 Thr Gly Ile Glu Leu Pro Gln Asp Thr Gly Lys His Val Ala Asp Glu  
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 Gln Leu Gln Arg Leu Asp Thr Ala Leu Glu His Val Arg Gly Glu Ile  
 20 25 30  
 Arg Ile Thr Leu Glu His Ala Arg Gln Arg Lys Asn Val Glu Glu Glu  
 35 40 45  
 Asp Ile Phe Ala Ala His Leu Ala Leu Leu Glu Asp Pro Thr Leu Leu  
 50 55 60  
 Asp Ala Ala Thr Gly Ala Ile Glu His Gly Ser Ala Ala Thr His Ala  
 65 70 75 80  
 Trp Arg Asp Ala Ile Gln Ala Gln Cys Ala Val Leu Leu Ala Leu Gly  
 85 90 95  
 Lys Pro Leu Phe Ala Glu Arg Ala Asn Asp Leu Arg Asp Leu Gln Gln  
 100 105 110  
 Arg Val Leu Arg Ala Leu Leu Gly Glu Ala Trp His Phe Glu Leu Pro  
 115 120 125  
 Ala Gly Pro Ile Phe Arg Xaa Ala Ile Asn Leu Pro Pro Ser Ala Leu  
 130 135 140  
 Leu Gln Leu Ser Ala Gln Asn Ala Val Gly Ile Cys Met Ala Glu Gly  
 145 150 155 160  
 Gly Ala Thr Ser His Val Ala Ile Leu Ala Arg Gly Lys Gly Leu Pro  
 165 170 175  
 Cys Val Val Ala Leu Gly Ala Glu Val Leu Asp Val Pro Gln  
 180 185 190

<210> 925  
 <211> 620  
 <212> DNA  
 <213> Homo sapiens

<400> 925  
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 gtgggtgtgta tgcattggtgt gtgcacgtgt gcactgtgtg tgtgtgtatg catgtgtgtg  
 180  
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 240  
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 300  
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 360  
 ggtgtgtggt gtgtatgcat gtgtgtgcac gtgtgcactg tgtggcaggg gtgtttggtg  
 420  
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 480

tgcccagcag catcacacgc actttggtgc tttataaatg catggtcagt gaggctgcca  
 540  
 gcaccaagct gtccctttac cataacacct ggaatagtca cctgtgataa gctatcacat  
 600  
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 620

<210> 926  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 926  
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys  
 1 5 10 15  
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met  
 20 25 30  
 Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val Cys  
 35 40 45  
 Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Val Cys Leu  
 50 55 60  
 Cys Val Cys Met Val Met Cys Val Cys Thr Val Trp Cys Val Cys Met  
 65 70 75 80  
 Cys Val His Val Cys Thr Val Tyr Ala  
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<210> 927  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 927  
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 240  
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 300  
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 360

<210> 928  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 928  
 Met Glu Leu Leu Glu Ile Val Arg His Asp Gln Arg Glu Glu Ala Phe  
 1 5 10 15  
 Gly Val Leu Phe Arg Ser Phe Gln Gln Gln Thr Gly His Gly Asp Pro

	20		25		30										
Ile	Ser	Gly	Leu	Cys	Phe	Ser	Gly	Gly	His	Pro	Ala	Ile	Leu	Pro	Thr
	35		40		45										
Ser	Ser	Glu	Ala	Gly	Thr	Lys	Pro	Ser	Gln	Glu	Ala	Ala	Gly	Ser	Lys
	50		55		60										
Gly	Gln	Pro	Ala	Gln	Trp	Gly	Gln	Ala	Gly	Thr	Thr	Trp	Lys	Pro	Gln
65			70		75									80	
Arg	Thr	Pro	Asp	Gly	Asn	Val	Thr	Arg	Pro	Ile	His	Gln	Ala	Pro	Val
			85		90									95	
Met	Pro	Ala	Ser	His	Arg	Gly	Glu	Pro	Asp	Pro	Gly	Thr	Ile	Leu	
	100							105						110	

&lt;210&gt; 929

&lt;211&gt; 2340

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 929

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1080

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 2220  
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 2340

<210> 930

<211> 702

<212> PRT

<213> Homo sapiens

<400> 930

Met	Val	Ala	His	Ile	Asn	Asn	Ser	Arg	Leu	Lys	Ala	Lys	Gly	Val	Gly
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Gln	His	Asp	Asn	Ala	Gln	Asn	Phe	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Leu
			20					25					30		
Arg	Ala	Ala	Cys	Leu	Arg	Lys	Gly	Glu	Leu	Phe	Glu	Asp	Pro	Leu	Phe

35	40	45
Pro Ala Glu Pro Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser		
50	55	60
Lys Asn Val Gln Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn		
65	70	75
Asn Pro Leu Phe Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln		80
	85	90
Gly Ile Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr		95
	100	105
Thr Cys Pro Lys Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe		110
	115	120
Lys Lys Asn Tyr Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly		125
	130	135
Gln Trp Val Asn Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp		140
145	150	155
Lys Leu Val Phe Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala		160
	165	170
Leu Leu Glu Lys Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu		175
	180	185
Ser Gly Gly Ser Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val		190
	195	200
Ala Gln Ser Phe Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu		205
	210	215
Leu Arg Lys Ala Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu		220
225	230	235
Val Thr Ser Asp Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val		240
	245	250
Arg Gly His Ala Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg		255
	260	265
Gly Lys Met Glu Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile		270
	275	280
Glu Trp Asn Gly Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val		285
	290	295
Ala Ser Asp Ile Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu		300
305	310	315
Phe Trp Met Ser Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu		320
	325	330
Ile Cys Asn Leu Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr		335
	340	345
Trp His Thr Thr Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala		350
	355	360
Gly Gly Cys Arg Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe		365
	370	375
Lys Ile Ser Leu Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly		380
385	390	395
Asn Val Val Val Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp		400
	405	410
Arg His Ala Arg Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val		415
	420	425
Leu Tyr Ala Val Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu		430
	435	440
Lys Lys Glu Phe Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile		445
	450	455
Phe Thr Asn Ser Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly		460

465                      470                      475                      480  
 Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp  
                                  485                      490                      495  
 Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu  
                                  500                      505                      510  
 Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Lys Val Ser Glu  
                                  515                      520                      525  
 Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly  
                                  530                      535                      540  
 Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg  
 545                      550                      555                      560  
 Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp  
                                  565                      570                      575  
 Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys  
                                  580                      585                      590  
 Leu Gly Leu Leu Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp  
                                  595                      600                      605  
 Met Asp Ile Phe Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn  
                                  610                      615                      620  
 Ser Tyr Glu Met Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn  
 625                      630                      635                      640  
 Asn Lys Val Met Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Gly Leu  
                                  645                      650                      655  
 Ile Ile Asp Phe Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr  
                                  660                      665                      670  
 Met Phe Thr Phe Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile  
                                  675                      680                      685  
 Cys Leu Ser Leu Glu Gln Trp Leu Gln Met Thr Met Trp Gly  
                                  690                      695                      700

<210> 931  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

<400> 931  
 tcgcgaaggg agcctgacat gggccagaaa atcaatcccc atggtttccg tctcggtgtg  
 60  
 acgaccgatc acaagaccgc ctggtacgcc gagaagcagt acgccgagct cgtgggtgag  
 120  
 gatgtcaaga tccgagagtg gctccacaag aatctggagc gcgccggtct ttcgtccatc  
 180  
 gagatcgagc gtcgctccga gcgcgtgacc attttccttt acgccgctcg cccgggcatc  
 240  
 gttatcgggc gcaatggccg ggaggccgag cgcgtgcgtn ntgagctcga aaagctt  
 297

<210> 932  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 932  
 Met Gly Gln Lys Ile Asn Pro His Gly Phe Arg Leu Gly Val Thr Thr



```

1           5           10           15
Asp His Lys Thr Arg Trp Tyr Ala Glu Lys Gln Tyr Ala Glu Leu Val
           20           25           30
Gly Glu Asp Val Lys Ile Arg Glu Trp Leu His Lys Asn Leu Glu Arg
           35           40           45
Ala Gly Leu Ser Ser Ile Glu Ile Glu Arg Arg Ser Glu Arg Val Thr
           50           55           60
Ile Phe Leu Tyr Ala Ala Arg Pro Gly Ile Val Ile Gly Arg Asn Gly
65           70           75           80
Arg Glu Ala Glu Arg Val Arg Xaa Glu Leu Glu Lys Leu
           85           90

```

&lt;210&gt; 933

&lt;211&gt; 305

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 933

```

nnacgcgtcg ccaagctggt gatggccgaa tacaaggggc tcaacgtcat cgtcaaaacc
60
tccgccgatc cggcaagcca agccaatgcc gtgcaggatc tggcgggggc aggcacgcac
120
gcgctggcca tcctgccgac cgaccgggat cagctggttt cggcgatcca gcaggtcaag
180
gacgacggca agttcgtggc gctggtcgac cgtgcgcctt ccgtcaacga caacacgatc
240
cgcgatctct acgtggccgg caacaaccgg gcgctcggcg aagtggcggg caaattcatg
300
ggcga
305

```

&lt;210&gt; 934

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 934

```

Xaa Arg Val Ala Lys Leu Leu Met Ala Glu Tyr Lys Gly Leu Asn Val
1           5           10           15
Ile Val Lys Thr Ser Ala Asp Pro Ala Ser Gln Ala Asn Ala Val Gln
           20           25           30
Asp Leu Ala Gly Ala Gly Ile Asp Ala Leu Ala Ile Leu Pro Thr Asp
           35           40           45
Pro Asp Gln Leu Val Ser Ala Ile Gln Gln Val Lys Asp Asp Gly Lys
           50           55           60
Phe Val Ala Leu Val Asp Arg Ala Pro Ser Val Asn Asp Asn Thr Ile
65           70           75           80
Arg Asp Leu Tyr Val Ala Gly Asn Asn Pro Ala Leu Gly Glu Val Ala
           85           90           95
Gly Lys Phe Met Gly
           100

```

&lt;210&gt; 935

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 935

acgcgtgaag ggctgatgag tgctatgaaa aagccagggg cccgaggaca ctgggggtgga  
60  
caggctcccc tggggaagtc ctcttagaac tgagggatca aactggagg agactgcaag  
120  
gggtacggga taaatgttcc tggatgaagga aacagcaggg gcaaaggccc tgcagcagaa  
180  
aggagcgagg ccctttggag taacagaaaag accatggtga caggagctca gaaagaccac  
240  
tgggtgttaag actataagcc agtggaggcc agattgggga atgggatggg aggggtgctt  
300  
gaagaccatg gtgaggctct cttggtcttt act  
333

&lt;210&gt; 936

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 936

Met	Val	Phe	Lys	His	Pro	Ser	His	Pro	Ile	Pro	Gln	Ser	Gly	Leu	His
1			5					10					15		
Trp	Leu	Ile	Val	Leu	Thr	Pro	Val	Val	Phe	Leu	Ser	Ser	Cys	His	His
		20						25					30		
Gly	Leu	Ser	Val	Thr	Pro	Lys	Gly	Leu	Ala	Pro	Phe	Cys	Cys	Arg	Ala
		35					40					45			
Phe	Ala	Pro	Ala	Val	Ser	Phe	Thr	Arg	Asn	Ile	Tyr	Pro	Val	Pro	Leu
	50					55					60				
Ala	Val	Ser	Ser	Ser	Val	Asp	Pro	Ser	Val	Leu	Arg	Gly	Leu	Pro	Gln
65					70					75				80	
Gly	Ser	Leu	Ser	Thr	Pro	Val	Ser	Ser	Gly	Pro	Trp	Leu	Phe	His	Ser
			85						90					95	
Thr	His	Gln	Pro	Phe	Thr	Arg									
															100

&lt;210&gt; 937

&lt;211&gt; 464

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 937

nnnttatctg cggagggggg ggccaccctg cccacactca tgctgcaggc ctccaccgac  
60  
cggcgggacg acgagctcaa ggatctgttg acggccgacc tcatggacca gcacaacctc  
120  
gaccgtgccc tggcaggggt gcgtgccagt cacgtcatcg acgaagctcg cgccgaggtg  
180  
cagcggcgtg ccgatctcgc ccgtggccat ctcgccatcc ttcccgcagg cgatgccctg  
240  
acggcggttg agaccctgtg cgacgaggtg ggttcccggg cggcctgaac cccgaccctg  
300

ccagntcgcg tcccatctcc tggccgggac cgtccagcg tctgctctct gacagctcat  
 360  
 cgttcttccg acaccaagga gtttctcgtg gcccgatc tcatctcat cggcattggg  
 420  
 cccggcaacc cggactggat caccctggct gccgtcaagg ccan  
 464

<210> 938  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 938  
 Xaa Leu Ser Ala Glu Gly Val Ala Thr Leu Pro Thr Leu Met Leu Gln  
 1 5 10 15  
 Ala Ser Thr Asp Pro Ala Asp Asp Glu Leu Lys Asp Leu Leu Thr Ala  
 20 25 30  
 Asp Leu Met Asp Gln His Asn Leu Asp Arg Ala Leu Ala Gly Leu Arg  
 35 40 45  
 Ala Ser His Val Ile Asp Glu Ala Arg Ala Glu Val Gln Arg Arg Ala  
 50 55 60  
 Asp Leu Ala Arg Gly His Leu Ala Ile Leu Pro Ala Gly Asp Ala Arg  
 65 70 75 80  
 Thr Ala Leu Glu Thr Leu Cys Asp Glu Val Gly Ser Arg Ala Ala  
 85 90 95

<210> 939  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<400> 939  
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 ggactgctgc cggtcgaggt ggacttcgcc gccacgaaga cccttgctt gtcgcacggg  
 120  
 acatggcggg ggatcgaggt tggcggctat gaaatccatc acgggcgtct gtcgttcgct  
 180  
 gaggacgtg aagccttctt cgacggcgta cacgtcggtc cggtatgggg gacgatgtgg  
 240  
 cacggggcat tcgagcacga cgaattccgt cgcacgtggc tggctgacgc ggcccgtcac  
 300  
 gctggatcat cctggcgtcc gactccgac gagctgggtt atcaggctcg acgcgaggcg  
 360  
 atgatcgaac ccctcgccga cgcgt  
 385

<210> 940  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 940  
 Xaa Thr Ile Leu Asp Pro Asp Gly Gln Glu Thr Thr Pro Gly Ser Val

```

      1             5             10             15
Ile Glu Gly Leu Gly Leu Leu Pro Val Glu Val Asp Phe Ala Ala Thr
      20             25             30
Lys Thr Leu Ala Leu Ser His Gly Thr Trp Arg Gly Ile Glu Val Gly
      35             40             45
Gly Tyr Glu Ile His His Gly Arg Leu Ser Phe Ala Glu Asp Ala Glu
      50             55             60
Ala Phe Leu Asp Gly Val His Val Gly Pro Val Trp Gly Thr Met Trp
65             70             75             80
His Gly Ala Phe Glu His Asp Glu Phe Arg Arg Thr Trp Leu Ala Asp
      85             90             95
Ala Ala Arg His Ala Gly Ser Ser Trp Arg Pro His Ser Asp Glu Leu
      100            105            110
Gly Tyr Gln Ala Arg Arg Glu Ala Met Ile Glu Thr Leu Ala Asp Ala
      115            120            125

```

&lt;210&gt; 941

&lt;211&gt; 348

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 941

```

atcttctggt cggcggtgat cacgctggtg accatcggcc tgctgtttgc cggcaacttc
60
gaagccatgc aaaccatggt cgtgctggcc gggetgcegt tctcgtggtg gctgattttc
120
ttcatgttcg gtttgcacaa ggcgatgcgc caggacgtgg ccatggagca ggagcaggca
180
caattggctg aacgtggctg ccggtggttc agcgagcgcc tgaccgcgct ggacctgcaa
240
ccgagccagg gcaccgtgca acgctttatg gacaaacatg tgacgccggc gttggaacaa
300
gcggcgactg cgttgctgta tcaagggtg gaagtgcaga ccctgctt
348

```

&lt;210&gt; 942

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 942

```

Ile Phe Trp Ser Ala Val Ile Thr Leu Val Thr Ile Gly Leu Leu Phe
 1             5             10             15
Ala Gly Asn Phe Glu Ala Met Gln Thr Met Val Val Leu Ala Gly Leu
      20             25             30
Pro Phe Ser Val Val Leu Ile Phe Met Phe Gly Leu His Lys Ala
      35             40             45
Met Arg Gln Asp Val Ala Met Glu Gln Glu Gln Ala Gln Leu Ala Glu
50             55             60
Arg Gly Arg Arg Gly Phe Ser Glu Arg Leu Thr Ala Leu Asp Leu Gln
65             70             75             80
Pro Ser Gln Gly Thr Val Gln Arg Phe Met Asp Lys His Val Thr Pro
      85             90             95
Ala Leu Glu Gln Ala Ala Thr Ala Leu Arg Asp Gln Gly Leu Glu Val

```

100  
Gln Thr Leu Leu  
115

105

110

<210> 943  
<211> 439  
<212> DNA  
<213> Homo sapiens

<400> 943  
ccatggcagg agcagagcag atagagcagg acctcgtctc cttctctttg cattttgtgc  
60  
ctcctctaata gcacccctggg ctccctgctaa cctgtgga aacaccgtct cttctctctc  
120  
ttgccctctt ctgtgatcac atcctcactt ctgagcctat ctgcccattc agtcaatccc  
180  
ccttggttct gggatgctat ttccctggcc gccctcctct aggagtgttt agaaccctca  
240  
ctgtgggcag aagggaggga agatggctga ggtacctgga aagggacgtg tggatccccg  
300  
ggcatggaag gaaggaggca ggagagctag aaaaagggat gagatctaata gttccctaag  
360  
gaacctggct tagtgctggc ccttcacata ctgagacatg gaatccttac tactgttctc  
420  
tgaggaaaga ggctgttcc  
439

<210> 944  
<211> 118  
<212> PRT  
<213> Homo sapiens

<400> 944  
Met Ala Gly Ala Glu Gln Ile Glu Gln Asp Leu Val Ser Phe Ser Leu  
1 5 10 15  
His Phe Val Pro Pro Leu Met His Pro Gly Leu Leu Leu Thr Leu Trp  
20 25 30  
Glu Thr Pro Ser Leu Leu Ser Phe Ala Leu Phe Cys Asp His Ile Leu  
35 40 45  
Thr Ser Glu Pro Ile Cys Pro Ser Ser Gln Ser Pro Leu Val Leu Gly  
50 55 60  
Cys Tyr Phe Pro Gly Arg Leu Pro Leu Gly Val Phe Arg Thr Leu Thr  
65 70 75 80  
Val Gly Arg Arg Glu Gly Arg Trp Leu Arg Tyr Leu Glu Arg Asp Val  
85 90 95  
Trp Ile Pro Gly His Gly Arg Lys Glu Ala Gly Glu Leu Glu Lys Gly  
100 105 110  
Met Arg Ser Asn Val Pro  
115

<210> 945  
<211> 339  
<212> DNA  
<213> Homo sapiens

<400> 945  
 ngaattcgtg aagcgttcca ttttttttc cttttaataa tttcaattgc actttatgtc  
 60  
 gagatggtga tatatatata tactcacaca catatatatg tgtgtgtgtg tatatatgta  
 120  
 tatatatata gcgtgtacaa caaaacatgc actgtttact cagcaccctg tgtttgtctc  
 180  
 agcaatagct tttctaaaga actgctacta tttgaaatgg agggggaggg gggtcctgga  
 240  
 cagagtattg tgcaagttga aagtctctgg atggggctat gtatatccta ccagccaatt  
 300  
 tgggtgcaaa ttggatttga aggcctgcct ctgtccacn  
 339

<210> 946  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 946  
 Xaa Ile Arg Glu Ala Phe His Ile Phe Phe Leu Leu Ile Ile Ser Ile  
 1 5 10 15  
 Ala Leu Tyr Val Glu Met Val Ile Tyr Ile Tyr Thr His Thr His Ile  
 20 25 30  
 Tyr Val Cys Val Cys Ile Tyr Val Tyr Ile Tyr Ser Val Tyr Asn Lys  
 35 40 45  
 Thr Cys Thr Val Tyr Ser Ala Pro Arg Val Cys Leu Ser Asn Ser Phe  
 50 55 60  
 Ser Lys Glu Leu Leu Leu Phe Glu Met Glu Gly Glu Gly Gly Pro Gly  
 65 70 75 80  
 Gln Ser Ile Val Gln Val Glu Ser Leu Trp Met Gly Leu Cys Ile Ser  
 85 90 95  
 Tyr Gln Pro Ile Trp Val Gln Ile Gly Phe Glu Gly Leu Pro Leu Ser  
 100 105 110  
 Thr

<210> 947  
 <211> 648  
 <212> DNA  
 <213> Homo sapiens

<400> 947  
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 ctctggcat cacacctgtg cacgggggtg ggaaggagt ggacaggagt ggacaagtca  
 120  
 agtagtgctg ccggctcaag cgatgcctca gcctttctgc tgtgtgcgaa gctttgcaga  
 180  
 ggagatgatg cttcaaagtt gtccctgttg gggatgagca gccaggcctt tatacactgg  
 240  
 gacagtcagt catggatacg tggatactct ggaaaccctc atccctggag gtctgagccc  
 300

ctggatacca tgcccttctt aggctggagt tgctgccctt gtccatttac cataaaaatt  
 360  
 ggacaagaga ataccaggac acacctgagt ttctcatcgt atgctaaacc tgttcttcca  
 420  
 cgtacatccc caatgtgtac agccctactt tttctgctg atcaagttca attacttctg  
 480  
 ctaagatggt gactattctt gcctgctggt ccttggatgc aaggacccca atgttcaggc  
 540  
 agcctttggt gccttctagc atacgaatca gagcattatc tttaggtgtg gaataagctg  
 600  
 ccccaaaaacc tgttgaagcc agccaggcac tgtgctccct tcacgcgt  
 648

<210> 948  
 <211> 154  
 <212> PRT  
 <213> Homo sapiens

<400> 948  
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 Leu Cys Thr Gly Val Gly Lys Glu Trp Thr Gly Val Asp Lys Ser Ser  
 20 25 30  
 Ser Ala Ala Gly Ser Ser Asp Ala Ser Ala Phe Leu Leu Cys Ala Lys  
 35 40 45  
 Leu Cys Arg Gly Asp Asp Ala Ser Lys Leu Ser Leu Leu Gly Met Ser  
 50 55 60  
 Ser Gln Ala Phe Ile His Trp Asp Ser Gln Ser Trp Ile Arg Gly Tyr  
 65 70 75 80  
 Ser Gly Asn Pro His Pro Trp Arg Ser Glu Pro Leu Asp Thr Met Pro  
 85 90 95  
 Phe Leu Gly Trp Ser Cys Cys Pro Cys Pro Phe Thr Ile Lys Ile Gly  
 100 105 110  
 Gln Glu Asn Thr Arg Thr His Leu Ser Phe Ser Ser Tyr Ala Lys Pro  
 115 120 125  
 Val Leu Pro Arg Thr Ser Pro Met Cys Thr Ala Leu Leu Phe Ser Ala  
 130 135 140  
 Asp Gln Val Gln Leu Leu Leu Arg Trp  
 145 150

<210> 949  
 <211> 661  
 <212> DNA  
 <213> Homo sapiens

<400> 949  
 acgcgtactg gttggctcat tcaactgaaaa tatgatgaca tttaaaggaa atgcaagaat  
 60  
 aagtaatgtg gaattttatc acagtgggtca agaaggcttc agggatagca cagatccaag  
 120  
 atatgctgta acgtttctta acctaggaca gattcaagaa catggctcat cttatatctg  
 180  
 aggctgtgct tttcaccatg gcttctctcc agcaattggt gtatttgga cagatggatt  
 240

ggacatagat gacaacatca ttcactttac agtgggggaa ggcataagaa tatgggggaa  
 300  
 tgccaaccga gtccgagggga atttgattgc actttcggtt tggccaggaa cctatcagaa  
 360  
 cagaaaagat ttaagttcaa ctctctggca tgcagcaatt gagataaata gagggaccaa  
 420  
 tacagtttta cagaataatg tagtggctgg atttggaaga gcaggatacc gcattgatgg  
 480  
 tgaaccttgc ccaggccagt ttaatcctgt ggaaaagtgg tttgacaatg aagcccatgg  
 540  
 aggtttatat gggatctata tgaaccaaga tggccttcct ggatgttctc ttatacaagg  
 600  
 atttaccatt tggacatgct gggattatgg aatttatttt cagaccacag agagtgtgca  
 660  
 c  
 661

<210> 950

<211> 210

<212> PRT

<213> Homo sapiens

<400> 950

Met	Met	Thr	Phe	Lys	Gly	Asn	Ala	Arg	Ile	Ser	Asn	Val	Glu	Phe	Tyr
1				5					10					15	
His	Ser	Gly	Gln	Glu	Gly	Phe	Arg	Asp	Ser	Thr	Asp	Pro	Arg	Tyr	Ala
			20					25					30		
Val	Thr	Phe	Leu	Asn	Leu	Gly	Gln	Ile	Gln	Glu	His	Gly	Ser	Ser	Tyr
		35				40						45			
Ile	Arg	Gly	Cys	Ala	Phe	His	His	Gly	Phe	Ser	Pro	Ala	Ile	Gly	Val
	50					55					60				
Phe	Gly	Thr	Asp	Gly	Leu	Asp	Ile	Asp	Asp	Asn	Ile	Ile	His	Phe	Thr
65					70					75				80	
Val	Gly	Glu	Gly	Ile	Arg	Ile	Trp	Gly	Asn	Ala	Asn	Arg	Val	Arg	Gly
			85						90					95	
Asn	Leu	Ile	Ala	Leu	Ser	Val	Trp	Pro	Gly	Thr	Tyr	Gln	Asn	Arg	Lys
			100					105					110		
Asp	Leu	Ser	Ser	Thr	Leu	Trp	His	Ala	Ala	Ile	Glu	Ile	Asn	Arg	Gly
		115					120						125		
Thr	Asn	Thr	Val	Leu	Gln	Asn	Asn	Val	Val	Ala	Gly	Phe	Gly	Arg	Ala
		130				135						140			
Gly	Tyr	Arg	Ile	Asp	Gly	Glu	Pro	Cys	Pro	Gly	Gln	Phe	Asn	Pro	Val
145					150					155				160	
Glu	Lys	Trp	Phe	Asp	Asn	Glu	Ala	His	Gly	Gly	Leu	Tyr	Gly	Ile	Tyr
			165						170					175	
Met	Asn	Gln	Asp	Gly	Leu	Pro	Gly	Cys	Ser	Leu	Ile	Gln	Gly	Phe	Thr
			180					185					190		
Ile	Trp	Thr	Cys	Trp	Asp	Tyr	Gly	Ile	Tyr	Phe	Gln	Thr	Thr	Glu	Ser
		195					200						205		
Val	His														
															210

<210> 951

<211> 2615



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 951

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60  
acaacccggc catgcttccc cgggtgccaa tgcgaggtgg agaccttcgg ccttttcgac  
120  
agcttcagcc tgactcgggt ggattgtagc ggcttgggccc cccacatcat gccggtgccc  
180  
atccctctgg acacagccca cttggacctg tcctccaacc ggctggagat ggtgaatgag  
240  
tcggtgttgg cggggccggg ctacacgacg ttggctggcc tggatctcag ccacaacctg  
300  
ctcaccagca tctcaccac tgcttctcc cgcttcgct acctggagtc gcttgacctc  
360  
agccacaatg gcctgacagc cctgccagcc gagagcttca ccagctcacc cctgagcgac  
420  
gtgaacctta gccacaacca gctccgggag gtctcagtgt ctgccttcac gacgcacagt  
480  
cagggccggg cactacagc ggacctctcc cacaacctct caccgectcg tgccccaccc  
540  
cacgagggcc ggctgcctg cgcccaccat tcagagcctg aacctggcct ggaaccggct  
600  
ccatgcctg cccaacctg agacttgccc ctgcgtacc tgagcctgga tgggaacct  
660  
ctagctgtca ttggtccggg tgcttcgcg gggctgggag gccttacaca cctgtctctg  
720  
gccagcctgc agaggtccc tgagctggcg cccagtggct tccgtgagct accgggcctg  
780  
caggtcctgg acctgtcggg caaccccaag cttaactggg caggagctga ggtgttttca  
840  
ggcctgagct ccctgcagga gctggacctt tcgggcacca acctggtgcc cctgcctgag  
900  
gcgctgctcc tccacctccc ggactgcag agcgtcagcg tgggccagga tgtgcggtgc  
960  
cggcgccctg tgcgggaggg cacctacccc cggaggcctg gctccagccc caaggtggcc  
1020  
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1080  
gtgtggccca gggccacata acagactgct gtcttgggct gcctcaggtc ccgagtaact  
1140  
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1200  
ggagttgtgg gcctaggaga ggctttggac ctgggagcca cacctaggag caaagtctca  
1260  
cccctttgtc tacgttgctt ccccaaacca tgagcagagg gacttcgatg ccaaaccaga  
1320  
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1380  
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 1680  
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 1740  
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 1860  
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 1980  
 gactggaaac ctaccatctt tccctgagc atcctctaga tgctgccccca aggagttgct  
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 aataaacact ataaaatgaa gactaaggaa acagcccagg gttcggaagc tgagatgcta  
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 2615

&lt;210&gt; 952

&lt;211&gt; 357

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 952

Xaa Pro Ala Pro Thr Met Pro Trp Pro Leu Leu Leu Leu Ala Val  
 1 5 10 15  
 Ser Gly Ala Gln Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu  
 20 25 30  
 Val Glu Thr Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp  
 35 40 45  
 Cys Ser Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp  
 50 55 60  
 Thr Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu

65                                      70                                      75                                      80  
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu  
    85                                      90                                      95  
 Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu  
    100                                      105                                      110  
 Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu Thr Ala Leu  
    115                                      120                                      125  
 Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser  
    130                                      135                                      140  
 His Asn Gln Leu Arg Glu Val Ser Val Ser Ala Phe Thr Thr His Ser  
 145                                      150                                      155                                      160  
 Gln Gly Arg Ala Leu His Val Asp Leu Ser His Asn Leu Ser Pro Pro  
    165                                      170                                      175  
 Arg Ala Pro Pro His Glu Gly Arg Pro Ala Cys Ala His His Ser Glu  
    180                                      185                                      190  
 Pro Glu Pro Gly Leu Glu Pro Ala Pro Cys Arg Ala Gln Pro Arg Asp  
    195                                      200                                      205  
 Leu Pro Leu Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile  
    210                                      215                                      220  
 Gly Pro Gly Ala Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu  
 225                                      230                                      235                                      240  
 Ala Ser Leu Gln Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu  
    245                                      250                                      255  
 Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn  
    260                                      265                                      270  
 Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu  
    275                                      280                                      285  
 Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu  
    290                                      295                                      300  
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys  
 305                                      310                                      315                                      320  
 Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser  
    325                                      330                                      335  
 Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg  
    340                                      345                                      350  
 Gly Pro Thr Ile Leu  
    355

&lt;210&gt; 953

&lt;211&gt; 347

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 953

acgcgtgaag ccatccctgt gcgcaggcca gtctcgcggg ggtcaccacg gagcgtgtgc  
 60  
 accacacttt ccccatccct tgatccatca ttgggcgttg aggttttccc atgtcttgac  
 120  
 tgttgtaact ggcggctctg cggagtaacc gctgcggaca cacagtagga cgggaggag  
 180  
 aagccattgc gtttcaccct ttcattggccc ttcctttccc cttccaagtg agctctttga  
 240  
 ggtgagtcac ggagggcagt gtccctctgc atcctgtctg gggttgtcaa atatggccaa  
 300

gtgggctcca tcggggcagc ggggtggggtg ggggggtgtct gtcagag  
347

<210> 954

<211> 103

<212> PRT

<213> Homo sapiens

<400> 954

Met	Glu	Pro	Thr	Trp	Pro	Tyr	Leu	Thr	Thr	Pro	Asp	Arg	Met	Gln	Arg
1				5				10					15		
Asp	Thr	Ala	Leu	His	Asp	Ser	Pro	Gln	Arg	Ala	His	Leu	Glu	Gly	Glu
		20						25				30			
Arg	Lys	Gly	His	Glu	Arg	Val	Lys	Arg	Asn	Gly	Phe	Ser	Leu	Pro	Ser
	35						40				45				
Tyr	Cys	Val	Ser	Ala	Ala	Val	Thr	Pro	Gln	Ser	Arg	Gln	Val	Gln	Gln
	50					55				60					
Ser	Arg	His	Gly	Lys	Thr	Ser	Thr	Pro	Asn	Asp	Gly	Ser	Arg	Asp	Gly
65				70					75					80	
Glu	Ser	Val	Val	His	Thr	Leu	Arg	Gly	Asp	Pro	Arg	Glu	Thr	Gly	Leu
				85				90						95	
Arg	Thr	Gly	Met	Ala	Ser	Arg									
				100											

<210> 955

<211> 634

<212> DNA

<213> Homo sapiens

<400> 955

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ctctgcagggt gaatgggttct gcagggtgaag ggctctgcag gtgaacgggt ctgcagggtga  
120  
agggctctgc aggtgaacgg ttctgcagggt gagcggctct gcaggtgagc ggctctgcat  
180  
gtgagtgcct ctgtgactgg ctgcgaagca gcatttgtgc acacttgact ggccacaaca  
240  
gaatgttctt ctctgttctc agcactgagg aggaagctcc tgcctaagcg accacagcca  
300  
ggcaccgct ccatggagac attgctctct ccagactcca ttcagactca ggaaacctga  
360  
gctcctggaa tgcaggctga ggcagctccc acacaaaagc tatctactct ggcagttatc  
420  
agaggctcc gttgcacaaa tcacacacct actgtgectg acgtggctgg gctccagca  
480  
ggacccgctc ctgagaacac acgggtgcta gtccaagttc acagcacggc tcaagtcact  
540  
cccacaaacc tctctataca aacacacaaa gctctgggag gctaccctgc atccaagagt  
600  
caccatctca cacctggaac aagggttacg gccg  
634

<210> 956

<211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 956  
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 Gly Arg Leu Gly Arg Ser Phe Leu Leu Ser Ala Asp Asn Arg Glu Glu  
 20 25 30  
 His Ser Val Val Ala Ser Gln Val Cys Thr Asn Ala Ala Cys Glu Pro  
 35 40 45  
 Val Thr Glu Ala Leu Thr Cys Arg Ala Ala His Leu Gln Ser Arg Ser  
 50 55 60  
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Leu His Leu Gln Asn Arg Ser  
 65 70 75 80  
 Pro Ala Glu Pro Phe Thr Cys Arg Thr Ile His Leu Gln Ser Arg Ser  
 85 90 95  
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Ala His Leu Gln Ser Pro Ser  
 100 105 110  
 Arg

<210> 957  
 <211> 823  
 <212> DNA  
 <213> Homo sapiens

<400> 957  
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 gcgctccaag cttcaggagg cccagggaga gcacgtcctg ccggccaccc agcacagcgt  
 120  
 gtacctctg gccaccacgc actgcgcagc cgtggtgtcc agcctcctgg gcagccctt  
 180  
 gcccttgga aggtaccacg ctcagactcc aggccttaggg gtccctctgg aatgatgctc  
 240  
 cccctggaat gatgctcccc gagccctcca cccggctctg caccctgact ttctgcatga  
 300  
 gttcccatgg ctgtaggcca cgtgggacag aaagtacat ggagccaggc cccagtctct  
 360  
 caggtaccca cggggacctc tcctctccag gcgttttggg atcctcactg gctccggtgg  
 420  
 gccctgcaca gcacccccac agggaagctg ctgtttctgc cttcctctaa ggtcccaaaa  
 480  
 ctgcctggct gctctgttgg cccaggtc cagcacacac tggaggctgc cctcaccct  
 540  
 gtgtcttgg tccggtact ccaagccttg tcctctgcag ggcctccact gctgcctgtg  
 600  
 agcagacccc tgggaactgc ctgatctgag cccctcagg agcccaagga caacctgtc  
 660  
 tgtaccatac atcactatgt cttcccaagc tcacacctcc cagctcccag caaagggcag  
 720  
 ggcggtgcta ccaccacca gccactggg gtcccccttc ctgcccagg cctccggagc  
 780

atgggtctgc tggcccttcc tttctttgcc tcttagtctg gaa  
823

<210> 958

<211> 105

<212> PRT

<213> Homo sapiens

<400> 958

Met	Ala	Val	Gly	His	Val	Gly	Gln	Lys	Val	Thr	Trp	Ser	Gln	Ala	Pro
1				5					10					15	
Val	Ser	Gln	Val	Pro	Thr	Gly	Thr	Ser	Pro	Leu	Gln	Ala	Phe	Trp	Asp
			20					25					30		
Pro	His	Trp	Leu	Arg	Trp	Ala	Leu	His	Ser	Thr	Pro	Thr	Gly	Lys	Leu
		35				40					45				
Leu	Phe	Leu	Pro	Ser	Ser	Lys	Val	Pro	Lys	Leu	Pro	Gly	Cys	Ser	Val
	50					55				60					
Gly	Pro	Arg	Leu	Gln	His	Thr	Leu	Glu	Ala	Ala	Pro	His	Pro	Val	Ser
65				70					75					80	
Trp	Phe	Arg	Leu	Leu	Gln	Ala	Leu	Ser	Ser	Ala	Gly	His	Pro	Leu	Leu
			85					90						95	
Pro	Val	Ser	Arg	Pro	Leu	Gly	Thr	Ala							
			100					105							

<210> 959

<211> 586

<212> DNA

<213> Homo sapiens

<400> 959

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120  
ctggcagtgt ggtgccagga taacaacctc tccctcaacg tgatcaagac cacgaagatg  
180  
atcgtggact acaggaaaag gagggctcag caccgccccca ttctcattga tggggctgta  
240  
tgaggagccag ttgagagctt caagttcctt ggtgtccaca tcaccatcga actatcatgg  
300  
tccaaacaca ccaagacagt agtgaagagg gtgcgacaat gcctattcca cctcggtaga  
360  
caaaaaagat ttggaatgga tcctcagacc ctcaaaaagt ttgacatcta caccatcgag  
420  
agcatcatga ctggttgcac caccgectgg tatggcaact gctcggcctc cgaccgcaag  
480  
gcactacaga gggtagtgcg tacggcccag tacatcactg gggctaagct tcctgccatc  
540  
caggacctct ataccaggcg gtgtcagcgg aagaccctga caattg  
586

<210> 960

<211> 195

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 960

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Xaa His Asp Cys Met Ala Lys His Asp Ser Asn Thr Ile Ile Lys Phe
 1           5           10           15
Ala Asp Asp Thr Thr Val Val Gly Leu Ile Thr Asp Asn Asp Glu Ala
      20           25           30
Ala Tyr Arg Glu Glu Val Arg Asp Leu Ala Val Trp Cys Gln Asp Asn
      35           40           45
Asn Leu Ser Leu Asn Val Ile Lys Thr Thr Lys Met Ile Val Asp Tyr
 50           55           60
Arg Lys Arg Arg Val Glu His Ala Pro Ile Leu Ile Asp Gly Ala Val
65           70           75           80
Trp Glu Pro Val Glu Ser Phe Lys Phe Leu Gly Val His Ile Thr Ile
      85           90           95
Glu Leu Ser Trp Ser Lys His Thr Lys Thr Val Val Lys Arg Val Arg
      100          105          110
Gln Cys Leu Phe His Leu Gly Arg Gln Lys Arg Phe Gly Met Asp Pro
      115          120          125
Gln Thr Leu Lys Lys Phe Asp Ile Tyr Thr Ile Glu Ser Ile Met Thr
      130          135          140
Gly Cys Ile Thr Ala Trp Tyr Gly Asn Cys Ser Ala Ser Asp Arg Lys
      145          150          155          160
Ala Leu Gln Arg Val Val Arg Thr Ala Gln Tyr Ile Thr Gly Ala Lys
      165          170          175
Leu Pro Ala Ile Gln Asp Leu Tyr Thr Arg Arg Cys Gln Arg Lys Thr
      180          185          190
Leu Thr Ile
      195

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&lt;210&gt; 961

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 961

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acgcgttgtc gtctctccgt agaccattca gtttggcaaa acttccactg gagtctgtgc
60
atgactggat ggtctctttg acagccctgt caaggaatac caacagaata ttgattctcc
120
taaaactgtat agtaacctgc taaccagtcg gaaagagcta ccaccaatg gagatactaa
180
atccatggta atggaccatc gagggcaacc tccagagttg gctgctcttc ccactcctga
240
gtctacaccc gtgcttcacc agaagaccct gcaggccatg aagagccact cagaaaaggc
300
ccatggccat ggagcttcaa ggaaagaaac cctcagttt tttccgtcta gtccgccacc
360
tcattcccca ataagtcatg ggcataatcc cagtgccatt gttcttccaa atgctaccca
420
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480
cattgatcac cccttcacgc gt
502

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<210> 962  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 962  
 Met Val Met Asp His Arg Gly Gln Pro Pro Glu Leu Ala Ala Leu Pro  
   1                  5                  10                  15  
 Thr Pro Glu Ser Thr Pro Val Leu His Gln Lys Thr Leu Gln Ala Met  
                   20                  25                  30  
 Lys Ser His Ser Glu Lys Ala His Gly His Gly Ala Ser Arg Lys Glu  
           35                  40                  45  
 Thr Pro Gln Phe Phe Pro Ser Ser Pro Pro Pro His Ser Pro Ile Ser  
   50                  55                  60  
 His Gly His Ile Pro Ser Ala Ile Val Leu Pro Asn Ala Thr His Asp  
 65                  70                  75                  80  
 Tyr Asn Thr Ser Phe Ser Asn Ser Asn Ala His Lys Ala Glu Lys Lys  
                   85                  90                  95  
 Leu Gln Asn Ile Asp His Pro Phe Thr Arg  
                   100                  105

<210> 963  
 <211> 1298  
 <212> DNA  
 <213> Homo sapiens

<400> 963  
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 120  
 acgccaccca gggccagtcg ggtctgctca cagcccagag aggccgcgtg tccagccgcg  
 180  
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 240  
 ggccctgtag agagccagca gccaccatgg cgaaggagga agatgaggag aagaaagcca  
 300  
 agaaagggaa gaaggggaag aaggcaccgg acccgagaga gcccaaacgg agcctgaagg  
 360  
 ggacgtcgcg ggtgttcatg ggcttccgcg accgaacacc caagatctac aagaagggcc  
 420  
 agttccgcag cgcctcgggc ttcttctggg gcctccacac cgccccccac aagaccaagc  
 480  
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 540  
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 600  
 caggccgcg tggctacggc cgcctcgggc cgcgcgcccc gtcactcagc aaagcgtcca  
 660  
 cggccatcaa ctggctcaca aaaaagttcc tcctcaagaa ggccgaggag tcgggcagcg  
 720  
 aacagggcac agtggacgcc tggctgcagc gctcagctc ccgcatgggc tcccgaaaac  
 780



tccccctccc gtcgggtgcc gagatcctgc ggcctggggg ccggtccgg aggttcccc  
 840  
 gcagccgcag catctacgcg tcaggcgagc ccctgggctt cctgcccttc gaggacgagg  
 900  
 ccccatcca tcaactcgggc tcccgcaagt cgctgtacgg gcttgagggc ttccaggacc  
 960  
 tgggcgagta ttatgactat caccgcgacg gcgacgacta ctacgaccgg cagtcaactcc  
 1020  
 accgctacga ggagcaggaa ccctacctgg cgggcctcgg cccctacagc ccggcctggc  
 1080  
 caccctacgg cgaccactac tacgggtacc cgcccaggga tccctacgac tactaccacc  
 1140  
 ccgactatta cggtagggccc gttgatccgg ggtacaccta cggctacggc tacgacgatt  
 1200  
 acgaaccccc atatgcgccc ccgtcggggg actcgtctcc ttacagctac cagcatgggt  
 1260  
 acgagggcga ggcgcaccct tatggctact acctggat  
 1298

<210> 964

<211> 235

<212> PRT

<213> Homo sapiens

<400> 964

Ser	Ala	Ser	Gln	Ala	Ala	Val	Ala	Thr	Ala	Ala	Cys	Gly	Arg	Ala	Pro
1			5					10						15	
Gly	His	Ser	Ala	Lys	Arg	Pro	Arg	Pro	Ser	Thr	Gly	Ser	Gln	Lys	Ser
			20					25					30		
Ser	Ser	Ser	Arg	Arg	Pro	Arg	Ser	Arg	Ala	Ala	Asn	Arg	Pro	Gln	Trp
			35				40					45			
Thr	Pro	Gly	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Trp	Ala	Pro	Ala	Asn	Ser
			50				55				60				
Pro	Ser	Arg	Arg	Val	Pro	Arg	Ser	Cys	Gly	Leu	Gly	Ala	Gly	Ser	Gly
65				70					75					80	
Gly	Ser	Pro	Ala	Ala	Ala	Ala	Ser	Thr	Arg	Gln	Ala	Ser	Pro	Trp	Ala
			85						90					95	
Ser	Cys	Pro	Ser	Arg	Thr	Arg	Pro	His	Ser	Ile	Thr	Arg	Ala	Pro	Ala
			100					105					110		
Ser	Arg	Cys	Thr	Gly	Leu	Arg	Ala	Ser	Arg	Thr	Trp	Ala	Ser	Ile	Met
			115				120					125			
Thr	Ile	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Gly	Ser	His	Ser	Thr	
			130				135					140			
Ala	Thr	Arg	Ser	Arg	Asn	Pro	Thr	Trp	Arg	Ala	Ser	Ala	Pro	Thr	Ala
145				150					155					160	
Arg	Pro	Gly	His	Pro	Thr	Ala	Thr	Thr	Thr	Thr	Gly	Thr	Arg	Pro	Arg
			165						170					175	
Ile	Pro	Thr	Thr	Thr	Thr	Thr	Pro	Thr	Ile	Thr	Val	Ala	Pro	Leu	Ile
			180					185					190		
Arg	Gly	Thr	Pro	Thr	Ala	Thr	Ala	Thr	Thr	Ile	Thr	Asn	Pro	His	Met
			195				200					205			
Arg	Pro	Arg	Arg	Gly	Thr	Arg	Leu	Leu	Thr	Ala	Thr	Thr	Met	Gly	Thr
			210				215					220			
Arg	Ala	Arg	Arg	Thr	Leu	Met	Ala	Thr	Thr	Trp					

947

cgggttcgcc agccaaatgg cggtgcaggc tccagcatcc agtccggtgc cttcggcacc  
 240  
 cccgcactgc gcagagaggc cgccagaaac gatggcaccg gcggcgcggg aggtgataca  
 300  
 ggcgcttcgg ccggagcgct cacggactcc ggcactacag gtgcagcttg cgcttcctgc  
 360  
 ggcggagcaa cagggctcact tcgaggcggg gat  
 393

<210> 968

<211> 125

<212> PRT

<213> Homo sapiens

<400> 968

Pro	Ala	Arg	Ser	Asp	Thr	Glu	Leu	Val	Val	Ser	Thr	Asp	Ser	Gly	Ala
1			5						10					15	
Glu	Ala	Ser	Gly	Ser	Ser	Ser	Ala	Ser	Ala	Pro	Val	Gly	Thr	Glu	Glu
		20					25					30			
Ser	Pro	Ser	Ala	Ser	Ala	Ser	Ala	Ala	Ala	Trp	Ala	Ala	Pro	Asp	Ser
		35				40					45				
Ala	Gly	Gly	Thr	Phe	Ser	Arg	Val	Arg	Gln	Pro	Asn	Gly	Val	Ala	Gly
	50					55				60					
Ser	Ser	Ile	Gln	Ser	Gly	Ala	Phe	Gly	Thr	Pro	Ala	Leu	Arg	Arg	Glu
65				70					75					80	
Ala	Ala	Arg	Asn	Asp	Gly	Thr	Gly	Gly	Ala	Gly	Gly	Asp	Thr	Gly	Ala
			85					90					95		
Ser	Ala	Gly	Ala	Leu	Thr	Asp	Ser	Gly	Thr	Thr	Gly	Ala	Ala	Cys	Ala
		100						105					110		
Ser	Cys	Gly	Gly	Ala	Thr	Gly	Ser	Leu	Arg	Gly	Gly	Asp			
		115					120					125			

<210> 969

<211> 880

<212> DNA

<213> Homo sapiens

<400> 969

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 120  
 atgaattttc gagtaaaactt acatagaatg cctatgagac acaggaagaa ggcagcagac  
 180  
 aagaatctta ccctgccgtc tttagtatgt gaagtactgg acctgatggg agagttttatt  
 240  
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 420  
 gccaaacaca acattttttac attagccctt atgattgtga acctatttaa tatgtttatc  
 480

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 780  
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<210> 970

<211> 263

<212> PRT

<213> Homo sapiens

<400> 970

Met	Thr	Met	His	Phe	Cys	Met	Met	Ile	Asn	Met	Asn	Phe	Arg	Val	Asn
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Leu	His	Arg	Met	Pro	Met	Arg	His	Arg	Lys	Lys	Ala	Ala	Asp	Lys	Asn
			20					25					30		
Leu	Thr	Leu	Pro	Ser	Leu	Val	Cys	Glu	Val	Leu	Asp	Leu	Met	Val	Glu
	35					40					45				
Phe	Ile	Val	Thr	His	Met	Met	Lys	Glu	Phe	Pro	Met	Asp	Leu	Tyr	Ile
50					55					60					
Arg	Cys	Ile	Gln	Val	Val	His	Lys	Leu	Leu	Cys	Tyr	Gln	Lys	Lys	Cys
65				70						75				80	
Arg	Val	Arg	Leu	His	Tyr	Thr	Trp	Arg	Glu	Leu	Trp	Ser	Ala	Leu	Ile
			85					90					95		
Asn	Leu	Leu	Lys	Phe	Leu	Met	Ser	Asn	Glu	Thr	Val	Leu	Leu	Ala	Lys
			100					105					110		
His	Asn	Ile	Phe	Thr	Leu	Ala	Leu	Met	Ile	Val	Asn	Leu	Phe	Asn	Met
	115						120					125			
Phe	Ile	Thr	Tyr	Gly	Asp	Thr	Phe	Leu	Pro	Thr	Pro	Ser	Ser	Tyr	Asp
130					135						140				
Glu	Leu	Tyr	Tyr	Glu	Ile	Ile	Arg	Met	His	Gln	Ser	Phe	Asp	Asn	Leu
145				150						155				160	
Tyr	Ser	Met	Val	Leu	Arg	Leu	Ser	Thr	Asn	Ala	Gly	Gln	Trp	Lys	Glu
			165					170					175		
Ala	Ala	Ser	Lys	Val	Thr	His	Ala	Leu	Val	Asn	Ile	Arg	Ala	Ile	Ile
			180					185					190		
Asn	His	Phe	Asn	Pro	Lys	Ile	Glu	Ser	Tyr	Ala	Ala	Val	Asn	His	Ile
	195						200					205			
Ser	Gln	Leu	Ser	Glu	Glu	Gln	Val	Leu	Glu	Val	Val	Arg	Ala	Asn	Tyr
	210				215						220				
Asp	Thr	Leu	Thr	Leu	Lys	Leu	Gln	Asp	Gly	Leu	Asp	Gln	Tyr	Glu	Arg
225				230						235				240	
Tyr	Ser	Glu	Gln	His	Lys	Glu	Ala	Ala	Phe	Phe	Lys	Glu	Leu	Val	Arg
			245					250					255		
Ser	Ile	Ser	Thr	Asn	Val	Arg									

260

<210> 971  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<400> 971  
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 120  
 aatcccaacc ccaatacct ggttgtaac ggagacgaat ccgaaccggg cacgtgcaag  
 180  
 gacatgccgc tcattatggc aagcccgac acgcttgctg aaggtgctct tatctccgc  
 240  
 tacgctttcg gatccgagca ggctttcacc tacctccgtg gagaagttgt tcaggtagcc  
 300  
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 337

<210> 972  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 972  
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 Asp Ser Gly Leu Arg Gly Arg Gly Gly Ala Gly Phe Pro Thr Gly Val  
 20 25 30  
 Lys Trp Ser Phe Val Pro Gln Asn Asn Pro Asn Pro Lys Tyr Leu Val  
 35 40 45  
 Val Asn Gly Asp Glu Ser Glu Pro Gly Thr Cys Lys Asp Met Pro Leu  
 50 55 60  
 Ile Met Ala Ser Pro His Thr Leu Val Glu Gly Ala Leu Ile Ser Arg  
 65 70 75 80  
 Tyr Ala Phe Gly Ser Glu Gln Ala Phe Ile Tyr Leu Arg Gly Glu Val  
 85 90 95  
 Val Gln Val Ala Arg Arg Leu Glu Glu Lys Lys Lys Met Arg Xaa Xaa  
 100 105 110

<210> 973  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 973  
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 120  
 ccgggacctt ctgtataggc atcacttagg aaccagtcag accatcagat tctcaggacc  
 180

cactggatca actgagtcag gaactcaggg ttttcaacac atcctccggg gggattccag  
 240  
 tggctgtgta actttgagga ccactggcaa agtggctctg gggtcagaga tccgagttca  
 300  
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 360

<210> 974

<211> 91

<212> PRT

<213> Homo sapiens

<400> 974

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Tyr	Arg	His	His	Leu	Gly	Thr	Ser	Gln	Thr	Ile	Arg	Phe	Ser	Gly	Pro
			20					25					30		
Thr	Gly	Ser	Thr	Glu	Ser	Gly	Thr	Gln	Gly	Phe	Gln	His	Ile	Leu	Arg
		35					40				45				
Gly	Asp	Ser	Ser	Gly	Cys	Val	Thr	Leu	Arg	Thr	Thr	Gly	Lys	Val	Ala
	50					55					60				
Leu	Gly	Ser	Glu	Ile	Arg	Val	His	Ile	Leu	Gly	Leu	Pro	Leu	Thr	Asp
65				70					75					80	
Cys	Asn	Gly	Gly	Gln	Val	Thr	Cys	Arg	Ala	Gln					
				85					90						

<210> 975

<211> 2604

<212> DNA

<213> Homo sapiens

<400> 975

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 120  
 ccttggataa gtggtttctg attttgagag gacagcagag ggctgtatca cacaagacat  
 180  
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 240  
 tgaccagcca cgatgcaggt tgaagaagcc accggtcagg ctgcggggccg tcgtcgggga  
 300  
 aacgtggtgc gaaggggtgtt tggccgcac cggcgctttt tcagtcgcag gcggaatgag  
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 420  
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 480  
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 540  
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 600  
 gcagtgggga tttttaccct tgaatactcc gtgcagcgag tgcgtcagct ccgtgaagaa  
 660

tttgatcaag gtctggatgt agtgctggat gacaatcaga atgtgcatga tgtggctgca  
720  
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1260  
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1380  
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1980  
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2160  
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 2580  
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 2604

<210> 976

<211> 411

<212> PRT

<213> Homo sapiens

<400> 976

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Asn	Val	Val	Arg	Arg	Val	Phe	Gly	Arg	Ile	Arg	Arg	Phe	Phe	Ser	Arg
			20					25					30		
Arg	Arg	Asn	Glu	Pro	Thr	Leu	Pro	Arg	Glu	Phe	Thr	Arg	Arg	Gly	Arg
		35					40					45			
Arg	Gly	Ala	Val	Ser	Val	Asp	Ser	Leu	Ala	Glu	Leu	Glu	Asp	Gly	Ala
	50					55					60				
Leu	Leu	Leu	Gln	Thr	Leu	Gln	Leu	Ser	Lys	Ile	Ser	Phe	Pro	Ile	Gly
65					70					75				80	
Gln	Arg	Leu	Leu	Gly	Ser	Lys	Arg	Lys	Met	Ser	Leu	Asn	Pro	Ile	Ala
			85						90					95	
Lys	Gln	Ile	Pro	Gln	Val	Val	Glu	Ala	Cys	Cys	Gln	Phe	Ile	Glu	Lys
			100					105					110		
His	Gly	Leu	Ser	Ala	Val	Gly	Ile	Phe	Thr	Leu	Glu	Tyr	Ser	Val	Gln
	115						120					125			
Arg	Val	Arg	Gln	Leu	Arg	Glu	Glu	Phe	Asp	Gln	Gly	Leu	Asp	Val	Val
	130					135					140				
Leu	Asp	Asp	Asn	Gln	Asn	Val	His	Asp	Val	Ala	Ala	Leu	Leu	Lys	Glu
145					150					155				160	
Phe	Phe	Arg	Asp	Met	Lys	Asp	Ser	Leu	Leu	Pro	Asp	Asp	Leu	Tyr	Met
			165						170					175	
Ser	Phe	Leu	Leu	Thr	Ala	Thr	Leu	Lys	Pro	Gln	Asp	Gln	Leu	Ser	Ala
			180					185					190		
Leu	Gln	Leu	Leu	Val	Tyr	Leu	Thr	Pro	Pro	Cys	His	Ser	Asp	Thr	Leu
	195						200					205			
Glu	Arg	Leu	Leu	Lys	Ala	Leu	His	Lys	Ile	Thr	Glu	Asn	Cys	Glu	Asp
	210					215					220				
Ser	Ile	Gly	Ile	Asp	Gly	Gln	Leu	Val	Pro	Gly	Asn	Arg	Met	Thr	Ser
225					230					235				240	
Thr	Asn	Leu	Ala	Leu	Val	Phe	Gly	Ser	Ala	Leu	Leu	Lys	Lys	Gly	Lys
			245						250					255	
Phe	Gly	Lys	Arg	Glu	Ser	Arg	Lys	Thr	Lys	Leu	Gly	Ile	Asp	His	Tyr
			260					265				270			
Val	Ala	Ser	Val	Asn	Val	Val	Arg	Ala	Met	Ile	Asp	Asn	Trp	Asp	Val



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      275              280              285
Leu Phe Gln Val Pro Pro His Ile Gln Arg Gln Val Ala Lys Arg Val
 290              295              300
Trp Lys Ser Ser Pro Glu Ala Leu Asp Phe Ile Arg Arg Arg Asn Leu
305              310              315              320
Arg Lys Ile Gln Ser Ala Arg Ile Lys Met Glu Glu Asp Ala Leu Leu
      325              330              335
Ser Asp Pro Val Glu Thr Ser Ala Glu Ala Arg Ala Ala Val Leu Ala
      340              345              350
Gln Ser Lys Pro Ser Asp Glu Gly Ser Ser Glu Glu Pro Ala Val Pro
      355              360              365
Ser Gly Thr Ala Arg Ser His Asp Asp Glu Glu Gly Ala Gly Asn Pro
      370              375              380
Pro Ile Pro Glu Gln Asp Arg Pro Leu Leu Arg Val Pro Arg Glu Lys
385              390              395              400
Glu Ala Lys Thr Gly Val Ser Tyr Phe Phe Pro
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<210> 977  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

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120
gagggcaacc ttaactatgg aggagtttgc ctggcgctcg acgcccagtt cagtgaattc
180
ctgggaagca.tggggccggc acagtttgtg ggccgccaga ccctggccac cacacccatg
240
ggggatgtgg agatcggctc gcaggagcgg aacggtcagt tggaggtgga cattatccag
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378

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<210> 978  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

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<400> 978
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Glu Met Pro Ser Arg Thr Leu Arg Gln Ala Ser His Glu Ser Ile Glu
      20              25              30
Asp Ser Met Asn Ser Tyr Gly Ser Glu Gly Asn Leu Asn Tyr Gly Gly
      35              40              45
Val Cys Leu Ala Ser Asp Ala Gln Phe Ser Asp Phe Leu Gly Ser Met
      50              55              60
Gly Pro Ala Gln Phe Val Gly Arg Gln Thr Leu Ala Thr Thr Pro Met

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65		70		75		80									
Gly	Asp	Val	Glu	Ile	Gly	Leu	Gln	Glu	Arg	Asn	Gly	Gln	Leu	Glu	Val
				85					90					95	
Asp	Ile	Ile	Gln	Ala	Arg	Gly	Leu	Thr	Ala	Lys	Pro	Gly	Ser	Lys	Thr
			100					105						110	
Leu	Pro	Ala	Ala	Tyr	Ile	Lys	Ala	Tyr	Leu	Leu	Glu	Met	Ala		
		115					120					125			

&lt;210&gt; 979

&lt;211&gt; 3500

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 979

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1200

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<213> Homo sapiens

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Thr	Ala	Pro	Val	Gly	Trp	Glu	Leu	Val	Arg	Val	Glu	His	Val	Glu	Leu
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Asp	Asp	Glu	Asp	Val	Asp	Asp	Glu	Asn	Thr	Asp	Ile	Thr	Ala	Leu	Ala
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<213> Homo sapiens

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Asp Ala Leu Pro Val Asp Gln Gln Val Ala Phe Phe Leu Asn Asn Met			
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Gly Phe			

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&lt;211&gt; 4224

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 987

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 <213> Homo sapiens

<400> 988

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Met	Leu	Leu	Arg	Gly	Leu	Thr	Gln	Ile	Gln	Ser	Arg	Ile	Leu	Gly	Pro
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Phe	Ala	Leu	Thr	Glu	Asp	Pro	Gln	Glu	Val	Ser	Ala	Thr	Val	Tyr	
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Leu	Asp	Lys	Leu	Ala	Thr	Val	Ile	Ser	Val	Trp	Asn	Ser	Asp	Thr	Gln
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Phe	Val	Gly	Cys	Glu	Phe	Leu	His	His	Leu	Leu	Arg	Glu	Trp	Gly	Glu
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Glu	Leu	Gln	Ala	Val	Leu	Arg	Ser	Ser	Gln	Gly	Thr	Ser	Tyr	Asp	Ser
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Tyr	Arg	Leu	Cys	Asp	Ser	Leu	Thr	Ser	Phe	Ser	Gln	Asn	Ala	Thr	Leu
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Tyr	Leu	Asn	Arg	Thr	Ser	Leu	Ser	Lys	Glu	Asp	Arg	Gln	Val	Val	Ser
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Glu	Leu	Ala	Glu	Cys	Val	Arg	Asp	Phe	Leu	Arg	Lys	Thr	Ser	Thr	Val
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Gly	Ser	Asn	Arg	Ala	Leu	Phe	Arg	Glu	Pro	Asp	Leu	Val	Leu	Arg	Leu
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Phe	Gln	Glu	Asp	Leu	Asn	Thr	Thr	Phe	Asn	Gln	Leu	Thr	Gln	Ser	Ala
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Pro Ala Leu Arg Phe Val Glu Val Gln Gly Pro Asn Ser Ser Ala Thr		400
	405	410
Phe Met Val Ser Cys Leu Lys Glu Thr Val Trp Met Lys Phe Ser Thr		415
	420	425
Pro Lys Glu Glu Lys Gln Phe Leu Glu Leu Leu Asn Cys Leu Met Ser		430
	435	440
Pro Val Lys Pro Gln Gly Ile Pro Val Ala Ala Leu Leu Glu Pro Asp		445
	450	455
Glu Val Leu Lys Glu Phe Val Leu Pro Phe Leu Arg Leu Asp Val Glu		460
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Glu Val Asp Leu Ser Leu Arg Ile Phe Ile Gln Thr Leu Glu Ala Asn		480
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	500	505
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Leu Pro Lys Glu Lys Arg Cys Leu Ser Leu Asp Arg Lys Asp Leu Ala		525
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Ile His Ile Leu Glu Leu Leu Cys Glu Ile Val Ser Ala Asn Ala Glu		540
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Thr Phe Ser Pro Asp Val Trp Ile Lys Ser Leu Ser Trp Leu His Arg		560
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	660	665
Val Gln Val Met Pro Trp Cys Ser Pro Gln Glu Trp Gln Arg Leu His		670
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Gln Leu Thr Arg Arg Leu Leu Glu Lys Gln Leu Leu His Val Pro Tyr		685
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Ser Leu Glu Tyr Ile Gln Phe Val Pro Leu Leu Asn Leu Lys Pro Phe		700
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His Val Val Lys Leu Leu Cys Gly Ser Leu Thr Arg Leu Leu Asp Ser		750
	755	760
Val Arg Ala Ile Gln Ala Ala Gly Pro Trp Val Gln Gly Pro Glu Gln		765
	770	775
Asp Leu Thr Gln Glu Ala Leu Phe Val Tyr Thr Gln Val Phe Cys His		780
785	790	795
Ala Leu His Ile Met Ala Met Leu His Pro Glu Val Cys Glu Pro Leu		800

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 <212> DNA  
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 gcccaatttt taggagtaga tggttattgg ttaacgacgg ggaatactga agattctttt  
 180  
 agagaaagtg atgtatttag cccgactgta gtgagtgcag aatctactga tcagtatggt  
 240  
 tggattgaag ttgtagaagc taacttttct tgcgggacag gtgaatctat tgaatttcac  
 300  
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 359

<210> 992  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 992  
 Ser Arg Ile Lys Ala Lys Lys Thr Gln Ala Glu Val Ala Glu Ala Val  
 1 5 10 15  
 Lys Met Ser Gln Pro Ala Tyr Gln Ala Leu Glu Ser Gly Lys Asn Leu  
 20 25 30  
 Lys Ser Ala Phe Leu Pro Leu Ile Ala Gln Phe Leu Gly Val Asp Gly  
 35 40 45  
 Tyr Trp Leu Thr Thr Gly Asn Thr Glu Asp Ser Phe Arg Glu Ser Asp  
 50 55 60  
 Val Phe Ser Pro Thr Val Val Ser Ala Glu Ser Thr Asp Gln Tyr Val  
 65 70 75 80  
 Trp Ile Glu Val Val Glu Ala Asn Phe Ser Cys Gly Thr Gly Glu Ser  
 85 90 95  
 Ile Glu Phe His Phe Asp Ala Ile Asn Gly Lys Ile Pro Phe Pro Ala  
 100 105 110  
 Ser Phe Phe Lys Glu Lys Arg  
 115

<210> 993  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<400> 993  
 ngcgcgccgg gcaccacata cgacgacggg acgttattca cctctaactg gtagccgccg  
 60  
 tcgcgggtccg gatccgcgat gatggccgcg tggcctgaag caatggggta ggtgcccggtg  
 120

atgcgctcgct ttggcgacag aggtttacgc cgtggggagt tcataaggga aataccagca  
180  
cagggtcgga ccagttgtta cgatcgctgc atgatctact tgcgcagga ttatatcggt  
240  
gagctaccca agcaacatat ctcgctggga aagtttgatc ccgacaatat tcctgcggag  
300  
ccgaacgaac tgtttgccac gtggtttaaa gaagccgttg agaacgaagt cggcgaccct  
360  
actgcgggtca ccgtggccac ggtggacgac aacggtcagc ccgatgcgcg agtcgctgac  
420  
cttctgtacc tcaactccga cggcttccac  
450

<210> 994

<211> 110

<212> PRT

<213> Homo sapiens

<400> 994

Met	Arg	Arg	Phe	Gly	Ala	Arg	Gly	Leu	Arg	Arg	Gly	Glu	Phe	Ile	Arg
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Glu	Ile	Pro	Ala	Gln	Gly	Arg	Thr	Ser	Cys	Tyr	Asp	Arg	Cys	Met	Ile
		20					25				30				
Tyr	Leu	Ser	Gln	Asp	Tyr	Ile	Gly	Glu	Leu	Pro	Lys	Gln	His	Ile	Ser
	35					40					45				
Leu	Gly	Lys	Phe	Asp	Pro	Asp	Asn	Ile	Pro	Ala	Asp	Pro	Asn	Glu	Leu
	50					55				60					
Phe	Ala	Thr	Trp	Phe	Lys	Glu	Ala	Val	Glu	Asn	Glu	Val	Gly	Asp	Pro
65				70				75				80			
Thr	Ala	Val	Thr	Val	Ala	Thr	Val	Asp	Asp	Asn	Gly	Gln	Pro	Asp	Ala
			85				90					95			
Arg	Val	Val	Asp	Leu	Leu	Tyr	Leu	Asn	Ser	Asp	Gly	Phe	His		
			100				105						110		

<210> 995

<211> 924

<212> DNA

<213> Homo sapiens

<400> 995

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gtggatggcg acgtggtccc cgatgaccct gagatcctca tgcagcaggg agaattcctc  
120  
aactacgaca tgctcatcgg cgtcaaccag ggagagggcc tcaagttcgt ggaggactct  
180  
gcagagagcg aggacggtgt gtctgccagc gcctttgact tcaactgtctc caactttgtg  
240  
gacaacctgt atggctaccc ggaaggcaag gatgtgcttc gggagaccat caagtttatg  
300  
tacacagact gggccgaccg ggacaatggc gaaatgcgcc gcaaaaccct gctggcgctc  
360  
tttactgacc accaatgggt ggcaccagct gtggccactg ccaagctgca cgccgactac  
420

cagtctcccg tctactttta caccttctac caccactgcc aggcggaggg ccggcctgag  
 480  
 tgggcagatg cggcgcacgg ggatgaactg ccctatgtct ttggcgtgcc catggtgggt  
 540  
 gccaccgacc tcttcccctg taacttctcc aagaatgacg tcatgtctag tgccgtggtc  
 600  
 atgacctact ggaccaactt cgccaagact ggggacccca accagccggt gccgcaggat  
 660  
 accaagtcca tccacaccaa gcccaatcgc ttcgaggagg tgggtgtggag caaattcaac  
 720  
 agcaaggaga agcagtatct gcacataggg ctgaagccac gcgtgctga caactaccgc  
 780  
 gccacaagg tggccttctg gctggagctc gtgccccacc tgcacaacct gcacacggag  
 840  
 ctcttcacca ccaccacgcg cctgcctccc tacgccacgc gctggccgcc tcgtccccc  
 900  
 gctggcgccc cgggcacacg ccgg  
 924

&lt;210&gt; 996

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 996

Arg	Glu	Leu	Val	Asp	Gln	Asp	Val	Gln	Pro	Ala	Arg	Tyr	His	Ile	Ala
1				5				10					15		
Phe	Gly	Pro	Val	Val	Asp	Gly	Asp	Val	Val	Pro	Asp	Asp	Pro	Glu	Ile
			20					25					30		
Leu	Met	Gln	Gln	Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Met	Leu	Ile	Gly	Val
		35					40					45			
Asn	Gln	Gly	Glu	Gly	Leu	Lys	Phe	Val	Glu	Asp	Ser	Ala	Glu	Ser	Glu
	50					55					60				
Asp	Gly	Val	Ser	Ala	Ser	Ala	Phe	Asp	Phe	Thr	Val	Ser	Asn	Phe	Val
65					70					75				80	
Asp	Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Val	Leu	Arg	Glu	Thr
			85						90					95	
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Arg	Asp	Asn	Gly	Glu	Met
			100					105						110	
Arg	Arg	Lys	Thr	Leu	Leu	Ala	Leu	Phe	Thr	Asp	His	Gln	Trp	Val	Ala
		115					120					125			
Pro	Ala	Val	Ala	Thr	Ala	Lys	Leu	His	Ala	Asp	Tyr	Gln	Ser	Pro	Val
	130					135					140				
Tyr	Phe	Tyr	Thr	Phe	Tyr	His	His	Cys	Gln	Ala	Glu	Gly	Arg	Pro	Glu
145					150					155				160	
Trp	Ala	Asp	Ala	Ala	His	Gly	Asp	Glu	Leu	Pro	Tyr	Val	Phe	Gly	Val
			165						170					175	
Pro	Met	Val	Gly	Ala	Thr	Asp	Leu	Phe	Pro	Cys	Asn	Phe	Ser	Lys	Asn
		180					185					190			
Asp	Val	Met	Leu	Ser	Ala	Val	Val	Met	Thr	Tyr	Trp	Thr	Asn	Phe	Ala
	195					200						205			
Lys	Thr	Gly	Asp	Pro	Asn	Gln	Pro	Val	Pro	Gln	Asp	Thr	Lys	Phe	Ile
	210					215					220				
His	Thr	Lys	Pro	Asn	Arg	Phe	Glu	Glu	Val	Val	Trp	Ser	Lys	Phe	Asn

225                      230                      235                      240  
 Ser Lys Glu Lys Gln Tyr Leu His Ile Gly Leu Lys Pro Arg Val Arg  
                                  245                      250                      255  
 Asp Asn Tyr Arg Ala Asn Lys Val Ala Phe Trp Leu Glu Leu Val Pro  
                                  260                      265                      270  
 His Leu His Asn Leu His Thr Glu Leu Phe Thr Thr Thr Thr Arg Leu  
                                  275                      280                      285  
 Pro Pro Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala Pro  
                                  290                      295                      300  
 Gly Thr Arg Arg  
 305

<210> 997

<211> 320

<212> DNA

<213> Homo sapiens

<400> 997

aaatttaata ccatagcctt ctcttggttg atccttctag gcatgagtta tggcattaaa  
 60  
 acgggcatcc atcttggtgt cgatatacgt cttaatgccg tgcctaaacg agtatcaaga  
 120  
 gccttgcttt tgttcggtgc ctttgccgct attatgtacg gtctcattct acttgattct  
 180  
 acctggttag ccttactcgg tatcgatgta cgagggtggtg ccatcgaata ttgggcgaag  
 240  
 atgttcaaaa taggtattgg tactgaagag cttcggtacc ctatctttat gcaagatatg  
 300  
 tttgatttgc gcccacgcgt  
 320

<210> 998

<211> 106

<212> PRT

<213> Homo sapiens

<400> 998

Lys Phe Asn Thr Ile Ala Phe Ser Trp Leu Ile Leu Leu Gly Met Ser  
 1                      5                      10                      15  
 Tyr Gly Ile Lys Thr Gly Ile His Leu Gly Val Asp Ile Val Leu Asn  
                                  20                      25                      30  
 Ala Val Pro Lys Arg Val Ser Arg Ala Leu Ser Leu Phe Gly Ala Phe  
                                  35                      40                      45  
 Ala Ala Ile Met Tyr Gly Leu Ile Leu Leu Asp Ser Thr Trp Leu Ala  
                                  50                      55                      60  
 Leu Leu Gly Ile Asp Val Arg Gly Gly Ala Ile Glu Tyr Trp Ala Lys  
 65                      70                      75                      80  
 Met Phe Lys Ile Gly Ile Gly Thr Glu Glu Leu Arg Tyr Pro Ile Phe  
                                  85                      90                      95  
 Met Gln Asp Met Phe Asp Leu Arg Pro Arg  
                                  100                      105

<210> 999

<211> 401



<212> DNA

<213> Homo sapiens

<400> 999

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acgcgttcag gcggttaaca atcgcgctaa gaagctgacc aaggaaaatg tcggcatggg
60
acatctgagc aagagcttca tcggtgttta tctctactca gaaggcaagt ttgtgaccag
120
caactatctc aatcgtggct acaaggacat tctgagctat gcagacgatg ctagtctttt
180
gcaaaagcct ccagcagtgg cttcagatga tctggataca ggtctcttga agagggcctt
240
ggatgagtgg gtggctgatg ctaagaacca cattctcaat actgaaaact tctttagecg
300
gtcaaccggg ctcaacattg acagtttcta cgtctttggg gaccaagaca tctgctggca
360
gttggcagct attctgaagc agagcatgaa tcgggaattg t
401
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<210> 1000

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1000

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Met Val His Leu Ser Lys Ser Phe Ile Gly Val Tyr Leu Tyr Ser Glu
 1             5             10            15
Gly Lys Phe Val Thr Ser Asn Tyr Leu Asn Arg Gly Tyr Lys Asp Ile
      20             25            30
Leu Ser Tyr Ala Asp Asp Ala Ser Leu Leu Gln Lys Pro Pro Ala Val
      35             40            45
Ala Ser Asp Asp Leu Asp Thr Gly Leu Leu Lys Arg Ala Leu Asp Glu
      50             55            60
Trp Val Ala Asp Ala Lys Asn His Ile Leu Asn Thr Glu Asn Phe Phe
      65             70            75            80
Ser Gly Ser Thr Gly Leu Asn Ile Asp Ser Phe Tyr Val Phe Gly Asp
      85             90            95
Gln Asp Ile Cys Trp Gln Leu Ala Ala Ile Leu Lys Gln Ser Met Asn
      100            105            110
Arg Glu Leu
      115
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<210> 1001

<211> 351

<212> DNA

<213> Homo sapiens

<400> 1001

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cgcggtattg caatgcgcct ggtgccgaat gctaaacctg ctcttgattg cccggtactg
60
ttcccttatg ccctaatagc ggtgattggt ggcttcctgg ccactaccgt tggttcaatt
120
atcggtatga ttgtcttccc gctgtttggt ctggcgatga tccttcgggg tctgctaact
180
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aacttcttcg ctggtggtgc cgctggagtc tttggcaacg cgatgggagg acgtaaaggg  
 240  
 gcaattattg gcggcgtagt gcacgggctg tttatcaccc tggtaccage gatgctaate  
 300  
 cccttactgg aaaccttcgg cttcaaaggc gtcaccttca gtgattccga t  
 351

<210> 1002

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1002

Arg	Gly	Ile	Ala	Met	Arg	Leu	Val	Pro	Asn	Ala	Lys	Pro	Ala	Leu	Asp
1				5				10					15		
Cys	Pro	Val	Leu	Phe	Pro	Tyr	Ala	Pro	Asn	Ala	Val	Ile	Val	Gly	Phe
		20					25					30			
Leu	Ala	Thr	Thr	Val	Gly	Ser	Ile	Ile	Gly	Met	Ile	Val	Phe	Pro	Leu
		35				40				45					
Phe	Gly	Leu	Ala	Met	Ile	Leu	Pro	Gly	Leu	Leu	Thr	Asn	Phe	Phe	Ala
	50				55				60						
Gly	Gly	Ala	Ala	Gly	Val	Phe	Gly	Asn	Ala	Met	Gly	Gly	Arg	Lys	Gly
65				70				75				80			
Ala	Ile	Ile	Gly	Gly	Val	Val	His	Gly	Leu	Phe	Ile	Thr	Leu	Leu	Pro
			85					90				95			
Ala	Met	Leu	Ile	Pro	Leu	Leu	Glu	Thr	Phe	Gly	Phe	Lys	Gly	Val	Thr
		100					105					110			
Phe	Ser	Asp	Ser	Asp											
		115													

<210> 1003

<211> 444

<212> DNA

<213> Homo sapiens

<400> 1003

acgcgtcctc ctttagtcga tcgcgaatat gataggcgaa gcgacgtgat ggtgtgacgc  
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 acgagcactg ccccatctcc taggcttagg gttatgcaga ctcccatcga cgctacctcc  
 120  
 acccccgcacat ggggcacact ctccggccta aagtcgccgt tcgctgacgg gccacataaa  
 180  
 ctgcgcggtt tgttcgacgc cgacctcac cgcgctgagc gctacacctt tgacgtcgcg  
 240  
 gatttgacag tcgatttata gaagaacctc cttaccgacg agattcgtga cgctctcttc  
 300  
 gaactggctg cgcagatgag cgtcaccgag cgtcgtgacg cgatgtatgc cgggtgagac  
 360  
 atcaacgtca ccgaggaccg cgccgtcctc cataccgcgc tgtgtcgtcc ccgcactgac  
 420  
 gagctgcatg ttgacggtca ggat  
 444

<210> 1004

<211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 1004  
 Met Gln Thr Pro Ile Asp Ala Thr Ser Thr Pro Ala Trp Gly Thr Leu  
 1 5 10 15  
 Ser Gly Leu Lys Ser Arg Phe Ala Asp Gly Pro His Lys Leu Arg Arg  
 20 25 30  
 Leu Phe Asp Ala Asp Pro His Arg Ala Glu Arg Tyr Thr Phe Asp Val  
 35 40 45  
 Ala Asp Leu His Val Asp Leu Ser Lys Asn Leu Leu Thr Asp Glu Ile  
 50 55 60  
 Arg Asp Ala Leu Leu Glu Leu Ala Ala Gln Met Arg Val Thr Glu Arg  
 65 70 75 80  
 Arg Asp Ala Met Tyr Ala Gly Glu His Ile Asn Val Thr Glu Asp Arg  
 85 90 95  
 Ala Val Leu His Thr Ala Leu Cys Arg Pro Arg Thr Asp Glu Leu His  
 100 105 110  
 Val Asp Gly Gln Asp  
 115

<210> 1005  
 <211> 299  
 <212> DNA  
 <213> Homo sapiens

<400> 1005  
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 60  
 tgggtgactcc caagtttaca cctccagcca gggcttctct cctggggttg catacccacc  
 120  
 tatctatctg ccttagccac tcgtgtctga cgagcacctc acacctccag aggctctca  
 180  
 tttcttccca tgctgtcttc tcccacactc ctccctctca catgagggca acttcaccc  
 240  
 cccagttgct caggcccaa acctccatca gttttgactc ttctctcgca cactactcg  
 299

<210> 1006  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 1006  
 Met Ala Ile Pro Leu Val Thr Ala Ser Ser Pro Met Asp Leu Asn Thr  
 1 5 10 15  
 Pro Asn Val Leu Val Thr Pro Lys Phe Thr Pro Pro Ala Arg Ala Ser  
 20 25 30  
 Leu Leu Gly Leu His Thr His Leu Ser Ile Cys Leu Ser His Ser Cys  
 35 40 45  
 Leu Thr Ser Thr Ser His Leu Gln Arg Leu Leu Ile Ser Ser His Ala  
 50 55 60  
 Cys Phe Ser His Thr Pro Pro Ser His Met Arg Ala Thr Ser Ser Ser

<400> 1009

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 cattccactg gtgtttcccc aggaaagcca accctacctg catctcagca gagcttccac  
 120  
 ggagttggaa ccccgctccg agaggggtgtg ggctcagggg ccaggggtca cacaaactcc  
 180  
 agaaggagga cgtagtgtgt ttgcaaggct gtcctttgcc ctggttgaat aaccttcggt  
 240  
 ctgccccgag aggaacgtgg gcattaggct gcacccgcag gaagccatgt attttctgag  
 300  
 aaacttgccc catggtgcag atct  
 324

<210> 1010  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 1010  
 Met Gly Gln Val Ser Gln Lys Ile His Gly Phe Leu Arg Val Gln Pro  
 1 5 10 15  
 Asn Ala His Val Pro Leu Gly Ala Asp Arg Arg Leu Phe Asn Gln Gly  
 20 25 30  
 Lys Gly Gln Pro Cys Lys Pro Thr Thr Ser Ser Phe Trp Ser Leu Cys  
 35 40 45  
 Asp Pro Trp Pro Leu Ser Pro His Pro Leu Gly Ala Gly Phe Gln Leu  
 50 55 60  
 Arg Gly Ser Ser Ala Glu Met Gln Val Gly Leu Ala Phe Leu Gly Lys  
 65 70 75 80  
 His Gln Trp Asn Val Ala Ile Val Thr Gly Ala Arg Asp Gly Asp Glu  
 85 90 95  
 Ala Arg His Xaa Ser His Glu Gly  
 100

<210> 1011  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 1011  
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 60  
 gatccctgcg gctgcctgca ctctggacca cgagctctga gagcagcagg ttgagggccg  
 120  
 gtgggcagca gctcggaggc tccgcgaggt gcaggagacg caggcatggc cgggtgagctg  
 180  
 actcctgagg aggaggccca gtacaaaaag gctttctccg cggttgacac ggatggaaac  
 240  
 ggcaccatca atgcccagga gctgggcgcg gcgctgaagg ccacgggcaa gaacctctcg  
 300  
 gaggcccagc taaagaaact catctccgag  
 330

<210> 1012

<211> 55  
 <212> PRT  
 <213> Homo sapiens

<400> 1012  
 Met Ala Gly Glu Leu Thr Pro Glu Glu Glu Ala Gln Tyr Lys Lys Ala  
 1 5 10 15  
 Phe Ser Ala Val Asp Thr Asp Gly Asn Gly Thr Ile Asn Ala Gln Glu  
 20 25 30  
 Leu Gly Ala Ala Leu Lys Ala Thr Gly Lys Asn Leu Ser Glu Ala Gln  
 35 40 45  
 Leu Lys Lys Leu Ile Ser Glu  
 50 55

<210> 1013  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

<400> 1013  
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 tggcggcgctc tcctcgtcgc cgggagcggc gaggaaggat taacgatgac cagcgacgctc  
 120  
 cccgggattg gctcgaacgc cgccactttg gcgcgttccc aggctcgcag tgacaaggctc  
 180  
 gaggctgatt tggcggtcca tcccgacaag tggcgcatte tgggggggga ccgtcctact  
 240  
 ggcagcctgc acatcgggtca ctacttcggg tcgctggcga atcgggtacg cgtgcagaac  
 300  
 aagggcattg agtctttcct tgctcgtcgt gactaccagg ttatctatga ccgcgggggg  
 360  
 ggtggtgacc tgcaggccaa tggtatgtcg aatgtcgccg attacctggc aatcggcatt  
 420  
 gacccaacgc gt  
 432

<210> 1014  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 1014  
 Met Thr Ser Asp Val Pro Gly Ile Gly Ser Asn Ala Ala Thr Leu Ala  
 1 5 10 15  
 Arg Ser Gln Ala Arg Ser Asp Lys Val Glu Ala Asp Leu Ala Val His  
 20 25 30  
 Pro Asp Lys Trp Arg Ile Leu Gly Gly Asp Arg Pro Thr Gly Ser Leu  
 35 40 45  
 His Ile Gly His Tyr Phe Gly Ser Leu Ala Asn Arg Val Arg Val Gln  
 50 55 60  
 Asn Lys Gly Ile Glu Ser Phe Leu Val Val Ala Asp Tyr Gln Val Ile  
 65 70 75 80  
 Tyr Asp Arg Gly Gly Gly Gly Asp Leu Gln Ala Asn Val Met Ser Asn

85 90 95  
 Val Ala Asp Tyr Leu Ala Ile Gly Ile Asp Pro Thr Arg  
 100 105

<210> 1015  
 <211> 467  
 <212> DNA  
 <213> Homo sapiens

<400> 1015  
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 60  
 gaaaacttcc cgatgaaagc gcgcacgggtt gaagagctga aagaattgga aagagtttta  
 120  
 cagcaaaaga agattgaagc agagtgtctt aaactacgga aggaaattgt agaggctcag  
 180  
 tctggagtta agttgattaa acagcgctcat gaagaggatg atgaagaaga ggaagaggaa  
 240  
 gacaagacag taaaatatag caatttgccc aattacctgc ttggtagtct gagtactgat  
 300  
 tttggggtag atacctcttt attgtcaagc caattggagc ttcattccag agaagagaaa  
 360  
 atcaacccaa ttatattatt gaaagatatc atttacaagg taaaaactgt tttcaataat  
 420  
 gagtttgacg ctgcatataa acaaaaagag tttgaaattg cagcgt  
 467

<210> 1016  
 <211> 155  
 <212> PRT  
 <213> Homo sapiens

<400> 1016  
 Xaa Asn Ser Met Ala Val Lys Gly Arg Ala Leu Lys Cys Phe His Ile  
 1 5 10 15  
 Pro Cys Val Val Glu Asn Phe Pro Met Lys Ala Arg Thr Val Glu Glu  
 20 25 30  
 Leu Lys Glu Leu Glu Arg Val Leu Gln Gln Lys Lys Ile Glu Ala Glu  
 35 40 45  
 Cys Leu Lys Leu Arg Lys Glu Ile Val Glu Ala Gln Ser Gly Val Lys  
 50 55 60  
 Leu Ile Lys Gln Arg His Glu Glu Asp Asp Glu Glu Glu Glu Glu  
 65 70 75 80  
 Asp Lys Thr Val Lys Tyr Ser Asn Leu Pro Asn Tyr Leu Leu Gly Ser  
 85 90 95  
 Leu Ser Thr Asp Phe Gly Val Asp Thr Ser Leu Leu Ser Ser Gln Leu  
 100 105 110  
 Glu Leu His Ser Arg Glu Glu Lys Ile Asn Gln Ile Ile Leu Leu Lys  
 115 120 125  
 Asp Ile Ile Tyr Lys Val Lys Thr Val Phe Asn Asn Glu Phe Asp Ala  
 130 135 140  
 Ala Tyr Lys Gln Lys Glu Phe Glu Ile Ala Arg  
 145 150 155

<210> 1017  
 <211> 335  
 <212> DNA  
 <213> Homo sapiens

<400> 1017  
 acgcgtggct ggttgggtat gtggaaccat gtgcgcgcta atgagaagga tgcaagggg  
 60  
 aacattaaag tgggtcgccc cggctacttt gcggaggtca tggatttcta tgccattat  
 120  
 ctgaaggggtg cggttacccg tttccgtccg aattttattg tgcaggataa tacgggccgt  
 180  
 tggcgtgttc agtcgtcgtg gccgcagccg aatcgactg ttacttttgc gggaccccg  
 240  
 ggcattgtcc gctacggtac gacgttggcg gccgcacgc atgggaatgg tcaggctatt  
 300  
 ccgcaggcgg atgcacagtc tcttaaccgc gagaa  
 335

<210> 1018  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 1018  
 Met Trp Asn His Val Arg Ala Asn Glu Lys Asp Ala Lys Gly Asn Ile  
 1 5 10 15  
 Lys Val Gly Arg Pro Gly Tyr Phe Ala Glu Val Met Asp Phe Tyr Ala  
 20 25 30  
 His Tyr Leu Lys Gly Ala Val Thr Arg Phe Arg Pro Asn Phe Ile Val  
 35 40 45  
 Gln Asp Asn Thr Gly Arg Trp Arg Val Gln Ser Ser Trp Pro Gln Pro  
 50 55 60  
 Asn Arg Thr Val Thr Phe Ala Gly Pro Arg Gly Ile Val Arg Tyr Gly  
 65 70 75 80  
 Thr Thr Leu Ala Ala Arg Thr His Gly Asn Gly Gln Ala Ile Pro Gln  
 85 90 95  
 Ala Asp Ala Gln Ser Leu Asn Arg Glu  
 100 105

<210> 1019  
 <211> 454  
 <212> DNA  
 <213> Homo sapiens

<400> 1019  
 acgcgtgaag gggtagtcgt agtagaagtc gtccacaaac acggggcccg gcagggtccag  
 60  
 ctctggagcc tcctcctcaa tggcgttgcc catggtgcct ggcttgggtg atgaggcggg  
 120  
 tgaagggcgt ggggccaggt ggtgcgggat gaagtcagcc tcgttgaaga gctcgtggct  
 180  
 ggaggagccg ctgcctgagc cttcagggcc cagtgtgccc aggggccacc gacagagtgg  
 240



cagagagcag gtgacttcct ggcactgcgg agcgaggacc cggagaagta cttcctcaat  
300  
ggtggctgga ccatccagtg gaacggggac taccagggtg cagggaccac cttcacatac  
360  
gcacgcaggg gcaactggga gaacctcacg tccccgggtc ccaccaagga gcctgtctgg  
420  
atccagctgc tgttccagga gagcaaccct gggg  
454

<210> 1020

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1020

Met	Ala	Leu	Pro	Met	Val	Pro	Gly	Leu	Gly	Asp	Glu	Ala	Gly	Glu	Gly
1				5				10					15		
Arg	Gly	Ala	Arg	Trp	Cys	Gly	Met	Lys	Ser	Ala	Ser	Leu	Lys	Ser	Ser
			20					25				30			
Trp	Leu	Glu	Glu	Pro	Leu	Pro	Glu	Pro	Ser	Gly	Pro	Ser	Val	Pro	Arg
		35					40					45			
Gly	His	Arg	Gln	Ser	Gly	Arg	Glu	Gln	Val	Thr	Ser	Trp	His	Cys	Gly
50						55				60					
Ala	Arg	Thr	Arg	Arg	Ser	Thr	Ser	Ser	Met	Val	Ala	Gly	Pro	Ser	Ser
65					70					75				80	
Gly	Thr	Gly	Thr	Thr	Arg	Trp	Gln	Gly	Pro	Pro	Ser	His	Thr	His	Ala
			85					90					95		
Gly	Ala	Thr	Gly	Arg	Thr	Ser	Arg	Pro	Arg	Val	Pro	Pro	Arg	Ser	Leu
			100					105					110		
Ser	Gly	Ser	Ser	Cys	Cys	Ser	Arg	Arg	Ala	Thr	Leu	Gly			
		115					120					125			

<210> 1021

<211> 366

<212> DNA

<213> Homo sapiens

<400> 1021

cagctgtgtc gtgacctcct gtagaccaga gagaggtaga gcatgaaaaa tgctcattga  
60  
gccgagatta tctgacagga ccaaagcata taaagttgac tgaagcagga gcaaacacgc  
120  
tggttgaggg tcaagtgtg gggcagcagc aacaacaaac caaaaaaag ccctttgaac  
180  
tcccttaatg ttgcccagg gttctggtag agaacaagtc acatgcctaa gaaggtcttt  
240  
taaagggcac tcttgagtt tcagcatttg gtccggggaa ttgcacaagg ctctgcttaa  
300  
atgcagagct ctttctagca tcttcatatt caaggcggaa aaactgagct tggcgaggaa  
360  
ccctgt  
366

<210> 1022

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1022

```

Met Lys Met Leu Glu Arg Ala Leu His Leu Ser Arg Ala Leu Cys Asn
 1             5             10             15
Ser Pro Asp Gln Met Leu Lys Leu Gln Glu Cys Pro Leu Lys Asp Leu
      20             25             30
Leu Arg His Val Thr Cys Ser Leu Pro Glu Pro Leu Gly Asn Ile Lys
      35             40             45
Gly Val Gln Arg Ala Phe Phe Trp Phe Val Val Ala Ala Ala Pro Ala
 50             55             60
Leu Asp Pro Gln Pro Ala Cys Leu Leu Leu Leu Gln Ser Thr Leu Tyr
65             70             75             80
Ala Leu Val Leu Ser Asp Asn Leu Gly Ser Met Ser Ile Phe His Ala
      85             90             95
Leu Pro Leu Ser Gly Leu Gln Glu Val Thr Thr Gln Leu
      100             105

```

&lt;210&gt; 1023

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1023

```

gccgggcttc gggctctctga agcgatcaac ctggccgact cggatgcaga tctggacggc
60
ggcatcctga ccatacagca gaccaagttt ggcaagtccc gcatgggtgcc gctacacccc
120
agcgtgatcg gtccgatggc agcctaccgg gccttgcgcc gccagtacgt gcctgcgaag
180
ccgcagatga cattcttcgt gggctcgcgt ggcgtgcacc ggggtgaacc gctgggagat
240
aggcaggtgc atcgagtgtt ctgtcagctg cgcgagcaat tgggttgat cgatcgcggc
300
ggccatggcc gaccgagggt gcatgacctg cgccatagct tcgccgtgag acggatgatc
360
ctgtggcacc agcagggagc gaaccttgac caacgaatgc tggccctgtc cacgtacatg
420
ggccac
426

```

&lt;210&gt; 1024

&lt;211&gt; 142

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1024

```

Ala Gly Leu Arg Val Ser Glu Ala Ile Asn Leu Ala Asp Ser Asp Ala
 1             5             10             15
Asp Leu Asp Gly Ile Leu Thr Ile Gln Gln Thr Lys Phe Gly Lys
      20             25             30
Ser Arg Met Val Pro Leu His Pro Ser Val Ile Gly Pro Met Ala Ala

```

```

      35              40              45
Tyr Arg Ala Leu Arg Arg Gln Tyr Val Pro Ala Lys Pro Gln Met Thr
  50              55              60
Phe Phe Val Gly Ser Arg Gly Val His Arg Gly Glu Pro Leu Gly Asp
  65              70              75              80
Arg Gln Val His Arg Val Phe Cys Gln Leu Arg Glu Gln Leu Gly Trp
      85              90              95
Ile Asp Arg Gly Gly His Gly Arg Pro Arg Val His Asp Leu Arg His
      100              105              110
Ser Phe Ala Val Arg Arg Met Ile Leu Trp His Gln Gln Gly Ala Asn
      115              120              125
Leu Asp Gln Arg Met Leu Ala Leu Ser Thr Tyr Met Gly His
      130              135              140

```

<210> 1025  
 <211> 518  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1025
naccgctggt gcgcgcaggt ggcgcgcggt tccctttgct ccctgcgcaa gccggagggg
  60
tgcccagaag gctaccacta gcctcagcga aggggtgcgcc ctgagagccg ggtagcctcg
  120
gatagcggcg ctgcgtacgc gatgatggat gagccgtggt gggaagggcg cgtgcctcg
  180
gacgtccact gcaccctgcg cgagaaggaa ctgaagctgc ccaccttcg agccactcc
  240
ccactcctga agagccgcg gttcttcgtg gacatcctga ccctgctgag cagccactgc
  300
cagctctgcc ctgcagcccg gcacctggcc gtctacctgc tggaccactt catggatcgc
  360
tacaacgtca ccacctccaa gcagctctac accgtggccg tctcctgcct cctgcttgca
  420
agtaagtctg aggatcgga agaccacgtc cccaagttgg agcaaataaa cagcagagg
  480
atcctgagca gccagaactt caccctcacc aagaagga
  518

```

<210> 1026  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1026
Met Met Asp Glu Pro Trp Trp Glu Gly Arg Val Ala Ser Asp Val His
  1              5              10              15
Cys Thr Leu Arg Glu Lys Glu Leu Lys Leu Pro Thr Phe Arg Ala His
      20              25              30
Ser Pro Leu Leu Lys Ser Arg Arg Phe Phe Val Asp Ile Leu Thr Leu
      35              40              45
Leu Ser Ser His Cys Gln Leu Cys Pro Ala Ala Arg His Leu Ala Val
      50              55              60
Tyr Leu Leu Asp His Phe Met Asp Arg Tyr Asn Val Thr Thr Ser Lys

```

```

65          70          75          80
Gln Leu Tyr Thr Val Ala Val Ser Cys Leu Leu Leu Ala Ser Lys Phe
          85          90          95
Glu Asp Arg Glu Asp His Val Pro Lys Leu Glu Gln Ile Asn Ser Thr
          100          105          110
Arg Ile Leu Ser Ser Gln Asn Phe Thr Leu Thr Lys Lys
          115          120          125

```

&lt;210&gt; 1027

&lt;211&gt; 465

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1027

```

ggcccaaaag tcatcaaaga aaagctgaca caggagctga aggaccacaa cgccaccagc
60
atcctgcagc agctgccgct gctcaaggcc atgcgggaaa agccagccgg aggcattcct
120
gtgtggggca gcctgggtgaa caccngtcct gaagcacatc atnnctggct gaaggtcac
180
acagctaaca tcctccagct gcaggtgaag ccctcggcca atgaccagga gctgctagtc
240
aagatcccc tggacatggg ggctggattc aacacgcccc tgggtcaagac catcgtggag
300
ttccacatga cgactgaggc ccaagccacc atccgcatgg acaccagtgc aagtggcccc
360
accgcctgg tcctcagtga ctgtgccacc agccatggga gcctgcgcat ccaactgctg
420
cataagctct ccttcaagct gaacgcctca gctaagcagg tcatg
465

```

&lt;210&gt; 1028

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1028

```

Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys Asp His
1          5          10          15
Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Lys Ala Met Arg
          20          25          30
Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser Leu Val Asn Thr
          35          40          45
Xaa Pro Glu Ala His His Xaa Trp Leu Lys Val Ile Thr Ala Asn Ile
          50          55          60
Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp Gln Glu Leu Leu Val
65          70          75          80
Lys Ile Pro Leu Asp Met Val Ala Gly Phe Asn Thr Pro Leu Val Lys
          85          90          95
Thr Ile Val Glu Phe His Met Thr Thr Glu Ala Gln Ala Thr Ile Arg
          100          105          110
Met Asp Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys
          115          120          125
Ala Thr Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser

```

130 135 140  
 Phe Lys Leu Asn Ala Ser Ala Lys Gln Val Met  
 145 150 155

<210> 1029  
 <211> 479  
 <212> DNA  
 <213> Homo sapiens

<400> 1029  
 acgcgtgaag ggaaactgtc ctcacagatg agtgtgaggg ttcaaaaaga tactgcctgc  
 60  
 caagcactgg ccacaaatgc ctggcagaac aactgctcat aagtgtgtag ttgttgttat  
 120  
 tattactaac caagtgagga aaattatccc tagcagggtcc agatgaccgt gtgcatgaat  
 180  
 cacagggaga ccctaaagga tttcctcctg taaagctctt tccccaccta tttgctactg  
 240  
 cctgaaattg ctttagcagg aaacagaatc tctcatgccca caagtgagca taaagtttaa  
 300  
 aatgtaaatg ctctaggaaa aggcaactca tctcttaaat tctctccaag gttcaaatcc  
 360  
 tttccaaaga ggaggctttt gtataagtca gaaggcccag tccctgaagg tcatggaaaa  
 420  
 ggtcatgaca cacggagggg gtgtcaaagg gagactggga aactgaagat gaagctagc  
 479

<210> 1030  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 1030  
 Met Ser Cys Leu Phe Leu Glu His Leu His Phe Lys Leu Tyr Ala His  
 1 5 10 15  
 Leu Trp His Glu Arg Phe Cys Phe Leu Leu Lys Gln Phe Gln Ala Val  
 20 25 30  
 Ala Asn Arg Trp Gly Lys Ser Phe Thr Gly Gly Asn Pro Leu Gly Ser  
 35 40 45  
 Pro Cys Asp Ser Cys Thr Arg Ser Ser Gly Pro Ala Arg Asp Asn Phe  
 50 55 60  
 Pro His Leu Val Ser Asn Asn Asn Asn Asn Tyr Thr Leu Met Ser Ser  
 65 70 75 80  
 Cys Ser Ala Arg His Leu Trp Pro Val Leu Gly Arg Gln Tyr Leu Phe  
 85 90 95  
 Glu Pro Ser His Ser Ser Val Arg Thr Val Ser Leu His Ala  
 100 105 110

<210> 1031  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

<400> 1031

nacgcgtttt atgtcagcgt tgaattggaa gacggcaagt ctatcgccat gctgccccag  
 60  
 gcagatggct ggtttgaagt ggaggtgaag tgcccggcgg gcactcacta ccgctataac  
 120  
 atcgacggcg aaaccgatgt acccgacccg gcatccaggg cgcaagccaa cgatgtgcat  
 180  
 ggggtggagcg tcgtcgtcga cccgctcgcc tatcaatggc gacaccctaa ctggcaaggc  
 240  
 cgcccctggc atgaggcggt gatttacgag ctgcacgttg gcgtactggg cgggtacgcc  
 300  
 gctgttgaac agcaactgcc gc  
 322

<210> 1032

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1032

Xaa	Ala	Phe	Tyr	Val	Ser	Val	Glu	Leu	Glu	Asp	Gly	Lys	Ser	Ile	Ala
1				5					10					15	
Met	Leu	Pro	Gln	Ala	Asp	Gly	Trp	Phe	Glu	Val	Glu	Val	Lys	Cys	Pro
			20					25					30		
Ala	Gly	Thr	His	Tyr	Arg	Tyr	Asn	Ile	Asp	Gly	Glu	Thr	Asp	Val	Pro
		35					40					45			
Asp	Pro	Ala	Ser	Arg	Ala	Gln	Ala	Asn	Asp	Val	His	Gly	Trp	Ser	Val
		50					55				60				
Val	Val	Asp	Pro	Leu	Ala	Tyr	Gln	Trp	Arg	His	Pro	Asn	Trp	Gln	Gly
65					70					75				80	
Arg	Pro	Trp	His	Glu	Ala	Val	Ile	Tyr	Glu	Leu	His	Val	Gly	Val	Leu
			85						90					95	
Gly	Gly	Tyr	Ala	Ala	Val	Glu	Gln	Gln	Leu	Pro					
			100						105						

<210> 1033

<211> 579

<212> DNA

<213> Homo sapiens

<400> 1033

tgcgtccacc ggggtgacct cctgactgcc tcagtcacga ttccttatgg tcgaagtgtc  
 60  
 acagcgccaa gggttgtgag gagggccctt cgcggggtcac ggataggtcc aaggtggcac  
 120  
 aattcacatt caaatccatc acttttcaca taattgctgt taatatgaac gtcatgagtc  
 180  
 gttgttgctc gcggttgcca gtgggactcc ccatacacgg cagcgagaca tggaggaacc  
 240  
 atgggactaa ggatcgttgt cgccgctgat ccggcggcag tcgagtacaa ggatgtcgtc  
 300  
 aaggctgacc tggaagcgga ttcgcgagtc gatgacgtta tcgacgtcgg cgttcaggct  
 360  
 ggtgacgaca ccctctaccc gcgcacggc atcaaggag ctcacgtcat caaggacgga  
 420

aaagccgata gaggaatctt tttctgcggc accgggatgg gcatggccat cacggccaac  
480  
aagggtgccag gcattcgcgc ctgcaccgcc cacgactcct tctccgtaga gcgggtcacc  
540  
atgtccaacg acgcccacgt gctatgcctc ggccaacgc  
579

<210> 1034  
<211> 113  
<212> PRT  
<213> Homo sapiens

<400> 1034  
Met Gly Leu Arg Ile Val Val Ala Ala Asp Pro Ala Ala Val Glu Tyr  
1 5 10 15  
Lys Asp Val Val Lys Ala Asp Leu Glu Ala Asp Ser Arg Val Asp Asp  
20 25 30  
Val Ile Asp Val Gly Val Gln Ala Gly Asp Asp Thr Leu Tyr Pro Arg  
35 40 45  
Ile Gly Ile Lys Gly Ala His Val Ile Lys Asp Gly Lys Ala Asp Arg  
50 55 60  
Gly Ile Phe Phe Cys Gly Thr Gly Met Gly Met Ala Ile Thr Ala Asn  
65 70 75 80  
Lys Val Pro Gly Ile Arg Ala Cys Thr Ala His Asp Ser Phe Ser Val  
85 90 95  
Glu Arg Leu Ile Met Ser Asn Asp Ala His Val Leu Cys Leu Gly Gln  
100 105 110  
Arg

<210> 1035  
<211> 363  
<212> DNA  
<213> Homo sapiens

<400> 1035  
naccgctgca atgtgtgtgt gtgtatngga ccatgtctct gtgtgtgtat gngcatatgt  
60  
gtgtgtatan gaatgtgtgt atgtgtantg gaatgtgtgt gtgtantgga agctgtgtgc  
120  
atatgtnaat gtctgtgtgc atgtacngga atgtgcgcgt gtatggaatg tatctgtgta  
180  
tgtgtatgga ccgtttgtgt gattatgcaa tatgtccgtg tgtgcgtatg gagggtctca  
240  
gtatggcatg tgtgtgtgta tctactgtgc gtctctgtgt gtgtantgac atgcatatgt  
300  
atagaaagcg tctgcgctgt gtgcatgtgt gtcagtatcg aacgagtcgg agatgtggta  
360  
atn  
363

<210> 1036  
<211> 121  
<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1036

Xaa Ala Cys Asn Val Cys Val Cys Met Xaa Pro Cys Leu Cys Val Cys  
 1 5 10 15  
 Met Xaa Ile Cys Val Cys Ile Xaa Met Cys Val Cys Val Xaa Glu Cys  
 20 25 30  
 Val Cys Val Xaa Glu Ala Val Cys Ile Cys Xaa Cys Leu Cys Ala Cys  
 35 40 45  
 Thr Xaa Met Cys Ala Cys Met Glu Cys Ile Cys Val Cys Val Trp Thr  
 50 55 60  
 Val Cys Val Ile Met Gln Tyr Val Arg Val Cys Val Trp Ser Val Ser  
 65 70 75 80  
 Val Trp His Val Cys Val Tyr Leu Leu Cys Val Ser Val Cys Val Xaa  
 85 90 95  
 Thr Cys Ile Cys Ile Glu Ser Val Cys Ala Val Cys Met Cys Val Ser  
 100 105 110  
 Ile Glu Arg Val Gly Asp Val Val Xaa  
 115 120

&lt;210&gt; 1037

&lt;211&gt; 5832

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1037

ccttctcctg ggggccagat gcatgctgga atcagtagct ttcagcagag taactcaagt  
 60  
 gggacttacg gtccacagat gagccagtat ggaccacaag gtaactactc cagaccccca  
 120  
 gcgtatagtg ggggtgcccag tgcaagctac agcggcccag ggcccgggtat gggatatcagt  
 180  
 gccaacaacc agatgcatgg acaagggcca agccagccat gtggtgctgt gcccctggga  
 240  
 cgaatgccat cagctgggat gcagaacaga ccatttcctg gaaatatgag cagcatgacc  
 300  
 cccagttctc ctggcatgtc tcagcagggga gggccaggaa tggggccgcc aatgccaaact  
 360  
 gtgaaccgta aggcacagga ggcagccgca gcagtgatgc aggctgctgc gaactcagca  
 420  
 caaagcaggc aaggcagttt ccccggcatg aaccagagtg gacttatggc ttccagctct  
 480  
 ccctacagcc agcccatgaa caacagctct agcctgatga acacgcaggc gccgcctac  
 540  
 agcatggcgc ccgccatggt gaacagctcg gcagcatctg tgggtcttgc agatatgatg  
 600  
 tctcctggtg aatccaaact gcccctgcct ctcaaagcag acggcaaaga agaaggcact  
 660  
 ccacagcccg agagcaagtc aaaggatagc tacagctctc aggggtatttc tcagcccca  
 720  
 accccaggca acctgccagt cccttccccca atgtccccca gctctgctag catctcctca  
 780  
 tttcatggag atgaaagtga tagcattagc agcccaggct ggccaaagac tccatcaagc  
 840



cctaagtcca gctcctccac cactactggg gagaagatca cgaagggtga cgagctgggg  
900  
aatgagccag agagaaagct ctgggtcgac cgatacctca ccttcattga agagagaggg  
960  
tctcctgtct caagtctgcc tgcctggggc aagaagcccc tggacctgtt ccgactctac  
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1080  
ctggcaacca acctaacgt tggcacctca agcagtgcag cgagctccct gaaaaagcag  
1140  
tatattcagt acctgtttgc ctttgagtgc aagatcgaac gtggggagga gccccgccg  
1200  
gaagtcttca gcaccgggga caccaaaaag cagcccaagc tccagccgcc atctcctgct  
1260  
aactcgggat ccttgcaagg ccacacagacc cccagtcga ctggcagcaa ttccatggca  
1320  
gaggttccag gtgacctgaa gccacctacc ccagcctcca cccctcacgg ccagatgact  
1380  
ccaatgcaag gtggaagaag cagtacaatc agtgtgcacg acccattctc agatgtgagt  
1440  
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1500  
agcatgcccg atgtgatggg caggatgccc tatgagccca acaaggaccc ctttggggga  
1560  
atgagaaaag tgcttgaag cagcgagccc tttatgacgc aaggacagat gcccaacagc  
1620  
agcatgcagg acatgtacaa ccaaagtccc tccggagcaa tgtctaacct gggcatgggg  
1680  
cagcgccagc agtttcccta tggagccagt tacgaccgaa ggcataacc ttatgggcag  
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1800  
ctgtaccac agcagccgaa ttacaaacgc catatggacg gcatgtacgg gccccagcc  
1860  
aagcgccagc agggcgacat gtacaacatg cagtacagca gccagcagca ggagatgtac  
1920  
aaccagtatg gaggtccta ctcgggcccg gaccgcaggc ccattccagg ccagtaccgc  
1980  
tatccctaca gcaggagag gatgcagggc ccggggcaga tccagacaca cggaatcccc  
2040  
cttcagatga tgggcggccc gctgcagtcg tctccagtg aggggcctca gcagaatatg  
2100  
tgggcagcac gcaatgatat gccttatccc taccagaaca ggcagggcc tggcgccct  
2160  
acacaggcgc ccccttacc aggcattgaac cgcacagacg atatgatggt acccgatcag  
2220  
aggataaatc atgagagcca gtggccttct cagtcagcc agcgtcagcc ttatatgtcg  
2280  
tctcagcct ccatgcagcc catcacacgc ccaccacagc cgtccacca gacgccaccg  
2340  
tcactgccaa atcacatctc cagggcgccc agcccagcgt ccttcagcg ctccctggag  
2400  
aaccgcatgt ctccaagcaa gtctcctttt ctgccgtcta tgaagatgca gaaggtcatg  
2460

cccacgggcc ccacatccca ggtcaccggg ccaccacccc aaccaccccc aatcagaagg  
2520  
gagatcacct ttctctctgg ctccagtagaa gcatcacaac cagtcttgaa acaaaggcga  
2580  
aagattacct ccaaagatat cggtactcct gaggcgtggc gtgtgatgat gtcccttaaa  
2640  
tcaggctctt tggctgagag tacgtgggct ttggacacta ttaatatctt tctgtatgat  
2700  
gacagcactg ttgctacttt caatctctcc cagttgtctg gatttctcga acttttagtc  
2760  
gagtacttta gaaaatgcct gattgacatt tttggaattc ttatggaata tgaagtggga  
2820  
gacccagcc aaaaagcact tgatcacaac gcagcaagga aggatgacag ccagtccttg  
2880  
gcagacgatt ctgggaaaga ggaggaagat gctgaatgta ttgatgacga cgaggaagac  
2940  
gaggaggatg aggaggaaga cagcgagaag acagaaagcg atgaaaagag cagcatcgct  
3000  
ctgactgccc cggacgccgc tgcagacca aaggagaagc ccaagcaagc cagtaagtcc  
3060  
gacaagctgc caataaagat agtcaaaaag aacaacctgt ttgttggtga ccgatctgac  
3120  
aagttggggc gtgtgcagga gttcaatagt ggccttctac actggcagct cggcgggggt  
3180  
gacaccaccg agcacattca gactcacttt gagagcaaga tggaaattcc tctcgcagg  
3240  
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<210> 1038

<211> 1485

<212> PRT

<213> Homo sapiens

<400> 1038

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			20					25					30		
Gln	Gly	Asn	Tyr	Ser	Arg	Pro	Pro	Ala	Tyr	Ser	Gly	Val	Pro	Ser	Ala
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Ser	Tyr	Ser	Gly	Pro	Gly	Pro	Gly	Met	Gly	Ile	Ser	Ala	Asn	Asn	Gln
	50					55					60				
Met	His	Gly	Gln	Gly	Pro	Ser	Gln	Pro	Cys	Gly	Ala	Val	Pro	Leu	Gly
65					70					75				80	
Arg	Met	Pro	Ser	Ala	Gly	Met	Gln	Asn	Arg	Pro	Phe	Pro	Gly	Asn	Met
				85					90					95	
Ser	Ser	Met	Thr	Pro	Ser	Ser	Pro	Gly	Met	Ser	Gln	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Met	Gly	Pro	Pro	Met	Pro	Thr	Val	Asn	Arg	Lys	Ala	Gln	Glu	Ala
		115					120					125			
Ala	Ala	Ala	Val	Met	Gln	Ala	Ala	Ala	Asn	Ser	Ala	Gln	Ser	Arg	Gln
	130					135					140				
Gly	Ser	Phe	Pro	Gly	Met	Asn	Gln	Ser	Gly	Leu	Met	Ala	Ser	Ser	Ser
145					150					155				160	
Pro	Tyr	Ser	Gln	Pro	Met	Asn	Asn	Ser	Ser	Ser	Leu	Met	Asn	Thr	Gln
				165					170					175	
Ala	Pro	Pro	Tyr	Ser	Met	Ala	Pro	Ala	Met	Val	Asn	Ser	Ser	Ala	Ala
			180					185					190		
Ser	Val	Gly	Leu	Ala	Asp	Met	Met	Ser	Pro	Gly	Glu	Ser	Lys	Leu	Pro
		195					200					205			
Leu	Pro	Leu	Lys	Ala	Asp	Gly	Lys	Glu	Glu	Gly	Thr	Pro	Gln	Pro	Glu
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Ser	Lys	Ser	Lys	Asp	Ser	Tyr	Ser	Ser	Gln	Gly	Ile	Ser	Gln	Pro	Pro
225					230					235				240	
Thr	Pro	Gly	Asn	Leu	Pro	Val	Pro	Ser	Pro	Met	Ser	Pro	Ser	Ser	Ala
			245						250					255	
Ser	Ile	Ser	Ser	Phe	His	Gly	Asp	Glu	Ser	Asp	Ser	Ile	Ser	Ser	Pro
			260					265					270		
Gly	Trp	Pro	Lys	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Ser	Ser	Ser	Thr	Thr
		275					280					285			
Thr	Gly	Glu	Lys	Ile	Thr	Lys	Val	Tyr	Glu	Leu	Gly	Asn	Glu	Pro	Glu
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Arg	Lys	Leu	Trp	Val	Asp	Arg	Tyr	Leu	Thr	Phe	Met	Glu	Glu	Arg	Gly
305					310					315				320	
Ser	Pro	Val	Ser	Ser	Leu	Pro	Ala	Val	Gly	Lys	Lys	Pro	Leu	Asp	Leu

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          325          330          335
Phe Arg Leu Tyr Val Cys Val Lys Glu Ile Gly Gly Leu Ala Gln Val
          340          345          350
Asn Lys Asn Lys Lys Trp Arg Glu Leu Ala Thr Asn Leu Asn Val Gly
          355          360          365
Thr Ser Ser Ser Ala Ala Ser Ser Leu Lys Lys Gln Tyr Ile Gln Tyr
          370          375          380
Leu Phe Ala Phe Glu Cys Lys Ile Glu Arg Gly Glu Glu Pro Pro Pro
385          390          395          400
Glu Val Phe Ser Thr Gly Asp Thr Lys Lys Gln Pro Lys Leu Gln Pro
          405          410          415
Pro Ser Pro Ala Asn Ser Gly Ser Leu Gln Gly Pro Gln Thr Pro Gln
          420          425          430
Ser Thr Gly Ser Asn Ser Met Ala Glu Val Pro Gly Asp Leu Lys Pro
          435          440          445
Pro Thr Pro Ala Ser Thr Pro His Gly Gln Met Thr Pro Met Gln Gly
          450          455          460
Gly Arg Ser Ser Thr Ile Ser Val His Asp Pro Phe Ser Asp Val Ser
465          470          475          480
Asp Ser Ser Phe Pro Lys Arg Asn Ser Met Thr Pro Asn Ala Pro Tyr
          485          490          495
Gln Gln Gly Met Ser Met Pro Asp Val Met Gly Arg Met Pro Tyr Glu
          500          505          510
Pro Asn Lys Asp Pro Phe Gly Gly Met Arg Lys Val Pro Gly Ser Ser
          515          520          525
Glu Pro Phe Met Thr Gln Gly Gln Met Pro Asn Ser Ser Met Gln Asp
530          535          540
Met Tyr Asn Gln Ser Pro Ser Gly Ala Met Ser Asn Leu Gly Met Gly
545          550          555          560
Gln Arg Gln Gln Phe Pro Tyr Gly Ala Ser Tyr Asp Arg Arg His Glu
          565          570          575
Pro Tyr Gly Gln Gln Tyr Pro Gly Gln Gly Pro Pro Ser Gly Gln Pro
          580          585          590
Pro Tyr Gly Gly His Gln Pro Gly Leu Tyr Pro Gln Gln Pro Asn Tyr
          595          600          605
Lys Arg His Met Asp Gly Met Tyr Gly Pro Pro Ala Lys Arg His Glu
610          615          620
Gly Asp Met Tyr Asn Met Gln Tyr Ser Ser Gln Gln Gln Glu Met Tyr
625          630          635          640
Asn Gln Tyr Gly Gly Ser Tyr Ser Gly Pro Asp Arg Arg Pro Ile Gln
          645          650          655
Gly Gln Tyr Pro Tyr Pro Tyr Ser Arg Glu Arg Met Gln Gly Pro Gly
          660          665          670
Gln Ile Gln Thr His Gly Ile Pro Leu Gln Met Met Gly Gly Pro Leu
          675          680          685
Gln Ser Ser Ser Ser Glu Gly Pro Gln Gln Asn Met Trp Ala Ala Arg
690          695          700
Asn Asp Met Pro Tyr Pro Tyr Gln Asn Arg Gln Gly Pro Gly Gly Pro
705          710          715          720
Thr Gln Ala Pro Pro Tyr Pro Gly Met Asn Arg Thr Asp Asp Met Met
          725          730          735
Val Pro Asp Gln Arg Ile Asn His Glu Ser Gln Trp Pro Ser His Val
          740          745          750
Ser Gln Arg Gln Pro Tyr Met Ser Ser Ser Ala Ser Met Gln Pro Ile

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755	760	765
Thr Arg Pro Pro Gln Pro Ser Tyr Gln Thr Pro Pro Ser Leu Pro Asn		
770	775	780
His Ile Ser Arg Ala Pro Ser Pro Ala Ser Phe Gln Arg Ser Leu Glu		
785	790	795
Asn Arg Met Ser Pro Ser Lys Ser Pro Phe Leu Pro Ser Met Lys Met		
805	810	815
Gln Lys Val Met Pro Thr Val Pro Thr Ser Gln Val Thr Gly Pro Pro		
820	825	830
Pro Gln Pro Pro Ile Arg Arg Glu Ile Thr Phe Pro Pro Gly Ser		
835	840	845
Val Glu Ala Ser Gln Pro Val Leu Lys Gln Arg Arg Lys Ile Thr Ser		
850	855	860
Lys Asp Ile Val Thr Pro Glu Ala Trp Arg Val Met Met Ser Leu Lys		
865	870	875
Ser Gly Leu Leu Ala Glu Ser Thr Trp Ala Leu Asp Thr Ile Asn Ile		
885	890	895
Leu Leu Tyr Asp Asp Ser Thr Val Ala Thr Phe Asn Leu Ser Gln Leu		
900	905	910
Ser Gly Phe Leu Glu Leu Leu Val Glu Tyr Phe Arg Lys Cys Leu Ile		
915	920	925
Asp Ile Phe Gly Ile Leu Met Glu Tyr Glu Val Gly Asp Pro Ser Gln		
930	935	940
Lys Ala Leu Asp His Asn Ala Ala Arg Lys Asp Asp Ser Gln Ser Leu		
945	950	955
Ala Asp Asp Ser Gly Lys Glu Glu Glu Asp Ala Glu Cys Ile Asp Asp		
965	970	975
Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu Asp Ser Glu Lys Thr Glu		
980	985	990
Ser Asp Glu Lys Ser Ser Ile Ala Leu Thr Ala Pro Asp Ala Ala Ala		
995	1000	1005
Asp Pro Lys Glu Lys Pro Lys Gln Ala Ser Lys Phe Asp Lys Leu Pro		
1010	1015	1020
Ile Lys Ile Val Lys Lys Asn Asn Leu Phe Val Val Asp Arg Ser Asp		
1025	1030	1035
Lys Leu Gly Arg Val Gln Glu Phe Asn Ser Gly Leu Leu His Trp Gln		
1045	1050	1055
Leu Gly Gly Gly Asp Thr Thr Glu His Ile Gln Thr His Phe Glu Ser		
1060	1065	1070
Lys Met Glu Ile Pro Pro Arg Arg Pro Pro Pro Pro Leu Ser Ser		
1075	1080	1085
Ala Gly Lys Lys Lys Glu Leu Ala Gly Lys Gly Asp Ser Glu Glu Gln		
1090	1095	1100
Gln Glu Lys Ser Ile Ile Ala Thr Ile Asp Asp Val Leu Ser Ala Arg		
1105	1110	1115
Pro Gly Ala Leu Pro Glu Asp Ala Asn Pro Gly Pro Gln Thr Glu Ser		
1125	1130	1135
Ser Lys Phe Pro Phe Gly Ile Gln Gln Ala Lys Ser His Arg Asn Ile		
1140	1145	1150
Lys Leu Leu Glu Asp Glu Pro Arg Ser Arg Asp Glu Thr Pro Leu Cys		
1155	1160	1165
Thr Ile Ala His Trp Gln Asp Ser Leu Ala Lys Arg Cys Ile Cys Val		
1170	1175	1180
Ser Asn Ile Val Arg Ser Leu Ser Phe Val Pro Gly Asn Asp Ala Glu		

1185                      1190                      1195                      1200  
 Met Ser Lys His Pro Gly Leu Val Leu Ile Leu Gly Lys Leu Ile Leu  
                          1205                      1210                      1215  
 Leu His His Glu His Pro Glu Arg Lys Arg Ala Pro Gln Thr Tyr Glu  
                          1220                      1225                      1230  
 Lys Glu Glu Asp Glu Asp Lys Gly Val Ala Cys Ser Lys Asp Glu Trp  
                          1235                      1240                      1245  
 Trp Trp Asp Cys Leu Glu Val Leu Arg Asp Asn Thr Leu Val Thr Leu  
                          1250                      1255                      1260  
 Ala Asn Ile Ser Gly Gln Leu Asp Leu Ser Ala Tyr Thr Glu Ser Ile  
 1265                      1270                      1275                      1280  
 Cys Leu Pro Ile Leu Asp Gly Leu Leu His Trp Met Val Cys Pro Ser  
                          1285                      1290                      1295  
 Ala Glu Ala Gln Asp Pro Phe Pro Thr Val Gly Pro Asn Ser Val Pro  
                          1300                      1305                      1310  
 Ser Pro Gln Arg Leu Val Leu Glu Thr Leu Cys Lys Leu Ser Ile Gln  
                          1315                      1320                      1325  
 Asp Asn Asn Val Asp Leu Ile Leu Ala Thr Pro Pro Phe Ser Arg Gln  
                          1330                      1335                      1340  
 Glu Lys Phe Tyr Ala Thr Leu Val Arg Tyr Val Gly Asp Arg Lys Asn  
 1345                      1350                      1355                      1360  
 Pro Val Cys Arg Glu Met Ser Met Ala Leu Leu Ser Asn Leu Ala Gln  
                          1365                      1370                      1375  
 Gly Asp Ala Leu Ala Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile  
                          1380                      1385                      1390  
 Gly Asn Leu Ile Ser Phe Leu Glu Asp Gly Val Thr Met Ala Gln Tyr  
                          1395                      1400                      1405  
 Gln Gln Ser Gln His Asn Leu Met His Met Gln Pro Pro Pro Leu Glu  
                          1410                      1415                      1420  
 Pro Pro Ser Val Asp Met Met Cys Arg Ala Ala Lys Ala Leu Leu Ala  
 1425                      1430                      1435                      1440  
 Met Ala Arg Val Asp Glu Asn Arg Ser Glu Phe Leu Leu His Glu Gly  
                          1445                      1450                      1455  
 Arg Leu Leu Asp Ile Ser Ile Ser Ala Val Leu Asn Ser Leu Val Ala  
                          1460                      1465                      1470  
 Ser Val Ile Cys Asp Val Leu Phe Gln Ile Gly Gln Leu  
                          1475                      1480                      1485

&lt;210&gt; 1039

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1039

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 gaattacctt ggcctgaggt gttacgagag cacagagaga aaccaggtac agacgcgggg  
 120  
 cagaggggag agaggggagag agtgtgagag ctaagggttc gggagaagac tttgtggaaa  
 180  
 aagtctttgg ctgggtcctg caacatagcc aggattcagt gacaggtgag gaccactcca  
 240  
 gattttgtat gtattgaagg cctgaatac ttttttgaaa gagaatgaca tgagtacacc  
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 360  
 agaaagacct cgccatagt  
 379

<210> 1040  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 1040  
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 Phe Gln Lys Ser Ile Gln Gly Leu Gln Tyr Ile Gln Asn Leu Glu Trp  
 35 40 45  
 Ser Ser Pro Val Thr Glu Ser Trp Leu Cys Cys Arg Thr Gln Pro Lys  
 50 55 60  
 Thr Phe Ser Thr Lys Ser Ser Pro Glu Thr Leu Ala Leu Thr Leu Ser  
 65 70 75 80  
 Pro Ser Leu Pro Ser Ala Pro Arg Leu Tyr Leu Val Ser Leu Cys Ala  
 85 90 95  
 Leu Val Thr Pro Gln Ala Lys Val Ile Pro Cys Gly Gly Gly Leu Ser  
 100 105 110  
 Arg Ala Leu Arg Asp Val Gln Gln His Pro Trp Leu Leu  
 115 120 125

<210> 1041  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<400> 1041  
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 120  
 ttgtcgatga tcccggccct gcacttcccg cattggccgt tgtgggcgtt ggcgcttacc  
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 accccgggtg tgttctgggg tgcctggccg ctgcaccacg ccgctgggac caacctgcgg  
 240  
 cacggcgccg ccatcatgga caccctggtg tcgctcgccg tcctcacttc gtacctctgg  
 300  
 tcggtatgga tgctgaccac aggcggcgag cacctctacc tggaggtagc cgtccaccgt  
 360  
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 388

<210> 1042  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens



&lt;400&gt; 1042

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 Asp Met Ser Ile Glu Thr Ala Tyr Leu Pro Arg Leu Leu Val Ser Leu  
 20 25 30  
 Ala Leu Thr Ile Pro Val Leu Ala Leu Ser Met Ile Pro Ala Leu His  
 35 40 45  
 Phe Pro His Trp Pro Leu Trp Ala Leu Ala Leu Thr Thr Pro Val Val  
 50 55 60  
 Phe Trp Gly Ala Trp Pro Leu His His Ala Ala Trp Thr Asn Leu Arg  
 65 70 75 80  
 His Gly Ala Ala Ile Met Asp Thr Leu Val Ser Leu Gly Val Leu Thr  
 85 90 95  
 Ser Tyr Leu Trp Ser Val Trp Met Leu Thr Thr Gly Gly Glu His Leu  
 100 105 110  
 Tyr Leu Glu Val Ala Val His Arg His Asp Ala Asp Pro Gly Arg Gln  
 115 120 125  
 Ile

&lt;210&gt; 1043

&lt;211&gt; 555

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1043

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 120  
 gatgcctacg gcgcgcaatt acgcgacgca ttgttggtgg aaggcatcga ttgccaggcc  
 180  
 gtcagcaccg tcgacgggtc cagcgggtgtg gcgctgatcg tgggtggatga cagcagccag  
 240  
 aatgcgatcg ttatcgtcgc cggtagcaat ggcgagctga ctccggccaa gttacagacc  
 300  
 tttgacagcg tgctgcaggc tgccgacgtg attgtctgcc agcttgagac gccgatggac  
 360  
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 420  
 gcgcgggcca ggggcccgct gcctgaggat tggtagccg ccatcgatta cctgattccc  
 480  
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 540  
 gtcgctgcta cgcgt  
 555

&lt;210&gt; 1044

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1044

Thr Gly Glu Thr Leu Ile Gly Gln Ser Phe Ser Thr Val Pro Gly Gly

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Lys Gly Ala Asn Gln Ala Val Ala Ser Ala Arg Leu Gly Ala Glu Val
      20           25           30
Ala Met Val Gly Cys Val Gly Thr Asp Ala Tyr Gly Ala Gln Leu Arg
      35           40           45
Asp Ala Leu Leu Val Glu Gly Ile Asp Cys Gln Ala Val Ser Thr Val
      50           55           60
Asp Gly Ser Ser Gly Val Ala Leu Ile Val Val Asp Asp Ser Ser Gln
      65           70           75           80
Asn Ala Ile Val Ile Val Ala Gly Ser Asn Gly Glu Leu Thr Pro Ala
      85           90           95
Lys Leu Gln Thr Phe Asp Ser Val Leu Gln Ala Ala Asp Val Ile Val
      100          105          110
Cys Gln Leu Glu Thr Pro Met Asp Thr Val Gly His Ala Pro Lys Arg
      115          120          125
Gly Arg Glu Leu Gly Lys Thr Val Ile Leu Asn Pro Ala Pro Ala Ser
      130          135          140
Gly Pro Leu Pro Glu Asp Trp Tyr Ala Ala Ile Asp Tyr Leu Ile Pro
      145          150          155          160
Asn Glu Ser Glu Ala Ser Ala Leu Ser Gly Val Val Val Asp Ser Leu
      165          170          175
Asp Ser Ala Lys Val Ala Ala Thr Arg
      180          185

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&lt;210&gt; 1045

&lt;211&gt; 371

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1045

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120
cgcgccatgc acgattacca cgcaccgccg gcagagcgca tgccaattgg gcaccgaagg
180
cagaccacca cccaggtgca aagcaacagt ggtagagcgg tcgctcatcg acgaaacgta
240
cggaagaaga cgaagagacg gagcaggaaa gacctgttat ggaatcacag aaccacatcg
300
ggcagggcgg cgagcacaaa accatatgcg catcgcgaca ttaaaccagg tacgtgctgc
360
aagctcctcg g
371

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&lt;210&gt; 1046

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1046

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Leu Leu Pro Tyr Tyr Arg Arg Gly Asn Leu Gln Asp Met Ile Asn Ala
1           5           10           15
Asn Leu Phe Asn His Ser Lys Phe Pro Glu Thr His Leu Met Asn Leu

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	20		25		30										
Phe	Leu	Gly	Val	Cys	Lys	Ala	Leu	Arg	Ala	Met	His	Asp	Tyr	His	Ala
	35		40		45										
Pro	Pro	Ala	Glu	Arg	Met	Pro	Ile	Gly	His	Arg	Arg	Gln	Thr	Thr	Thr
	50		55		60										
Gln	Val	Gln	Ser	Asn	Ser	Gly	Arg	Ala	Val	Ala	His	Arg	Arg	Asn	Val
65			70		75									80	
Arg	Lys	Lys	Thr	Lys	Arg	Arg	Ser	Arg	Lys	Asp	Leu	Leu	Trp	Asn	His
			85		90									95	
Arg	Thr	Thr	Ser	Gly	Arg	Ala	Ala	Ser	Thr	Lys	Pro	Tyr	Ala	His	Arg
			100		105									110	
Asp	Ile	Lys	Pro	Gly	Thr	Cys	Cys	Lys	Leu	Leu					
	115				120										

&lt;210&gt; 1047

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1047

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 60  
 cgcaacctca acaagaacga agtgacctag gtacgtgcca tgcagcggcc acccccgggt  
 120  
 gtgaaactgg tcatagaagc tgtgtgcatt atgaaaggca tcaagcccaa gaagggtgcct  
 180  
 ggagaaaagc caggcaccaa ggtggatgac tactgggagc ctggcaagggt gctgctgcag  
 240  
 gaccggggcc acttccttga gagcctcttc aagtttgaca aggacaacat tggagatgtg  
 300  
 gtgatcaaag ccatccagcc gtacatcgat aatgaagagt tccagccagc caccattgcc  
 360  
 aagggtgtcca agggttgccc ctcatcttgg ccgtgggggg gggcaatgcc caagtacccc  
 420  
 tttgtggcca aggcctgga gcccaagcgg caagccctgc tggaggccca ggatgacctg  
 480  
 ggggtgacac agaggatcct ggatgaggca aaacagcgcc ttcgtgaggt ggaggacggc  
 540  
 atcgccacaa tgcaggctaa gtaccgggaa tgcattacca agaaggagga gctggagctg  
 600  
 aagtgtgagc agtgtgagca gcggtgggc cacgctggca aggtgcgcac cctcctcctg  
 660  
 caaggcctgc aagcggggcc ggcccagaca ggggccagaa aggaccagggt cgccggtggg  
 720  
 tcctgggggtg gctgtccaac cccctcctg gcaa  
 754

&lt;210&gt; 1048

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1048

Xaa Ala Gln Lys Asp Leu Asp Glu Ala Leu Pro Ala Leu Asp Ala Ala

1	5	10	15
Leu Ala Ser Leu Arg Asn Leu Asn Lys Asn Glu Val Thr Gln Val Arg			
20	25	30	
Ala Met Gln Arg Pro Pro Pro Gly Val Lys Leu Val Ile Glu Ala Val			
35	40	45	
Cys Ile Met Lys Gly Ile Lys Pro Lys Lys Val Pro Gly Glu Lys Pro			
50	55	60	
Gly Thr Lys Val Asp Asp Tyr Trp Glu Pro Gly Lys Gly Leu Leu Gln			
65	70	75	80
Asp Pro Gly His Phe Leu Glu Ser Leu Phe Lys Phe Asp Lys Asp Asn			
85	90	95	
Ile Gly Asp Val Val Ile Lys Ala Ile Gln Pro Tyr Ile Asp Asn Glu			
100	105	110	
Glu Phe Gln Pro Ala Thr Ile Ala Lys Val Ser Lys Gly Cys Pro Phe			
115	120	125	
Ile Trp Pro Trp Gly Gly Ala Met Pro Lys Tyr Pro Phe Val Ala Lys			
130	135	140	
Ala Val Glu Pro Lys Arg Gln Ala Leu Leu Glu Ala Gln Asp Asp Leu			
145	150	155	160
Gly Val Thr Gln Arg Ile Leu Asp Glu Ala Lys Gln Arg Leu Arg Glu			
165	170	175	
Val Glu Asp Gly Ile Ala Thr Met Gln Ala Lys Tyr Arg Glu Cys Ile			
180	185	190	
Thr Lys Lys Glu Glu Leu Glu Leu Lys Cys Glu Gln Cys Glu Gln Arg			
195	200	205	
Leu Gly His Ala Gly Lys Val Arg Thr Leu Leu Leu Gln Gly Leu Gln			
210	215	220	
Ala Gly Pro Ala Gln Thr Gly Ala Arg Lys Asp Gln Gly Ala Gly Gly			
225	230	235	240
Ser Trp Gly Gly Cys Pro Thr Pro Ser Leu Ala			
245	250		

&lt;210&gt; 1049

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1049

cgcagcaata gctgcacttg accagactgg gctttgcaat aagcgcattc cccgggctga  
 60  
 atgctgcaga tccttacagg ctgactgcag ggtgtttcag attctcctgg agtcacacgt  
 120  
 gccagcttga tttcaagaaa caactagaat aacagttttc tgataagaag tctatagcac  
 180  
 tttatggctt acataatcca gagatagatg ggctgggcat gattccattt ttctgttggg  
 240  
 gaaaccgact cacagagaag ttaagggaca agtataaagt gatgaaactg tgtactgaac  
 300  
 ctcatgtctc ccagactccc ggggtccccg gctttttctc ggggcgggcc cattcacatt  
 360  
 gcaattcatg gccggggcaa atgctcacc acagagatat taagcactcc aacactccat  
 420  
 ccaccagggt gcagccaaag gattcagaag acaatgatca ttccatcagc atgcactatg  
 480

cagctaaaga aagggttttgg catgctctgc tttattgttt cacagaagat aagaaaataa  
540

actgcaaagt aacttaag  
558

<210> 1050

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1050

Met	Ile	Pro	Ile	Phe	Cys	Trp	Gly	Asn	Arg	Leu	Thr	Glu	Lys	Leu	Arg
1				5				10						15	
Asp	Lys	Tyr	Lys	Val	Met	Lys	Leu	Cys	Thr	Glu	Pro	His	Val	Ser	Gln
			20				25					30			
Thr	Pro	Gly	Ser	Pro	Gly	Phe	Phe	Ser	Gly	Arg	Pro	His	Ser	His	Cys
		35				40						45			
Asn	Ser	Trp	Pro	Gly	Gln	Met	Leu	Thr	His	Arg	Asp	Ile	Lys	His	Ser
50					55					60					
Asn	Thr	Pro	Ser	Thr	Arg	Leu	Gln	Pro	Lys	Asp	Ser	Glu	Asp	Asn	Asp
65				70					75					80	
His	Ser	Ile	Ser	Met	His	Tyr	Ala	Ala	Lys	Glu	Arg	Phe	Trp	His	Ala
			85					90						95	
Leu	Leu	Tyr	Cys	Phe	Thr	Glu	Asp	Lys	Lys	Ile	Asn	Cys	Lys	Val	Thr
			100					105						110	

<210> 1051

<211> 317

<212> DNA

<213> Homo sapiens

<400> 1051

gcgttgagtc gggatgtcgc attcatgccc ggcgaacctt tttttgccga accggagcgt  
60  
aatccgggta atcttcgtct caatttcagt cacatcgcac cggagcgtct ggacgaagggt  
120  
ctcaagcgcc tggctgctgt catccgtcac gcacaggctg cacaagcggc ttaaggggag  
180  
ggccatgtac aagggttatg gcgattacca gtcgggcaat tgctacaaga tcaagctgat  
240  
gctgcacctg ctggggcagg aatatcgctg gcacccgggg gacatcctca aggtgacacc  
300  
gagaccccg aattttt  
317

<210> 1052

<211> 57

<212> PRT

<213> Homo sapiens

<400> 1052

Ala	Leu	Ser	Arg	Asp	Val	Ala	Phe	Met	Pro	Gly	Glu	Pro	Phe	Phe	Ala
1					5				10					15	
Glu	Pro	Glu	Arg	Asn	Pro	Gly	Asn	Leu	Arg	Leu	Asn	Phe	Ser	His	Ile

```

                20                25                30
Ala Pro Glu Arg Leu Asp Glu Gly Leu Lys Arg Leu Ala Ala Val Ile
                35                40                45
Arg His Ala Gln Ala Ala Gln Ala Ala
                50                55

```

<210> 1053  
 <211> 318  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1053
caattggcta cgcatccga acgggcgcac gggctctctat gactggcaag ccgtcgctcg
60
cggggagtg ggcctcgact atgcctacgc gatgctgggtg aacctgacca ccgagaaccg
120
gcgtgcctgg gaacgcgacc tgctcgagcg ttatctgtgg cgctcgccg aagaggggtg
180
cgccaaccgg ccctcggtcg agcaagcgtg gctacgctac cggcaacagc cgttccacgt
240
cgggatcttc tcaactctga ccacgcggcg cggaagcttt caaccggcca tgcaaccggc
300
ggactcnnnn ccccnenc
318

```

<210> 1054  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1054
Met Gly Leu Tyr Asp Trp Gln Ala Val Ala Arg Gly Glu Trp Ala Leu
 1      5      10      15
Asp Tyr Ala Tyr Ala Met Ser Val Asn Leu Thr Thr Glu Asn Arg Arg
      20      25      30
Ala Trp Glu Arg Asp Leu Leu Glu Arg Tyr Leu Trp Arg Leu Ala Glu
      35      40      45
Glu Gly Val Ala Asn Pro Pro Ser Phe Glu Gln Ala Trp Leu Arg Tyr
      50      55      60
Arg Gln Gln Pro Phe His Val Gly Ile Phe Ser Leu Leu Thr Ile Gly
65      70      75      80
Ala Gly Arg Phe Gln Pro Ala Met Gln Pro Ala Asp Ser Xaa Pro Xaa
      85      90      95

```

<210> 1055  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1055
tacaatgtat catcaaccag aaatacaatg agaaccacct gccagtctcc caaatactat
60
ctgcagccac tcatttaact ctctgggcta gctccacgtg ggccgtctga actctcttag
120

```

aagaatcatc tctctgctca ggcaccggga gcaaggggca tctgtcgctc tgcagaacgg  
 180  
 aggggaccag gcctgatgaa caccatcctg ggcccagaaa cctgggaggg taaagagaac  
 240  
 tgccaggggt gaagtccaag gatgggaaaa aggcctccgg ggcagagtcc tgaaatgtca  
 300  
 gaagtacacc aaagaggaaa cagcatcacg ttattgctga ggcagggcct cattctgttg  
 360  
 ccaaggctgc agtgcagtgg tgacaccatg g  
 391

<210> 1056

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1056

Met	Val	Ser	Pro	Leu	His	Cys	Ser	Leu	Gly	Asn	Arg	Met	Arg	Pro	Cys
1				5					10					15	
Leu	Ser	Asn	Asn	Val	Met	Leu	Phe	Pro	Leu	Trp	Cys	Thr	Ser	Asp	Ile
			20					25					30		
Ser	Gly	Leu	Cys	Pro	Gly	Gly	Leu	Phe	Pro	Ile	Leu	Gly	Leu	His	Pro
		35					40					45			
Trp	Gln	Phe	Ser	Leu	Pro	Ser	Gln	Val	Ser	Gly	Pro	Arg	Met	Val	Phe
	50					55				60					
Ile	Arg	Pro	Gly	Pro	Leu	Arg	Ser	Ala	Glu	Arg	Gln	Met	Pro	Leu	Ala
65					70					75				80	
Pro	Gly	Ala													

<210> 1057

<211> 341

<212> DNA

<213> Homo sapiens

<400> 1057

gaattccctg cgcgtgtgac gccggtcgcc gagcaactcg gcgtgtcgct gacgctgcat  
 60  
 cccgatgac cgcgcgtcc gctgttcggg ttgccgcgca ttgcgtccag cgccgaggac  
 120  
 tatcaggcgc tggtcgatgc ggtaccgtcc aaggcgaacg gcattctgcct gtgcacgggt  
 180  
 tcgctcggcg tgcgcgcgga gaacgatctg cctgaaatgg ccgaacgttt cgccccgcgt  
 240  
 atcgcccttg cgcattctgcg cgcgaccaag cgcgacgccg atggcctgtc gtttcatgaa  
 300  
 tccgaccatc tcgacggcga tgtcgacatg gtcgcgtgct c  
 341

<210> 1058

<211> 113

<212> PRT

<213> Homo sapiens

&lt;400&gt; 1058

Glu Phe Pro Ala Arg Val Thr Pro Val Ala Glu Gln Leu Gly Val Ser  
 1 5 10 15  
 Leu Thr Leu His Pro Asp Asp Pro Pro Arg Pro Leu Phe Gly Leu Pro  
 20 25 30  
 Arg Ile Ala Ser Ser Ala Glu Asp Tyr Gln Ala Leu Phe Asp Ala Val  
 35 40 45  
 Pro Ser Lys Ala Asn Gly Ile Cys Leu Cys Thr Gly Ser Leu Gly Val  
 50 55 60  
 Arg Ala Glu Asn Asp Leu Pro Glu Met Ala Glu Arg Phe Gly Pro Arg  
 65 70 75 80  
 Ile Ala Phe Ala His Leu Arg Ala Thr Lys Arg Asp Ala Asp Gly Leu  
 85 90 95  
 Ser Phe His Glu Ser Asp His Leu Asp Gly Asp Val Asp Met Val Ala  
 100 105 110  
 Cys

&lt;210&gt; 1059

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1059

nagctgaccg gctggcagat caacatcatg acgccggaag aaagcgtgaa ccgccgggaa  
 60  
 gtcgagcggtt cgggcctgcg caccacgttc atgaacaagc tggacgtcga tgaggaagtc  
 120  
 gccgacatcc tgatcgacga aggtttcacc ggtatcgagg aaatcgcccta cgtccccatg  
 180  
 caggaactgc tggagatcga ggcgttcgac gaagacacca tcaacgagtt gcgcgcccgt  
 240  
 gcccgcaatg cgctgctgac cgaggccatc gcccggaag agcgccctga gaccgcgcag  
 300  
 gatctgcttg aactcgaagg cgtgacgccg gaactggctg ccaagctggc cgagcgtcaa  
 360  
 gtgcgtacgc gt  
 372

&lt;210&gt; 1060

&lt;211&gt; 124

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1060

Xaa Leu Thr Gly Trp Gln Ile Asn Ile Met Thr Pro Glu Glu Ser Val  
 1 5 10 15  
 Asn Arg Arg Glu Val Glu Arg Ser Gly Leu Arg Thr Thr Phe Met Asn  
 20 25 30  
 Lys Leu Asp Val Asp Glu Glu Val Ala Asp Ile Leu Ile Asp Glu Gly  
 35 40 45  
 Phe Thr Gly Ile Glu Glu Ile Ala Tyr Val Pro Met Gln Glu Leu Leu  
 50 55 60  
 Glu Ile Glu Ala Phe Asp Glu Asp Thr Ile Asn Glu Leu Arg Ala Arg



```

65              70              75              80
Ala Arg Asn Ala Leu Leu Thr Glu Ala Ile Ala Gln Glu Glu Arg Leu
              85              90              95
Glu Thr Ala Gln Asp Leu Leu Glu Leu Glu Gly Val Thr Pro Glu Leu
              100              105              110
Ala Ala Lys Leu Ala Glu Arg Gln Val Arg Thr Arg
              115              120

```

<210> 1061  
 <211> 456  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1061
tctagactcc atggcaccgg gctgagcggg taagtaagaa agataaaaag tgccttttgc
60
cccttcgagg aaaccctttt gcaggccaag caagggtgc aagtgtttgg gagctgagag
120
gagaaggagg attctggagc attgtatttg gcagccggag cgggcagtgg gcgggggggtt
180
gggacacgaa gggctcttcg gaccctgtg cctcttctgc cccaagggcg agaagacggg
240
cttcgcagcg accctcgggg gtccatggag ccgcctgcct tcgccccctc gctcttccca
300
ggtctgaacc tggatgggga gaagaaattg aagtgttttg gagacggggg ggcttaaaac
360
actagggagc ctcatcgccc agccttgggc ccactttcct ttcgatcgtg aggattccgc
420
accccgaaagc cgtcttctcg gggctccggg gcgcgc
456

```

<210> 1062  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1062
Met Arg Leu Pro Ser Val Leu Ser Pro Pro Val Ser Lys Ala Leu Gln
1      5      10      15
Phe Leu Leu Pro Ile Gln Val Gln Thr Trp Glu Glu Arg Gly Gly Glu
20     25     30
Gly Arg Arg Leu His Gly Pro Pro Arg Val Ala Ala Lys Pro Val Phe
35     40     45
Ser Pro Leu Gly Gln Lys Arg His Arg Gly Pro Lys Ser Pro Ser Cys
50     55     60
Pro Asn Pro Pro Pro Thr Ala Arg Ser Gly Cys Gln Ile Gln Cys Ser
65     70     75     80
Arg Ile Leu Leu Leu Leu Ser Ala Pro Lys His Leu Gln Pro Leu Leu
85     90     95
Gly Leu Gln Lys Gly Phe Leu Glu Gly Ala Lys Gly Thr Phe Tyr Leu
100    105    110
Ser Tyr Leu Pro Ala Gln Pro Gly Ala Met Glu Ser Arg
115    120    125

```

&lt;210&gt; 1063

&lt;211&gt; 3760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1063

ntagtagaga cagggtttca ccatgttggc caggctggc ttgaactcct gagcttgtga  
60  
tccaccgcgc tcagcctccc aaagtgtgg gattacaggc gtgacgactg caccagcct  
120  
taaggtctta taactagtaa atatctgcat taaagaacga gttgaatgaa aattctgata  
180  
aattcctact taaagtgtat ccaaagaaaa cggaaaaagt ctaggagtta gtgatattag  
240  
attcagaaga atgagctttg taattcttaa aaattagtct cagaatagaa aggattttaa  
300  
aagtaattga gtaaagtcac aggaaatgtg accatataaa ggaatggctc taaatgtatt  
360  
aatccagaag gaagcaacag gttaaacagt aagaggtaag aaacaaaaaa taaggaacga  
420  
gagagagaga gtgacaggga gagagagaca gagcggggaa ggagagaatg agaaggaaaa  
480  
tcaggaaaac gaggagaaac agaattaagg aggtgatact ggaatagtat cagaccattc  
540  
tgaatcaatt taagaattgc catgtctaata tcttatatgg aagatttgaa atacaaggat  
600  
attgaaagga ataacaaatt ataatgaatg catagaaatc cttatgtaat ccaaggtcac  
660  
taatttgaag gaagacatca agaaaatgtg atctagaaat aaagggtgag attgctccat  
720  
ttacaaaatt attatgctct ataattcttc catatgcaaa tatttcatat tccctctttt  
780  
gtcccatgga catatttcac agcaacaacg aatcaagtgc tgacctaaat ggggtatctg  
840  
ttaaaaactta gtatattgat atccttcacc ccaactccagg aacgttcgct acgctaggac  
900  
tgcactcttg gaacagaatt ttagagatga tcactcttta catcagaagc aggatctaaa  
960  
tgatccctgg atgcccatt tccctgacct gctattgttg tgggtggcaa gataagagga  
1020  
gttgcatcac agatgaaaaa gtaaggccga agaagaccag agaagagttg gttgaatgtg  
1080  
tagatataag atccatctgt gacattgtag aatgaaattt caccggcttc atagtccaag  
1140  
aaaatcccaa tgcagtgagg actttccagt tggagaagag gcaactgatgg ggaggcaagg  
1200  
accatgtact cattcccttt cagcagccac agggcccgaga cccattctc aggagatggc  
1260  
gtgggtttccc cctttcttgg cagtgtgtct tgacagaccc cttaaacccta ctctgctcct  
1320  
tctcccacca gaacctccca gtaatgcctc cctgatgaga agctctgcaa acccaggatg  
1380  
cagggccatg tgtcaaactg ctcagggttg ttggggacat cctccatgg ttctccatcc  
1440

tgcacactgc gcaggtcggc ggtcaagagc agactcgggt gcgccgtggc gggatccagc  
1500  
tttacatcca cttggaactt ccttaagagc tccctcctcc cagggatgca gcatgctgtc  
1560  
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1620  
actccttca caccctccag cagacccagg gctgggcgct ggcacctctc ctgcagctca  
1680  
tccgccagct ccttcagggc cttgctctgc tggaccagcc ggctcttgct ctcccgcagt  
1740  
ctctgcagcg tcgctcgctc ctccgcctcc agccgcctca gctaccaggt aaagctccag  
1800  
atggctctgg aacttatgag gaaagagttg gaggacgcct tgactcagga ggccaacgtg  
1860  
gggaaaaaga ctgtcatttg gaaggagaaa gtggaaatgc agaggcagcg cttcagattg  
1920  
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1980  
gaggcggagg agcgagcgac gctgcagaga ctgcgggaga gcaagagccg gctggtccag  
2040  
cagagcaagg ccctgaagga gctggcggat gagctgcagg agaggtgcca gcgccagcc  
2100  
ctgggtctgc tggaggggtg gagaggagtc ctgagcagaa gtaaggctgt cacaaggctg  
2160  
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2220  
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2280  
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2340  
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2460  
gacacactgc caagaaaggg ggaaccatg ccatctcctg agaatggggt ctgggccctg  
2520  
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2580  
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2640  
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2700  
cggccttact ttttcatctg tgatgcaact cctcttatct tgccaccac gacaatagca  
2760  
gggtcaggaa attgggcatc cagggatcat ttagatcctg cttctgatgt aagagatgat  
2820  
catctctaaa attctgttcc caagatgcag tcctagcgta gcgaacgttc ctggagtggg  
2880  
gtgaaggata tcaatatact aagttttaac agatacccca tttaggtcag cacttgattc  
2940  
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3000  
gaagattata gagcataata attttgtaaa tggagcaatc tcaacctcta tttctagatc  
3060

acattttctt gatgtcttcc ttcaaattaa tgaccttgga ttacataagg atttctatgc  
 3120  
 attcattata atttgttatt cttttcaata tccttgtatt tcaaattcttc catataagaa  
 3180  
 ttagacatgg caattcttaa attgattcag aatgggtctga tactattcca gtatcacctc  
 3240  
 ctttaattctg tttctcctcg ttttctgat tttccttctc attctctcct tccccgctct  
 3300  
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 3360  
 ctgtttaacc tgttgcttcc ttctggatta atacatttag agccattcct ttatatggtc  
 3420  
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 3480  
 taagaattac aaagctcatt cttctgaatc taatatcact aactcctaga ctttttccgt  
 3540  
 tttctttgga tacactttaa gtaggaattt atcagaattt tcattcaact cgttctttaa  
 3600  
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 3660  
 ccagcgcttt ggggggctga ggcgggtgga tcacaggctc gggagttcgg ggccagcctg  
 3720  
 gccagcatgg tgaaaccctg tctctactag aaaaaaaaaa  
 3760

<210> 1064

<211> 483

<212> PRT

<213> Homo sapiens

<400> 1064

Met	Gln	Gly	His	Val	Ser	Asn	Arg	Ser	Gly	Leu	Leu	Gly	Thr	Ser	Leu
1				5					10					15	
His	Gly	Ser	Pro	Ser	Cys	Thr	Leu	Arg	Arg	Ser	Ala	Val	Lys	Ser	Arg
			20					25					30		
Leu	Gly	Cys	Ala	Val	Ala	Gly	Ser	Ser	Phe	Thr	Ser	Thr	Trp	Asn	Phe
		35					40					45			
Leu	Lys	Ser	Ser	Leu	Leu	Pro	Gly	Met	Gln	His	Ala	Val	Phe	Ser	Ser
	50					55					60				
Met	Gly	Met	Phe	Ser	Ala	Ser	Ser	Leu	Val	Thr	Ala	Leu	Leu	Leu	Leu
65					70					75				80	
Arg	Thr	Pro	Leu	Thr	Pro	Ser	Ser	Arg	Pro	Arg	Ala	Gly	Arg	Trp	His
				85					90					95	
Leu	Ser	Cys	Ser	Ser	Ser	Ala	Ser	Ser	Phe	Arg	Ala	Leu	Leu	Cys	Trp
			100					105					110		
Thr	Ser	Arg	Leu	Leu	Leu	Ser	Arg	Ser	Leu	Cys	Ser	Val	Ala	Arg	Ser
		115					120					125			
Ser	Ala	Ser	Ser	Arg	Leu	Ser	Tyr	Gln	Val	Lys	Leu	Gln	Met	Ala	Leu
	130					135					140				
Glu	Leu	Met	Arg	Lys	Glu	Leu	Glu	Asp	Ala	Leu	Thr	Gln	Glu	Ala	Asn
145					150					155				160	
Val	Gly	Lys	Lys	Thr	Val	Ile	Trp	Lys	Glu	Lys	Val	Glu	Met	Gln	Arg
				165					170					175	
Gln	Arg	Phe	Arg	Leu	Glu	Phe	Glu	Lys	His	Arg	Gly	Phe	Leu	Ala	Gln

	180		185		190
Glu	Glu	Gln	Arg	Gln	Leu
	195		200		205
Leu	Gln	Arg	Leu	Arg	Glu
	210		215		220
Ala	Leu	Lys	Glu	Leu	Gln
	225		230		235
Ala	Leu	Gly	Leu	Glu	Gly
		245		250	
Ala	Val	Thr	Arg	Leu	Glu
		260		265	
Ala	Cys	Cys	Ile	Pro	Gly
		275		280	
Asp	Val	Lys	Leu	Asp	Pro
		290		295	
Ala	Asp	Leu	Arg	Ser	Val
		305		310	
Asn	Asn	Pro	Glu	Arg	Phe
			325		330
Ser	Phe	Ser	Ser	Gly	Arg
			340		345
Ala	Glu	Trp	Gly	Leu	Gly
		355		360	
Glu	Thr	Met	Pro	Ser	Pro
		370		375	
Lys	Gly	Asn	Glu	Tyr	Met
		385		390	
Gln	Leu	Glu	Ser	Pro	Arg
			405		410
Gly	Glu	Ile	Ser	Phe	Tyr
		420		425	
Phe	Asn	Gln	Leu	Phe	Ser
		435		440	
Asp	Ala	Thr	Pro	Leu	Ile
		450		455	
Asn	Trp	Ala	Ser	Arg	Asp
		465		470	
Asp	His	Leu			

&lt;210&gt; 1065

&lt;211&gt; 892

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1065

nacgcgtggt gtcattggga ggtgggctgc agtgatgaga aaaggccggg ggctgtgcaa  
 60  
 taccatgctt cacaaggga gaagatcaaa gtgacctcc cccatggctt tggaaccttc  
 120  
 ttgtccagtc tggaaggggg gaagaagaga tgaggggaag gctgtccagg ggggtgcaag  
 180  
 gccctagaga cccagcagag aagggaactct ggccactgaa ggggacctcc cattgtggct  
 240

ctggttcctt agagcagctc cagcttcttg gcctcccccg tctgatgctt agctcatccc  
 300  
 atccccctgga gtgctgtgga gcttagatga aacagcccag tgctcactct tcaatgagcc  
 360  
 caccagagc agcatcaaga tgcagttggc ggggtactgg aactggcttg gcaagggctg  
 420  
 cgcaggcaac aggtcccagc aagagtcagc tagcctagct cagccctgca cacctggaga  
 480  
 cctgggggtg ctccagacac ctcgccctt taggtccctt taattgaatg tgtgtggatc  
 540  
 agtgaagggt gaggaatcat ttctctatgg cccaagacgt ttctctctgc agttgtcatg  
 600  
 ttagtacctg ccagcttttc ctctcttaca taaatttcat gccagagcct ggaaatgtgt  
 660  
 gccctttgta ggaggggcat cacaggtctg ctcacctcag cagtgccagg cagagcccgt  
 720  
 ccctctcatt gcaggaggcg catgaagcgt gtctgggacc gagctgtgga gttcctggcc  
 780  
 tccaacgaat cccggatcca gacggagtcc caccgcgttg caggagagga catgctgggt  
 840  
 ttgagatgga ctaagccctc ttccttctct gactcagagc gataagcccg gg  
 892

&lt;210&gt; 1066

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1066

Met	Cys	Ala	Leu	Cys	Arg	Arg	Gly	Ile	Thr	Gly	Trp	Leu	Thr	Ser	Ala
1				5					10					15	
Val	Pro	Gly	Arg	Ala	Arg	Pro	Ser	His	Cys	Arg	Arg	Arg	Met	Lys	Arg
			20					25					30		
Val	Trp	Asp	Arg	Ala	Val	Glu	Phe	Leu	Ala	Ser	Asn	Glu	Ser	Arg	Ile
		35				40						45			
Gln	Thr	Glu	Ser	His	Arg	Val	Ala	Gly	Glu	Asp	Met	Leu	Val	Leu	Arg
	50				55						60				
Trp	Thr	Lys	Pro	Ser	Ser	Phe	Ser	Asp	Ser	Glu	Arg				
65					70					75					

&lt;210&gt; 1067

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1067

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 60  
 gttctcaccg atcccgaggg caaccgtcac ctactgaca tgcaccaggt cgagccctgg  
 120  
 ggactagaca tctggaaagc ccgagtctcc gctgacatcg aaggcgactg gactatgcac  
 180  
 gttgaaggct ggtcagacac ctggggcacg tggcatcaca atgccaatgc caagctcgcc  
 240

gctgccatcg acgtcgaact ggtgtgccc gaaggccatg cccatcataa cgaggcggtc  
 300  
 cggcacgccc agcaatccgg ggatactgac gcgatcacgg ctctgcgcga gaccgatgcc  
 360  
 aacctaaccc ttgaccgtgc ccccgactcg ctacaacagg tcatcaacac ctacgcgt  
 418

<210> 1068  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 1068  
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 Gly Ala Ser Val Val Leu Thr Asp Pro Glu Gly Asn Arg His Leu Thr  
 20 25 30  
 Asp Met His Gln Val Glu Pro Trp Gly Leu Asp Ile Trp Lys Ala Arg  
 35 40 45  
 Val Ser Ala Asp Ile Glu Gly Asp Trp Thr Met His Val Glu Gly Trp  
 50 55 60  
 Ser Asp Thr Trp Gly Thr Trp His His Asn Ala Asn Ala Lys Leu Ala  
 65 70 75 80  
 Ala Ala Ile Asp Val Glu Leu Val Cys Ala Glu Gly His Ala Leu Ile  
 85 90 95  
 Asn Glu Ala Val Arg His Ala Glu Gln Ser Gly Asp Thr Asp Ala Ile  
 100 105 110  
 Thr Ala Leu Arg Glu Thr Asp Ala Asn Leu Thr Leu Asp Arg Ala Pro  
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 130 135

<210> 1069  
 <211> 371  
 <212> DNA  
 <213> Homo sapiens

<400> 1069  
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 cagttcatat gccgtcactc ccagggaacca ccagtcaaca gcaaaggaat agcctgctcc  
 120  
 ttttctggag ctgaacatct caggtgccat gtaaggcttg gtgccagcca tgggtggagac  
 180  
 ctgcgttatc acctgcaaca gaacgtccac ttcaaggaag aaacagtga gctcttcac  
 240  
 tgtgagctgg tcatggccct ggactacctg cagaaccagc gcatcattca cagggatatg  
 300  
 aagcctgaca atattttact tgacgaacat gggcacgtgc acatcacaga tttcaacatt  
 360  
 gctgcgatgc t  
 371

<210> 1070

<211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 1070  
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 Pro Ala Ser Gln Gln Phe Ile Cys Arg His Ser Gln Gly Pro Pro Val  
 20 25 30  
 Asn Ser Lys Gly Ile Ala Cys Ser Phe Ser Gly Ala Glu His Leu Arg  
 35 40 45  
 Cys His Val Arg Leu Gly Ala Ser His Gly Gly Asp Leu Arg Tyr His  
 50 55 60  
 Leu Gln Gln Asn Val His Phe Lys Glu Glu Thr Val Lys Leu Phe Ile  
 65 70 75 80  
 Cys Glu Leu Val Met Ala Leu Asp Tyr Leu Gln Asn Gln Arg Ile Ile  
 85 90 95  
 His Arg Asp Met Lys Pro Asp Asn Ile Leu Leu Asp Glu His Gly His  
 100 105 110  
 Val His Ile Thr Asp Phe Asn Ile Ala Ala Met  
 115 120

<210> 1071  
 <211> 998  
 <212> DNA  
 <213> Homo sapiens

<400> 1071  
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 120  
 cccacccgaa gtacgtggcc ttggagtgcc attcgactc cacttgcca ccgtttgcat  
 180  
 tcgacctaac cagcaattgc atctcgtttg acctgctcgc gttgtcaaca tcatagcaac  
 240  
 gagcggccaa tagcagagtt ctggtcatec tgttccgcc ttcctcctat ttgaagcctc  
 300  
 agtttcagca aagagctggt tatgagtttt ccgtcaaacg gcgcttgat aggcataagg  
 360  
 ggtataccta tgatgcgtgt attcacagtt aaaaagggtt ctctcatggg ccatacagat  
 420  
 tcaaacaaag acgatcttct caaacgcgtg aaacgcacg cggggcaaat ccaggccgtt  
 480  
 gagcgtgcac tggagtcgga tgccgattgc gcgaaaacat tgcattctgt agctgccaca  
 540  
 cgtggagcta tcaacggctt gatggacgaa attattgagg atcacgccag aaaacatgtg  
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 660  
 attcgccgct actccaagtg aagaatccag gtacatgtcc atgagtagca gcccataat  
 720  
 cgagattagc cacatacatg accatgtgtt ccttgggtca gcacgcgaag aaaatgccaa  
 780



gcgtaccctt tgggttggtg cgcttacggt ggtgatgatg gttggcgaaa tcgtcgccgg  
840  
ctatctcact ggctcaatgg ctttacttgc cgacggggtt tcacaaggca accccatgca  
900  
ggcgctttgg gcatcgctgc agctgcctac ggttacgcaa aacgccacgc ttccagcagt  
960  
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998

<210> 1072

<211> 72

<212> PRT

<213> Homo sapiens

<400> 1072

Met	Gly	His	Thr	Ala	Ser	Asn	Lys	Asp	Asp	Leu	Leu	Lys	Arg	Val	Lys
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Arg	Ile	Ala	Gly	Gln	Ile	Gln	Ala	Val	Glu	Arg	Ala	Leu	Glu	Ser	Asp
		20					25				30				
Ala	Asp	Cys	Ala	Lys	Thr	Leu	His	Leu	Val	Ala	Ala	Thr	Arg	Gly	Ala
		35				40					45				
Ile	Asn	Gly	Leu	Met	Asp	Glu	Ile	Ile	Glu	Asp	His	Ala	Arg	Lys	His
	50				55					60					
Val	Ala	Ser	Pro	Thr	Leu	Ser	Asp								
65					70										

<210> 1073

<211> 468

<212> DNA

<213> Homo sapiens

<400> 1073

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120  
ttccccact gataaaatct tgcttctctt caaactccta ggcaaatctt tcttacttca  
180  
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240  
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300  
cactctctgt ataatatctg gttttcacct ctttatgaac tcttttgat tctcattact  
360  
ggctctggaa cccagaacat accacggggt caaggatatgt tttaatgaat tgaatggaat  
420  
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468

<210> 1074

<211> 134

<212> PRT

<213> Homo sapiens

&lt;400&gt; 1074

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Met Asp Asn Phe Leu Phe Phe Lys Tyr Thr Leu Pro Met Ser Gln Leu
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Gly Cys Phe Ser Pro Thr Asp Lys Ile Leu Leu Leu Phe Lys Leu Leu
          20           25           30
Gly Lys Phe Leu Leu Leu Gln Lys Val Leu Phe Leu His Ile Leu Arg
          35           40           45
Asn His His Leu Val His Met Leu Lys Ala Glu Phe Ile Val Ser Ser
          50           55           60
Pro Ser Leu Ser Asn Ser Phe Ala Gln Thr Leu Arg Tyr Ser Phe Ile
65           70           75           80
Leu Cys Ile Ile Phe Gly Phe His Leu Phe Met Asn Ser Phe Val Phe
          85           90           95
Ser Leu Leu Ala Leu Glu Pro Arg Thr Tyr His Gly Phe Lys Val Cys
          100          105          110
Phe Asn Glu Leu Asn Gly Ile Asn Phe Val Val Leu Met Gln Ile Gln
          115          120          125
Met Pro Leu Asn Thr Asp
          130

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&lt;210&gt; 1075

&lt;211&gt; 1633

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1075

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gcgcgccagg gatgagtcac agtacttccg cttcatgct gacgaggaga tggaggggac
60
cagcagcaag aacaaacagc ttcgcaacga cttcaagctg gtggagaaca ttctggccaa
120
gcgcctgctg atcctgcccc aggaggagga ctatggcttt gacatcgagg agaagaacaa
180
ggctgtggtg gtgaagtccg tccagagggg cttgctggct gaggtggctg gcctgcaggt
240
ggggaggaag atctactcca tcaatgagga cctggtgttc ctgcggccgt tttcagaggt
300
ggagtccatc ctcaaccagt cttctgctc ccgccgccct ctgcgcctcc tggtagggcc
360
gaaggccaaa gagatcatca aaatccccga ccagccggac aactgtgtct tccagattcg
420
tgagctgcc ccaccgtacg tctatgtgtg ggggagagga tctgaggcca tggtgcagg
480
gctctgtgct ggtcagtgc tctgaaggt caatggcagc aacgtgatga acgatggtgc
540
ccctgaggtc ctggagcact tccaggcatt ccggagtcgg cgcaagagg ccctgggcct
600
gtaccagtgg atctaccaca cccatgagga tgcccaggaa gcacgagcca gtcaggaggc
660
ctccactgag gaccccgctg gcgagcaggc ccaggaggaa gaccaggctg attcagcctt
720
cccactgctg tccctgggtc cccggctgag cctgtgtgag ggcagcccca tggtcaccct
780
gactgtggac aacgtgcacc tggaacacgg cgtggtgtat gagtatgtga gcacggcagg
840

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cgtcagggtgc catgtgctgg agaagatcgt ggagccccgc ggctgcttcg gcctcaccgc  
 900  
 caagatcctc gaggcctttg ctgccaatga cagcgtcttc gtggagaact gcaggcggct  
 960  
 catggccctg agcagcgcca tcgtgacat gccccaactt gagttccgca acatctgtga  
 1020  
 caccaagctg gagagcattg gccagaggat tgctgtctac caggagtttg cagcccaact  
 1080  
 gaagagcagg gtcagcccac ccttcaaaca agccccctg gagccccacc cgctgtgtgg  
 1140  
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 1200  
 cccctcagt gggcagggtcc ttcagcatcc gctttggacg caaacctcc ctcatcgcc  
 1260  
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 1320  
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 1380  
 tccatgatgg cagcttcggg ccagccagtg ggacccttg tcaggaagac cggggcctca  
 1440  
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 1620  
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 1633

<210> 1076

<211> 87

<212> PRT

<213> Homo sapiens

<400> 1076

His	Gln	Ala	Gly	Glu	His	Trp	Pro	Glu	Asp	Cys	Leu	Leu	Pro	Gly	Val
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Cys	Ser	Pro	Thr	Glu	Glu	Gln	Gly	Gln	Pro	Thr	Leu	Gln	Thr	Ser	Pro
		20					25					30			
Pro	Gly	Ala	Pro	Pro	Ala	Val	Trp	Pro	Thr	Ser	Ala	Pro	Pro	Ile	Ala
	35					40				45					
Thr	Ser	Thr	Ser	Trp	Lys	Cys	Pro	Thr	Pro	Arg	Pro	Pro	Pro	Gln	Trp
	50				55				60						
Ala	Gly	Pro	Ser	Ala	Ser	Ala	Leu	Asp	Ala	Asn	Pro	Pro	Ser	Ser	Ala
65				70					75					80	
Leu	Thr	Arg	Ser	Lys	Ala	Thr									
				85											

<210> 1077

<211> 419

<212> DNA

<213> Homo sapiens

<400> 1077

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 gcaaacgagg caacatgttt gcgcctcgcc ggagcaccct caccagcga tgctttgttt  
 120  
 caccagagt ttacatatcc aatttttgga gaggtgagg caatttacgg ctacaacggc  
 180  
 ttgcacatga atcttgctt tgcgagcggc agcctggtgc cgtcgctcga aatcacttac  
 240  
 cgcgctaaga atacgacgac gtccgctaaa gtagatgacg tggagcaggc tctgcgcgga  
 300  
 gtgtcccgcc cagatgtcgt tactcctgca gaacttgatg ctatcgttgc acgcgacgcc  
 360  
 agggcggtcc gggcgcatTT acgccgccgg gcaccaagat tgcgacgtac actcgcgcg  
 419

<210> 1078

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1078

Xaa	Arg	Val	Thr	Arg	Leu	Ala	Thr	Arg	Leu	His	Ser	Met	Ser	Thr	Lys
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Trp	Thr	Cys	Asn	Ala	Asn	Glu	Ala	Thr	Cys	Leu	Arg	Leu	Ala	Gly	Ala
			20					25					30		
Pro	Ser	Pro	Ser	Asp	Ala	Leu	Phe	His	Pro	Glu	Phe	Thr	Tyr	Pro	Ile
			35					40					45		
Phe	Gly	Glu	Ala	Glu	Ala	Ile	Tyr	Gly	Tyr	Asn	Gly	Leu	His	Met	Asn
			50					55				60			
Leu	Ala	Phe	Ala	Ser	Gly	Ser	Leu	Val	Pro	Ser	Leu	Glu	Ile	Thr	Tyr
					70					75				80	
Arg	Ala	Lys	Asn	Thr	Thr	Thr	Ser	Ala	Lys	Val	Asp	Asp	Val	Glu	Gln
				85					90					95	
Ala	Leu	Arg	Gly	Val	Leu	Pro	Pro	Asp	Val	Val	Thr	Pro	Ala	Glu	Leu
				100				105					110		
Asp	Ala	Ile	Val	Ala	Arg	Asp	Ala	Arg	Ala	Val	Arg	Ala	His	Leu	Arg
			115				120					125			
Arg	Arg	Ala	Pro	Arg	Leu	Arg	Arg	Thr	Leu	Ala					
			130				135								

<210> 1079

<211> 584

<212> DNA

<213> Homo sapiens

<400> 1079

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 120  
 gctcaaaactg cttcccaagc cagcagggag gggaaccatg ctgcctgctg acctgggtag  
 180  
 ttctatttag gtcttgtgac acaacagtgg gcaaggtgat gccctctgtg accaaaagta  
 240

ttaccccaa gtccccag gccctccctt tcgtctgcaa agacacacat ctgtttcact  
 300  
 gtgtcttctg caaagacaca catctgtttc actgggggtt tctgcaaaga caccatttg  
 360  
 tttccctttt taagggtttt cccctccatc ttgtctattt ttaaaaaaat aaaccgggtt  
 420  
 cccaggatag ccttcccccc cagatcaaga gcccatgtga aatgaggggg ccgacttgac  
 480  
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 caagggcaca ggccatggtt tgctctcagg ctccctccac gcgt  
 584

<210> 1080  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 1080  
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 Phe Pro Ser Gln Gln Gly Gly Glu Pro Cys Cys Leu Leu Thr Trp Val  
 35 40 45  
 Val Leu Phe Arg Ser Cys Asp Thr Thr Val Gly Lys Val Met Pro Ser  
 50 55 60  
 Val Thr Lys Ser Ile Tyr Pro Lys Phe Pro Gln Ala Leu Pro Phe Val  
 65 70 75 80  
 Cys Lys Asp Thr His Leu Phe His Cys Val Phe Cys Lys Asp Thr His  
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 Leu Phe His Trp Gly Phe Leu Gln Arg His Pro Phe Val Ser Pro Phe  
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 Lys Gly Phe Pro Leu His Leu Val Tyr Phe  
 115 120

<210> 1081  
 <211> 3077  
 <212> DNA  
 <213> Homo sapiens

<400> 1081  
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 120  
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 180  
 cagacatctc ttaagatgat gcaggcagta ggaggtgcac ctgcacgtcc cactggagaa  
 240  
 tatatctgta atcaatgtgg tgctaagtac acatccctag acagctttca gactcaccta  
 300  
 aaaactcatc tcgacactgt gtttccaaaa ttgacctgtc ctcaagtcaa caaggaattc  
 360

cccaaccaag aatccttgcg gaagcatggt accattcact ttatgatcac ttcaacgtat  
420  
tacatctgtg agagttgtga caagcaattc acatcagtgg atgaccttca gaaacacctg  
480  
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540  
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600  
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660  
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720  
accgaggtgg agctgcaatg ccacatcacc actcacagta agaagtacaa ctgcaagttc  
780  
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1020  
gcctacacta tggaaacttt gctgcagaat caccagctcc gagaccacaa catcagacct  
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ggagaaagtg ccatcgtgaa aaagaaagct gagctcatta aagggaatta caagtgcagc  
1140  
gtgtgctctc gaaccttctt ctccgaaaat ggctccggg aacatatgca gaccaccta  
1200  
ggcctgtca aacactacat gtgcctatt tgcggagagc ggtttccctc ccttttaact  
1260  
cttactgaac acaaagtcac gcatagtaag agtcttgata ctggaaactg ccggatttgc  
1320  
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1380  
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1440  
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2040

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 3077

&lt;210&gt; 1082

&lt;211&gt; 757

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1082

Xaa	Pro	Val	Val	Glu	Val	Tyr	Ser	Cys	Ser	Tyr	Cys	Thr	Asn	Ser	Pro
1				5					10					15	
Ile	Phe	Asn	Ser	Val	Leu	Lys	Leu	Asn	Lys	His	Ile	Lys	Glu	Asn	His
		20					25					30			
Lys	Asn	Ile	Pro	Leu	Ala	Leu	Asn	Tyr	Ile	His	Asn	Gly	Lys	Lys	Ser
	35					40					45				
Arg	Ala	Leu	Ser	Pro	Leu	Ser	Pro	Val	Ala	Ile	Glu	Gln	Thr	Ser	Leu
	50				55					60					
Lys	Met	Met	Gln	Ala	Val	Gly	Gly	Ala	Pro	Ala	Arg	Pro	Thr	Gly	Glu
65			70					75					80		
Tyr	Ile	Cys	Asn	Gln	Cys	Gly	Ala	Lys	Tyr	Thr	Ser	Leu	Asp	Ser	Phe

1017



515 520 525  
 Lys Leu Asp Ile Asn Gly Leu Pro Tyr Gly Leu Cys Ala Gly Cys Val  
 530 535 540  
 Asn Leu Ser Lys Ser Ala Ser Pro Gly Ile Asn Val Pro Pro Gly Thr  
 545 550 555 560  
 Asn Arg Pro Gly Leu Gly Gln Asn Glu Asn Leu Ser Ala Ile Gly Glu  
 565 570 575  
 Arg Gln Gly Gly Gly Thr Glu Thr Arg Cys Ser Ser Cys Asn Val Lys  
 580 585 590  
 Phe Glu Ser Glu Ser Glu Leu Gln Asn His Ile Gln Thr Ile His Arg  
 595 600 605  
 Glu Leu Val Pro Asp Ser Asn Ser Thr Gln Leu Lys Thr Pro Gln Val  
 610 615 620  
 Ser Pro Met Pro Arg Ile Ser Pro Ser Gln Ser Asp Glu Lys Lys Thr  
 625 630 635 640  
 Tyr Gln Cys Ile Lys Cys Gln Met Val Phe Tyr Asn Glu Trp Asp Ile  
 645 650 655  
 Gln Val His Val Ala Asn His Met Ile Asp Glu Gly Leu Asn His Glu  
 660 665 670  
 Cys Lys Leu Cys Ser Gln Thr Phe Asp Ser Pro Ala Lys Leu Gln Cys  
 675 680 685  
 His Leu Ile Glu His Ser Phe Glu Gly Met Gly Gly Thr Phe Lys Cys  
 690 695 700  
 Pro Val Cys Phe Thr Val Phe Val Gln Ala Asn Lys Leu Gln Gln His  
 705 710 715 720  
 Ile Phe Ser Ala His Gly Gln Glu Asp Lys Ile Tyr Asp Cys Thr Gln  
 725 730 735  
 Cys Pro Gln Lys Phe Phe Phe Gln Thr Glu Leu Gln Asn His Thr Met  
 740 745 750  
 Thr Gln His Ser Ser  
 755

&lt;210&gt; 1083

&lt;211&gt; 516

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1083

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 60  
 agatccgaat aacctgcccg ctcccgtga gcccgaggaa gaggagaaga agtgaccgat  
 120  
 ccactgaccc cggttctgtc ggccaattgg gatgaagagc gcagttggaa gctgcttaac  
 180  
 tacgagcgac agggcggata caccggcctt cgtaaggctt tgacgatgcc gcctgacgac  
 240  
 gttgtctcgc tggtaagga cgtaacctg cgtggccgtg gtggcgccgg gttccccacc  
 300  
 ggcatgaagt ggtccttcgt gcctaaggac aatcccaacc cgacctacct cgttgtcaac  
 360  
 ggcgacgagt ctgagccggg cacgtgcaag gacatgccgc tcatgatggc ctccccgcac  
 420  
 accctcgtcg agggcgatcat cattgcctcc tacgccatca aggccaaagat ggccttcac  
 480

tacatccgcg gtgaggtgct gcacgtcgtc cgacgc  
516

<210> 1084

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1084

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Ser	Ala	Asn	Trp	Asp	Glu	Glu	Arg	Ser	Trp	Lys	Leu	Leu	Asn	Tyr	Glu
		20						25					30		
Arg	Gln	Gly	Gly	Tyr	Thr	Gly	Leu	Arg	Lys	Ala	Leu	Thr	Met	Pro	Pro
		35					40					45			
Asp	Asp	Val	Val	Ser	Leu	Val	Lys	Asp	Ala	Asn	Leu	Arg	Gly	Arg	Gly
		50					55				60				
Gly	Ala	Gly	Phe	Pro	Thr	Gly	Met	Lys	Trp	Ser	Phe	Val	Pro	Lys	Asp
65					70					75				80	
Asn	Pro	Asn	Pro	Thr	Tyr	Leu	Val	Val	Asn	Gly	Asp	Glu	Ser	Glu	Pro
			85						90					95	
Gly	Thr	Cys	Lys	Asp	Met	Pro	Leu	Met	Met	Ala	Ser	Pro	His	Thr	Leu
			100					105					110		
Val	Glu	Gly	Val	Ile	Ile	Ala	Ser	Tyr	Ala	Ile	Lys	Ala	Lys	Met	Ala
		115					120					125			
Phe	Ile	Tyr	Ile	Arg	Gly	Glu	Val	Leu	His	Val	Val	Arg	Arg		
	130						135					140			

<210> 1085

<211> 374

<212> DNA

<213> Homo sapiens

<400> 1085

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aaatcgtaga gtgtctctga gctgcctagg gggctgtttg cgatcttgcg gacagtgtct  
120  
atatccacaa ggttcagctc cgccaggaga ctgtcgccga tcattttcag gaagttttct  
180  
ttgctgcgtt cgtagtcttg gtgcaggctg aagctgtagt cgcttttgta gatgtcccgg  
240  
tagaagaact cgggcagggt gcctttcatg gcttccagga tgacggggtt gctcatcccc  
300  
tgcccgtca gaacacccgg gtacaccagg gaagagcgga tcatgtcgtc ctcaaggtag  
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ggggcggcga attc  
374

<210> 1086

<211> 110

<212> PRT

<213> Homo sapiens

&lt;400&gt; 1086

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Met Ile Arg Ser Ser Leu Val Tyr Pro Gly Val Leu Ser Gly His Gly
 1           5           10           15
Met Ser Lys Pro Val Ile Leu Glu Ala Met Lys Gly Thr Leu Pro Glu
          20           25           30
Phe Phe Tyr Arg Asp Ile Tyr Lys Ser Asp Tyr Ser Phe Asp Leu His
          35           40           45
Gln Asp Tyr Glu Arg Ser Lys Glu Asn Phe Leu Lys Met Ile Gly Asp
 50           55           60
Ser Leu Leu Ala Glu Leu Asn Leu Val Asp Ile Asp Thr Val Arg Lys
65           70           75           80
Ile Ala Asn Ser Pro Leu Gly Ser Ser Glu Thr Leu Tyr Asp Phe Glu
          85           90           95
Arg Met Thr His Met Glu Val Trp Leu Arg Glu Asn Tyr Val
          100          105          110

```

&lt;210&gt; 1087

&lt;211&gt; 423

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1087

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ggcatccacc cgcacgacct cggccaggtc ctgcacgacc acggcgtgag catccgggtg
120
nggcaccact gtgcctggcc catccaccgg agtctagggg tgcaatccac cgcccgtgca
180
tcgttctact tctacaacac tttcccggaa gtggatgcgt tagcgtcggc ggtgcggggc
240
gcccggaat ttttcggagt gcattaggat tggctctgaac gtgaaccttg aatccatgta
300
ccaggaagtc atcctggacc actacaagaa tcccacgcac gcagggttga aggtccctt
360
tgatgccgaa gtgcaccatg tgaacccttc ctgcggtgac ganaccgtct ccgggtgaag
420
ctt
423

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&lt;210&gt; 1088

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1088

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Met Thr Ile Val Ala Pro Pro Pro Pro Thr Ala Gly Ala Ala Ile Ser
 1           5           10           15
Phe Leu Val Asp Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp
          20           25           30
Asp His Gly Val Ser Ile Arg Val Xaa His His Cys Ala Trp Pro Ile
          35           40           45
His Arg Ser Leu Gly Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Phe
 50           55           60
Tyr Asn Thr Phe Pro Glu Val Asp Ala Leu Ala Ser Ala Val Arg Ala

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80

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Cys	Glu	Asp	Lys	Thr	Lys	Gly	Gly	Arg	Val	Gly	Gln	Arg	Gln	Tyr	Ile
			20					25					30		
Arg	Val	Val	Arg	Met	Gly	Leu	Gly	Glu	Glu	Ala	Leu	Pro	Leu	Phe	Phe
		35					40					45			
Phe	Asn	Leu	Ala	Lys	Gly	Leu	Leu	Gly	Gln	Gly	His	Pro	Ser	Leu	Leu
	50					55					60				
Leu	Gly	Ala	Ser	Ile	Phe	Leu	His	Ser	Val	Lys	Asn	Gly	Gly	Val	Ile
65					70					75					80
Gln	Lys	Tyr	Pro	Pro	Tyr	Cys	Gln	Gly	Phe	Gly	Glu	Gly	Ser	Lys	Lys

85  
Lys Leu Ala Trp Glu Asn Thr  
100

90

95

<210> 1091  
<211> 438  
<212> DNA  
<213> Homo sapiens

<400> 1091  
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gcgattatta cggcttatat gaacgaagtg tatttggtc aagtaggtaa tgaggggctt  
120  
catggctttg ccgaggcgag tcagcacttt tttggacgac ctttaaaaga acttaatatc  
180  
gacgagtttg ccttgtagt aggaatgggt aaagggcctt ctatttataa tcctgaacga  
240  
caccctaaac gtgctttatc acgcagaaat acggtattag caattttaaa aagccaagat  
300  
cgtttaaccg agtcggatta taatatttta cggaaacaac ccattcgctt ggcagataaa  
360  
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420  
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438

<210> 1092  
<211> 146  
<212> PRT  
<213> Homo sapiens

<400> 1092  
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Tyr Ser Lys Ser Ala Ile Ile Thr Ala Tyr Met Asn Glu Val Tyr Leu  
20 25 30  
Ala Gln Val Gly Asn Glu Gly Leu His Gly Phe Ala Glu Ala Ser Gln  
35 40 45  
His Phe Phe Gly Arg Pro Leu Lys Glu Leu Asn Ile Asp Glu Phe Ala  
50 55 60  
Leu Leu Val Gly Met Val Lys Gly Pro Ser Ile Tyr Asn Pro Glu Arg  
65 70 75 80  
His Pro Lys Arg Ala Leu Ser Arg Arg Asn Thr Val Leu Ala Ile Leu  
85 90 95  
Lys Ser Gln Asp Arg Leu Thr Glu Ser Asp Tyr Asn Ile Leu Arg Lys  
100 105 110  
Gln Pro Ile Arg Leu Ala Asp Lys His Gln Glu Arg Ser Val Tyr Gly  
115 120 125  
Asp Tyr Leu Asp Leu Val Ser Met Gln Leu Ser Arg Asp Phe Asp Arg  
130 135 140  
Cys Met  
145

&lt;210&gt; 1093

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1093

cgcgttctct acttcgagag ctatgtcggt atcgatccag gcatgaccac ccttgagaaa  
 60  
 ggtcagctgc tgaacgacga gcagtacttc gaagcgctgg aagagttcgg cgacgatttc  
 120  
 gatgcccga tgggtgccga agctgtccgt gaactgctgc acgctatcga cctggaacac  
 180  
 gagattggcc gtctgcgtga acaaattccg caaaccaact ccgaaaccaa gatcaagaag  
 240  
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 300  
 atggtgctga ccgttctgcc ggttctgccg ccagatctgc gtccgctggt a  
 351

&lt;210&gt; 1094

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1094

Arg	Val	Leu	Tyr	Phe	Glu	Ser	Tyr	Val	Val	Ile	Asp	Pro	Gly	Met	Thr
1				5					10					15	
Thr	Leu	Glu	Lys	Gly	Gln	Leu	Leu	Asn	Asp	Glu	Gln	Tyr	Phe	Glu	Ala
			20					25					30		
Leu	Glu	Glu	Phe	Gly	Asp	Asp	Phe	Asp	Ala	Arg	Met	Gly	Ala	Glu	Ala
		35					40					45			
Val	Arg	Glu	Leu	Leu	His	Ala	Ile	Asp	Leu	Glu	His	Glu	Ile	Gly	Arg
	50				55						60				
Leu	Arg	Glu	Gln	Ile	Pro	Gln	Thr	Asn	Ser	Glu	Thr	Lys	Ile	Lys	Lys
65				70					75					80	
Leu	Ser	Lys	Arg	Leu	Lys	Leu	Met	Glu	Ala	Phe	Gln	Gly	Ser	Gly	Asn
			85					90					95		
Leu	Pro	Glu	Trp	Met	Val	Leu	Thr	Val	Leu	Pro	Val	Leu	Pro	Pro	Asp
		100						105					110		
Leu	Arg	Pro	Leu	Val											
			115												

&lt;210&gt; 1095

&lt;211&gt; 619

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1095

nnacgcgtga gatccagcca ggccctcaac gaggacatcg tgcgagtgtc cagccggctg  
 60  
 gagcacctgg agaaggagct gtccgagaag agcgggcagc tgcggcaggg cagcgcccag  
 120  
 agccagcggc agatccgcgg ggagatcgac agcctgcgcc aggagaagga ctcaactgctc  
 180

aagcagcgcc tggagatcga cggcaagctg aggcagggga gtctgctgtc ccccgaggag  
240  
gagcggagcg tgttccagtt ggatgaggcc atcgaggccc tggatgctgc cattgagtat  
300  
aagaatgagg ccatcacatg ccgccagcgg gtgcttcggg cctcagcctc gttgctgtcc  
360  
cagtgcgaga tgaacctcat ggccaagctc agctacctct catcctcaga gaccagagcc  
420  
ctcctctgca agtattttga caaggtgggc cagcagccca tggccccccc agtcctcct  
480  
cacggcacgt gtggggaggt gtctcatggc agctgctcca gcggatatcc cgtttcctcc  
540  
cagactgggg gacagaatca ggaccaactc atctgcaggg ccgcctgacc ttaaagccta  
600  
ttttacttgt gaacctaag  
619

&lt;210&gt; 1096

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1096

Xaa	Arg	Val	Arg	Ser	Ser	Gln	Ala	Leu	Asn	Glu	Asp	Ile	Val	Arg	Val
1				5					10					15	
Ser	Ser	Arg	Leu	Glu	His	Leu	Glu	Lys	Glu	Leu	Ser	Glu	Lys	Ser	Gly
			20					25					30		
Gln	Leu	Arg	Gln	Gly	Ser	Ala	Gln	Ser	Gln	Arg	Gln	Ile	Arg	Gly	Glu
		35					40					45			
Ile	Asp	Ser	Leu	Arg	Gln	Glu	Lys	Asp	Ser	Leu	Leu	Lys	Gln	Arg	Leu
	50					55				60					
Glu	Ile	Asp	Gly	Lys	Leu	Arg	Gln	Gly	Ser	Leu	Leu	Ser	Pro	Glu	Glu
65					70					75				80	
Glu	Arg	Thr	Leu	Phe	Gln	Leu	Asp	Glu	Ala	Ile	Glu	Ala	Leu	Asp	Ala
			85						90					95	
Ala	Ile	Glu	Tyr	Lys	Asn	Glu	Ala	Ile	Thr	Cys	Arg	Gln	Arg	Val	Leu
		100					105						110		
Arg	Ala	Ser	Ala	Ser	Leu	Leu	Ser	Gln	Cys	Glu	Met	Asn	Leu	Met	Ala
		115					120					125			
Lys	Leu	Ser	Tyr	Leu	Ser	Ser	Ser	Glu	Thr	Arg	Ala	Leu	Leu	Cys	Lys
	130					135					140				
Tyr	Phe	Asp	Lys	Val	Gly	Gln	Gln	Pro	Met	Ala	Pro	Pro	Ala	Pro	Pro
145				150						155				160	
His	Gly	Thr	Cys	Gly	Glu	Val	Ser	His	Gly	Ser	Cys	Ser	Ser	Gly	Tyr
			165						170					175	
Pro	Val	Ser	Ser	Gln	Thr	Gly	Gly	Gln	Asn	Gln	Asp	Gln	Leu	Ile	Cys
			180					185					190		
Arg	Ala	Ala													
			195												

&lt;210&gt; 1097

&lt;211&gt; 5108

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1097

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180  
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240  
cggaacttga ctttcccaa taatggatgt aaaatcatct tttgcagacc tgatttccac  
300  
acactgatct tgaacagcag ccaaaagctt tccattgctt gcaagtacca aatgccagtt  
360  
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420  
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480  
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780  
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840  
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900  
gaaagaggat atggtgataa gacagaggca accacaaagc ttcatgacat ggtagaccaa  
960  
ctggaacaaa ttctcagtgt gtcagagctt ttggaaaaac atggactcga gaaaccaatt  
1020  
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1080  
acgaggcaca ctggccggaa gcagcctcct gtcagtgtgt ctcatggag aacgttgctg  
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1200  
gagatattta cagaaagcct tctgtgctct agtcgccttg aaaacatcca cctggctgga  
1260  
cagatgatgc actgcagtgc ttgttcagaa aatcctccag ctggtatagc ccataaaggg  
1320  
aaacccact acagggtcag ctacgaaaag agtattgact tggttttggc tgccagcaga  
1380  
gagtacttca attcttctac caacctcact gatagctgca tggatctagc caggtgtgc  
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1500  
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1560



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1680  
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1740  
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1800  
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1920  
ctgcagacag aaattcttta tcaaagagt gatttccaga tccatcatga aggaggggaa  
1980  
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<210> 1098

<211> 1336

<212> PRT

<213> Homo sapiens

<400> 1098

Met	Val	Asp	Gln	Leu	Glu	Gln	Ile	Leu	Ser	Val	Ser	Glu	Leu	Leu	Glu
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Lys	His	Gly	Leu	Glu	Lys	Pro	Ile	Ser	Phe	Val	Lys	Asn	Thr	Gln	Ser
			20					25					30		
Ser	Ser	Glu	Glu	Ala	Arg	Lys	Leu	Met	Val	Arg	Leu	Thr	Arg	His	Thr
			35				40					45			
Gly	Arg	Lys	Gln	Pro	Pro	Val	Ser	Glu	Ser	His	Trp	Arg	Thr	Leu	Leu
			50				55				60				
Gln	Asp	Met	Leu	Thr	Met	Gln	Gln	Asn	Val	Tyr	Thr	Cys	Leu	Asp	Ser
65					70					75				80	
Asp	Ala	Cys	Tyr	Glu	Ile	Phe	Thr	Glu	Ser	Leu	Leu	Cys	Ser	Ser	Arg
			85					90						95	
Leu	Glu	Asn	Ile	His	Leu	Ala	Gly	Gln	Met	Met	His	Cys	Ser	Ala	Cys
			100					105					110		
Ser	Glu	Asn	Pro	Pro	Ala	Gly	Ile	Ala	His	Lys	Gly	Lys	Pro	His	Tyr
			115				120						125		
Arg	Val	Ser	Tyr	Glu	Lys	Ser	Ile	Asp	Leu	Val	Leu	Ala	Ala	Ser	Arg
			130				135					140			
Glu	Tyr	Phe	Asn	Ser	Ser	Thr	Asn	Leu	Thr	Asp	Ser	Cys	Met	Asp	Leu
145					150					155				160	
Ala	Arg	Cys	Cys	Leu	Gln	Leu	Ile	Thr	Asp	Arg	Pro	Pro	Ala	Ile	Gln
			165					170						175	
Glu	Glu	Leu	Asp	Leu	Ile	Gln	Ala	Val	Gly	Cys	Leu	Glu	Glu	Phe	Gly
			180					185						190	
Val	Lys	Ile	Leu	Pro	Leu	Gln	Val	Arg	Leu	Cys	Pro	Asp	Arg	Ile	Ser
			195				200						205		
Leu	Ile	Lys	Glu	Cys	Ile	Ser	Gln	Ser	Pro	Thr	Cys	Tyr	Lys	Gln	Ser
			210				215						220		
Thr	Lys	Leu	Leu	Gly	Leu	Ala	Glu	Leu	Leu	Arg	Val	Ala	Gly	Glu	Asn
225					230					235				240	
Pro	Glu	Glu	Arg	Arg	Gly	Gln	Val	Leu	Ile	Leu	Leu	Val	Glu	Gln	Ala
			245					250						255	
Leu	Arg	Phe	His	Asp	Tyr	Lys	Ala	Ala	Ser	Met	His	Cys	Gln	Glu	Leu
			260					265						270	
Met	Ala	Thr	Gly	Tyr	Pro	Lys	Ser	Trp	Asp	Val	Cys	Ser	Gln	Leu	Gly

275	280	285
Gln Ser Glu Gly Tyr Gln Asp Leu Ala Thr Arg Gln Glu Leu Met Ala		
290	295	300
Phe Ala Leu Thr His Cys Pro Pro Ser Ser Ile Glu Leu Leu Leu Ala		
305	310	315
Ala Ser Ser Ser Leu Gln Thr Glu Ile Leu Tyr Gln Arg Val Asn Phe		
325	330	335
Gln Ile His His Glu Gly Gly Glu Asn Ile Ser Ala Ser Pro Leu Thr		
340	345	350
Ser Lys Ala Val Gln Glu Asp Glu Val Gly Val Pro Gly Ser Asn Ser		
355	360	365
Ala Asp Leu Leu Arg Trp Thr Thr Ala Thr Thr Met Lys Val Leu Ser		
370	375	380
Asn Thr Thr Thr Thr Thr Lys Ala Val Leu Gln Ala Val Ser Asp Gly		
385	390	395
Gln Trp Trp Lys Lys Ser Leu Thr Tyr Leu Arg Pro Leu Gln Gly Gln		
405	410	415
Lys Cys Gly Gly Ala Tyr Gln Ile Gly Thr Thr Ala Asn Glu Asp Leu		
420	425	430
Glu Lys Gln Gly Cys His Pro Phe Tyr Glu Ser Val Ile Ser Asn Pro		
435	440	445
Phe Val Ala Glu Ser Glu Gly Thr Tyr Asp Thr Tyr Gln His Val Pro		
450	455	460
Val Glu Ser Phe Ala Glu Val Leu Leu Arg Thr Gly Lys Leu Ala Glu		
465	470	475
Ala Lys Asn Lys Gly Glu Val Phe Pro Thr Thr Glu Val Leu Leu Gln		
485	490	495
Leu Ala Ser Glu Ala Leu Pro Asn Asp Met Thr Leu Ala Leu Ala Tyr		
500	505	510
Leu Leu Ala Leu Pro Gln Val Leu Asp Ala Asn Arg Cys Phe Glu Lys		
515	520	525
Gln Ser Pro Ser Ala Leu Ser Leu Gln Leu Ala Ala Tyr Tyr Tyr Ser		
530	535	540
Leu Gln Ile Tyr Ala Arg Leu Ala Pro Cys Phe Arg Asp Lys Cys His		
545	550	555
Pro Leu Tyr Arg Ala Asp Pro Lys Glu Leu Ile Lys Met Val Thr Arg		
565	570	575
His Val Thr Arg His Glu His Glu Ala Trp Pro Glu Asp Leu Ile Ser		
580	585	590
Leu Thr Lys Gln Leu His Cys Tyr Asn Glu Arg Leu Leu Asp Phe Thr		
595	600	605
Gln Ala Gln Ile Leu Gln Gly Leu Arg Lys Gly Val Asp Val Gln Arg		
610	615	620
Phe Thr Ala Asp Asp Gln Tyr Lys Arg Glu Thr Ile Leu Gly Leu Ala		
625	630	635
Glu Thr Leu Glu Glu Ser Val Tyr Ser Ile Ala Ile Ser Leu Ala Gln		
645	650	655
Arg Tyr Ser Val Ser Arg Trp Glu Val Phe Met Thr His Leu Glu Phe		
660	665	670
Pro Phe Thr Asp Ser Gly Leu Ser Thr Leu Glu Ile Glu Asn Arg Ala		
675	680	685
Gln Asp Leu His Leu Phe Glu Thr Leu Lys Thr Asp Pro Glu Ala Phe		
690	695	700
His Gln His Met Val Lys Tyr Ile Tyr Pro Thr Ile Gly Gly Phe Asp		

705 710 715 720  
 His Glu Arg Leu Gln Tyr Tyr Phe Thr Leu Leu Glu Asn Cys Gly Cys  
 725 730 735  
 Ala Asp Leu Gly Asn Cys Ala Ile Lys Pro Glu Thr His Ile Arg Leu  
 740 745 750  
 Leu Lys Lys Phe Lys Val Val Ala Ser Gly Leu Asn Tyr Lys Lys Leu  
 755 760 765  
 Thr Asp Glu Asn Met Ser Pro Leu Glu Ala Leu Glu Pro Val Leu Ser  
 770 775 780  
 Ser Gln Asn Ile Leu Ser Ile Ser Lys Leu Val Pro Lys Ile Pro Glu  
 785 790 795 800  
 Lys Asp Gly Gln Met Leu Ser Pro Ser Ser Leu Tyr Thr Ile Trp Leu  
 805 810 815  
 Gln Lys Leu Phe Trp Thr Gly Asp Pro His Leu Ile Lys Gln Val Pro  
 820 825 830  
 Gly Ser Ser Pro Glu Trp Leu His Ala Tyr Asp Val Cys Met Lys Tyr  
 835 840 845  
 Phe Asp Arg Leu His Pro Gly Asp Leu Ile Thr Val Val Asp Ala Val  
 850 855 860  
 Thr Phe Ser Pro Lys Ala Val Thr Lys Leu Ser Val Glu Ala Arg Lys  
 865 870 875 880  
 Glu Met Thr Arg Lys Ala Ile Lys Thr Val Lys His Phe Ile Glu Lys  
 885 890 895  
 Pro Arg Lys Arg Asn Ser Glu Asp Glu Ala Gln Glu Ala Lys Asp Ser  
 900 905 910  
 Lys Val Thr Tyr Ala Asp Thr Leu Asn His Leu Glu Lys Ser Leu Ala  
 915 920 925  
 His Leu Glu Thr Leu Ser His Ser Phe Ile Leu Ser Leu Lys Asn Ser  
 930 935 940  
 Glu Gln Glu Thr Leu Gln Lys Tyr Ser His Leu Tyr Asp Leu Ser Arg  
 945 950 955 960  
 Ser Glu Lys Glu Lys Leu His Asp Glu Ala Val Ala Ile Cys Leu Asp  
 965 970 975  
 Gly Gln Pro Leu Ala Met Ile Gln Gln Leu Leu Glu Val Ala Val Gly  
 980 985 990  
 Pro Leu Asp Ile Ser Pro Lys Asp Ile Val Gln Ser Ala Ile Met Lys  
 995 1000 1005  
 Ile Ile Ser Ala Leu Ser Gly Gly Ser Ala Asp Leu Gly Gly Pro Arg  
 1010 1015 1020  
 Asp Pro Leu Lys Val Leu Glu Gly Val Val Ala Ala Val His Thr Ser  
 1025 1030 1035 1040  
 Val Asp Lys Gly Glu Glu Leu Val Ser Pro Glu Asp Leu Leu Glu Trp  
 1045 1050 1055  
 Leu Arg Pro Phe Cys Ala Asp Asp Ala Trp Pro Val Arg Pro Arg Ile  
 1060 1065 1070  
 His Val Leu Gln Ile Leu Gly Gln Ser Phe His Leu Thr Glu Glu Asp  
 1075 1080 1085  
 Ser Lys Leu Leu Val Phe Phe Arg Thr Glu Ala Ile Leu Lys Ala Ser  
 1090 1095 1100  
 Trp Pro Gln Arg Gln Val Asp Ile Ala Asp Ile Glu Asn Glu Glu Asn  
 1105 1110 1115 1120  
 Arg Tyr Cys Leu Phe Met Glu Leu Leu Glu Ser Ser His His Glu Ala  
 1125 1130 1135  
 Glu Phe Gln His Leu Val Leu Leu Leu Gln Ala Trp Pro Pro Met Lys

```

      1140      1145      1150
Ser Glu Tyr Val Ile Thr Asn Asn Pro Trp Val Arg Leu Ala Thr Val
      1155      1160      1165
Met Leu Thr Arg Cys Thr Met Glu Asn Lys Glu Gly Leu Gly Asn Glu
      1170      1175      1180
Val Leu Lys Met Cys Arg Ser Leu Tyr Asn Thr Lys Gln Met Leu Pro
      1185      1190      1195      1200
Ala Glu Gly Val Lys Glu Leu Cys Leu Leu Leu Leu Asn Gln Ser Leu
      1205      1210      1215
Leu Leu Pro Ser Leu Lys Leu Leu Leu Glu Ser Arg Asp Glu His Leu
      1220      1225      1230
His Glu Met Ala Leu Glu Gln Ile Thr Ala Val Thr Thr Val Asn Asp
      1235      1240      1245
Ser Asn Cys Asp Gln Glu Leu Leu Ser Leu Leu Leu Asp Ala Lys Leu
      1250      1255      1260
Leu Val Lys Cys Val Ser Thr Pro Phe Tyr Pro Arg Ile Val Asp His
      1265      1270      1275      1280
Leu Leu Ala Ser Leu Gln Gln Gly Arg Trp Asp Ala Glu Glu Leu Gly
      1285      1290      1295
Arg His Leu Arg Glu Ala Gly His Glu Ala Glu Ala Gly Ser Leu Leu
      1300      1305      1310
Leu Ala Val Arg Gly Thr His Gln Ala Phe Arg Thr Phe Ser Thr Ala
      1315      1320      1325
Leu Arg Ala Ala Gln His Trp Val
      1330      1335

```

&lt;210&gt; 1099

&lt;211&gt; 309

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1099

```

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60

```

```

tgaaccattt cttccagttg cgatttttca gaaagcagcg tcgattgacc ttcggtcagc
120

```

```

ttgcgcacat agcgcttggt gcggctggca aggatatagg cgagtatcaa tgcacctgcg
180

```

```

agggcgagga tcgaggcaat ggtagccag aagcgcaact tgtccatggc tatgttgcgg
240

```

```

gcgattagcc gacgatcttc ttcacccagg aaactgttga tggttttcct gacgtcatcc
300

```

atctggcca

309

&lt;210&gt; 1100

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1100

Met Asp Asp Val Arg Lys Thr Ile Asn Ser Phe Leu Gly Glu Glu Asp

1

5

10

15

Arg Arg Leu Ile Ala Arg Asn Ile Ala Met Asp Lys Leu Arg Phe Trp

```

      20      25      30
Leu Thr Ile Ala Ser Ile Leu Ala Leu Ala Gly Ala Leu Ile Leu Ala
      35      40      45
Tyr Ile Leu Ala Ser Arg Thr Lys Arg Tyr Val Arg Lys Leu Thr Glu
      50      55      60
Gly Gln Ser Thr Leu Leu Ser Glu Lys Ser Gln Leu Glu Glu Met Val
      65      70      75      80
Gln Leu Arg Thr Ala Glu Leu Glu Lys Ala Met Leu Ile Ala Lys Arg
      85      90      95
Glu Arg Ala Arg
      100

```

<210> 1101  
 <211> 540  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1101
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120
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180
gccattggcc tggctggcgt catgggtggg gcggccaccg aagtgactgc tgagacgacg
240
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300
cacaagctcg gttcggaggc ctcccgcgc tttgagcggg gcgttgatcc gatttgcgcc
360
cataccgcag ccgttcgcgc agcggaattg ctgcccagt acggcggtgc caccgtcggg
420
gagccaccg tcgttggtga ggtccccgag atgccacgac aaacgatcaa cgctgattta
480
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```

<210> 1102  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1102
Val Asp Val Thr Asn Tyr Val Met Leu Glu Ser Gly Gln Pro Leu His
1      5      10      15
Ala Tyr Asp Ala Asp Asn Val Ser Gly Thr Ile Val Val Arg Lys Ala
20      25      30
His Glu Gly Glu His Leu Leu Thr Leu Asp Asp Thr Asp Arg Thr Leu
35      40      45
Asp Pro Asp Asp Leu Val Ile Ala Asp Asp Ser Gly Ala Ile Gly Leu
50      55      60
Ala Gly Val Met Gly Gly Ala Ala Thr Glu Val Thr Ala Glu Thr Thr
65      70      75      80
Ser Ile Ile Leu Glu Gly Ala His Phe Asp Pro Met Thr Gly Ala Arg

```

```

      85              90              95
Ala Tyr Arg Arg His Lys Leu Gly Ser Glu Ala Ser Arg Arg Phe Glu
      100              105              110
Arg Gly Val Asp Pro Ile Cys Ala His Thr Ala Ala Val Arg Ala Ala
      115              120              125
Glu Leu Leu Ala Gln Tyr Gly Gly Ala Thr Val Gly Glu Pro Thr Val
      130              135              140
Val Gly Glu Val Pro Glu Met Pro Arg Gln Thr Ile Asn Ala Asp Leu
      145              150              155              160
Pro Asn Arg Ile Leu Gly Thr Lys Val Pro Thr Glu Glu Val Ile Glu
      165              170              175
Ile Leu Thr Arg
      180

```

&lt;210&gt; 1103

&lt;211&gt; 537

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1103

```

cctttcctcc aaccaggcgc tgcggcgccg gcacttgccc gacgttataa aacaattcaa
60
cgtcagggttt accatcgctg tactcaacca aatggtagcc gtatccacct tccccaccga
120
tcgcgaccca ggtgatcttt cctcggcat agattgacgt ggcattctcg tcggagtga
180
tcaagcagcg cttaggcagc tgctgggccc gcggcttcgc ctagctcgcc ggagcacacg
240
aacccttccc gaagataacc gccaaaggcct ggcacacctt ctgctgcacc cattccggct
300
tgacgccgac cgccaccgca ctggtgaaca tagccgcaat aaggagaatt gcgatgtatt
360
ccggcgccggc ggcaccccca tcgtcccttg tccgcatggg tctccctccc actacctacc
420
caatacaggg gagagcataa aaagaaaccc atagccgcac ctgagcccat ggccccaaac
480
cgggggcccaa gccgggcccc aaccatggga tcaaccggat gtccgtacat caccgct
537

```

&lt;210&gt; 1104

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1104

```

Met Tyr Gly His Pro Val Asp Pro Met Val Trp Ala Arg Leu Gly Pro
 1              5              10              15
Arg Phe Gly Ala Met Gly Ser Gly Ala Ala Met Gly Phe Phe Leu Cys
      20              25              30
Ser Pro Leu Tyr Trp Val Gly Ser Gly Gly Glu Thr His Ala Asp Lys
      35              40              45
Gly Arg Ser Gly Cys Arg Arg Ala Gly Ile His Arg Asn Ser Pro Tyr
      50              55              60
Cys Gly Tyr Val His Gln Cys Gly Gly Gly Arg Arg Gln Ala Gly Met

```



```

65              70              75              80
Gly Ala Ala Glu Gly Val Pro Gly Leu Gly Gly Tyr Leu Arg Glu Gly
              85              90              95
Phe Val Cys Ser Gly Glu Leu Gly Glu Ala Ala Gly Pro Ala Ala Ala
              100              105              110

```

&lt;210&gt; 1105

&lt;211&gt; 448

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1105

```

agggacctgg ggcagcacgt gcacgtgggt gggaggctcc ttgctaccga cagccagcca
60
tgggggtgggc ccttccgagg ctgcctccag gacctgcgac tcgatggctg ccacctcccc
120
ttctttcctc tgccactgga taactcaagc cagcccagcg agctcggcgg caggcagtc
180
tggaacctca ctgcgggctg cgtctccgag gacatgtgca gtcctgaccc ctgtttcaat
240
gggtgggactt gcctcgtcac ctggaatgac ttccactgta cctgccctgc caatttcacg
300
gggcctacat gtgccagca gctgtggtgt cccggccagc cctgtctccc acctgccacg
360
tgtgaggagg tcctgatgg ctttgtgtgt gtggcggagg ccacgttccg cgagggtccc
420
cccgcgcgt tcagcgggca caacgcgt
448

```

&lt;210&gt; 1106

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1106

```

Arg Asp Leu Gly Gln His Val His Val Gly Gly Arg Leu Leu Ala Thr
1              5              10              15
Asp Ser Gln Pro Trp Gly Gly Pro Phe Arg Gly Cys Leu Gln Asp Leu
20              25              30
Arg Leu Asp Gly Cys His Leu Pro Phe Phe Pro Leu Pro Leu Asp Asn
35              40              45
Ser Ser Gln Pro Ser Glu Leu Gly Gly Arg Gln Ser Trp Asn Leu Thr
50              55              60
Ala Gly Cys Val Ser Glu Asp Met Cys Ser Pro Asp Pro Cys Phe Asn
65              70              75              80
Gly Gly Thr Cys Leu Val Thr Trp Asn Asp Phe His Cys Thr Cys Pro
85              90              95
Ala Asn Phe Thr Gly Pro Thr Cys Ala Gln Gln Leu Trp Cys Pro Gly
100              105              110
Gln Pro Cys Leu Pro Pro Ala Thr Cys Glu Glu Val Pro Asp Gly Phe
115              120              125
Val Cys Val Ala Glu Ala Thr Phe Arg Glu Gly Pro Pro Ala Ala Phe
130              135              140
Ser Gly His Asn Ala

```

145

&lt;210&gt; 1107

&lt;211&gt; 618

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1107

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 60  
 tctttgttat cgatgagacc gaacgcaaac tcaccgaaga ggcctgcgc cacctcaacg  
 120  
 agaacctcga agagcgcgct gccagcgca cacaggcgct ggctgaagcc aaccaacgcc  
 180  
 tggcaaaaca aaatgttcaa acgcaagcgc gccgaagacg cgctgcgtca cgcgagaaaa  
 240  
 atggaagccg ggggccagct caccggcggc atcgcccatg atttcaacaa catgctgacc  
 300  
 gggattatcg gcagcctgga cttgatgcag cgctacatcn aggcggggcg cagcgacgaa  
 360  
 atcggccgnc ttactgacgc cgccgtatcg tccgcccatc gcgcggccgc cctcacccat  
 420  
 cggctgctgg cgttctcgcg ccgccagtcg ctggccccc gcccgctgga cccaaccag  
 480  
 ctggtagcgt ccctggagga tctgttccag cgaaccaaag gcgcgcatat cagctcaaa  
 540  
 gtgcaactgg gccgcgatat ctggcccgtg aataccgatg ccagccagtt ggaaaacgcc  
 600  
 ctgctcaacc tggcgatc  
 618

&lt;210&gt; 1108

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1108

Met	Arg	Pro	Asn	Ala	Asn	Ser	Pro	Lys	Arg	Pro	Cys	Ala	Thr	Ser	Thr
1			5					10					15		
Arg	Thr	Ser	Lys	Ser	Ala	Ser	Pro	Ser	Ala	His	Arg	Arg	Trp	Leu	Lys
		20					25					30			
Pro	Thr	Asn	Ala	Trp	Gln	Asn	Lys	Met	Phe	Lys	Arg	Lys	Arg	Ala	Glu
		35				40					45				
Asp	Ala	Leu	Arg	His	Ala	Gln	Lys	Met	Glu	Ala	Gly	Gly	Gln	Leu	Thr
	50					55				60					
Gly	Gly	Ile	Ala	His	Asp	Phe	Asn	Asn	Met	Leu	Thr	Gly	Ile	Ile	Gly
65				70					75				80		
Ser	Leu	Asp	Leu	Met	Gln	Arg	Tyr	Ile	Xaa	Ala	Gly	Arg	Ser	Asp	Glu
		85				90					95				
Ile	Gly	Arg	Leu	Thr	Asp	Ala	Ala	Val	Ser	Ser	Ala	His	Arg	Ala	Ala
	100					105					110				
Ala	Leu	Thr	His	Arg	Leu	Leu	Ala	Phe	Ser	Arg	Arg	Gln	Ser	Leu	Ala
	115					120					125				
Pro	Arg	Pro	Leu	Asp	Pro	Asn	Gln	Leu	Val	Ala	Ser	Leu	Glu	Asp	Leu

130		135		140											
Phe	Gln	Arg	Thr	Lys	Gly	Ala	His	Ile	Thr	Leu	Lys	Val	Gln	Leu	Gly
145		150		155		160									
Arg	Asp	Ile	Trp	Pro	Val	Asn	Thr	Asp	Ala	Ser	Gln	Leu	Glu	Asn	Ala
		165		170		175									
Leu	Leu	Asn	Leu	Ala	Ile										
		180													

<210> 1109  
 <211> 325  
 <212> DNA  
 <213> Homo sapiens

<400> 1109  
 accggtgagc atcagggagg caccatgcag acgactctcc catccagtct caagccgtcc  
 60  
 agcctcaaga tcgtcgaccc gctggggggc atcctcgtgc ccctggatca ggtgcccgat  
 120  
 cccgttttcg cccagaagat ggtgggagac gggatctccc tggaccccat ctcaaacgaa  
 180  
 ttgctggcgc cggtcgccgg caccgtgacc cagctccaca acgcccacca cgcgctcacg  
 240  
 atcacgaccc cggaaggcat cgaggttctg gtccatctcg gactggatac cgtgatgctg  
 300  
 cgcgggcgaca gctatccccc ccccn  
 325

<210> 1110  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 1110  
 Thr Gly Glu His Gln Gly Gly Thr Met Gln Thr Thr Leu Pro Ser Ser  
 1 5 10 15  
 Leu Lys Pro Ser Ser Leu Lys Ile Val Ala Pro Leu Gly Gly Ile Leu  
 20 25 30  
 Val Pro Leu Asp Gln Val Pro Asp Pro Val Phe Ala Gln Lys Met Val  
 35 40 45  
 Gly Asp Gly Ile Ser Leu Asp Pro Ile Ser Asn Glu Leu Leu Ala Pro  
 50 55 60  
 Val Ala Gly Thr Val Thr Gln Leu His Asn Ala His His Ala Leu Thr  
 65 70 75 80  
 Ile Thr Thr Pro Glu Gly Ile Glu Val Leu Val His Ile Gly Leu Asp  
 85 90 95  
 Thr Val Met Leu Arg Gly Asp Ser Tyr Pro Pro Pro  
 100 105

<210> 1111  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<400> 1111

nnacgcgtcg ccccggtgcg cctggcagtg ggagaagagc atgaccttac cgagctcgcg  
 60  
 actgaactcg tcaacgccgc ctatagccgg gttgacatgg tggaacgccg tggcgaattc  
 120  
 gcagtacgtg gcggcatcgt cgacgtcttc ccaccggtgc tagaacaccc ggtccgtatc  
 180  
 gatttttttg gtgacgagat cgaggaaatg acctccttcg cggtagccga ccagcgatcc  
 240  
 accgacgaga ctcaccaaga actgatctgc gctccttgcc gtgagctcat cctcaccgac  
 300  
 gaggtacgtt cccgagccaa ggctttgctg accgaccatc ccgaattagc tgacatgttg  
 360  
 gagcggatcg gcaacggtca agctt  
 385

<210> 1112  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 1112  
 Xaa Arg Val Ala Pro Val Arg Leu Ala Val Gly Glu Glu His Asp Leu  
 1 5 10 15  
 Thr Glu Leu Ala Thr Glu Leu Val Asn Ala Ala Tyr Ser Arg Val Asp  
 20 25 30  
 Met Val Glu Arg Arg Gly Glu Phe Ala Val Arg Gly Gly Ile Val Asp  
 35 40 45  
 Val Phe Pro Pro Val Leu Glu His Pro Val Arg Ile Asp Phe Phe Gly  
 50 55 60  
 Asp Glu Ile Glu Glu Met Thr Ser Phe Ala Val Ala Asp Gln Arg Ser  
 65 70 75 80  
 Thr Asp Glu Thr His Gln Glu Leu Ile Cys Ala Pro Cys Arg Glu Leu  
 85 90 95  
 Ile Leu Thr Asp Glu Val Arg Ser Arg Ala Lys Ala Leu Leu Thr Asp  
 100 105 110  
 His Pro Glu Leu Ala Asp Met Leu Glu Arg Ile Gly Asn Gly Gln Ala  
 115 120 125

<210> 1113  
 <211> 400  
 <212> DNA  
 <213> Homo sapiens

<400> 1113  
 nnncgaccga tgagcgatcg cgaaccgcgc aacctgggat acccctacgt cgagtctttc  
 60  
 cactcggact tctcggggac cggcggagtc gatcagaccg accgttctac caatatcgac  
 120  
 gagcacacca tcgaggagat gcatcagatc gcctcgcgtt accccgactc ccgttcggcg  
 180  
 ttgctgccga tcctgcacct ggttcagtcg gtggacggac gcatctcgcc ggtcggtatt  
 240  
 gagactgcgg ctgaagtgct cggcattacc accgcccagg tatccggggg ggcgaccttc  
 300

tacaccatgt ataagaagca ccttgccggc cagcatcaca tcggtgtctg caccacggcg  
 360  
 ctgtgcgcgcg tcatgggtgg cgaggaggtg cttgcccgtg  
 400

<210> 1114  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 1114  
 Xaa Arg Pro Met Ser Asp Arg Glu Pro Val Asn Leu Gly Tyr Pro Tyr  
 1 5 10 15  
 Val Glu Ser Phe His Ser Asp Phe Ser Gly Thr Gly Gly Val Asp Gln  
 20 25 30  
 Thr Asp Arg Ser Thr Asn Ile Asp Glu His Thr Ile Glu Glu Met His  
 35 40 45  
 Gln Ile Ala Ser Arg Tyr Pro Asp Ser Arg Ser Ala Leu Leu Pro Ile  
 50 55 60  
 Leu His Leu Val Gln Ser Val Asp Gly Arg Ile Ser Pro Val Gly Ile  
 65 70 75 80  
 Glu Thr Ala Ala Glu Val Leu Gly Ile Thr Thr Ala Gln Val Ser Gly  
 85 90 95  
 Val Ala Thr Phe Tyr Thr Met Tyr Lys Lys His Pro Ala Gly Gln His  
 100 105 110  
 His Ile Gly Val Cys Thr Thr Ala Leu Cys Ala Val Met Gly Gly Glu  
 115 120 125  
 Glu Val Leu Ala Arg  
 130

<210> 1115  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<400> 1115  
 tctccgactg cacagattag agaaaggact gcgatgacca ttcgcaccac tcatgttggt  
 60  
 tcctgcccc gcacccccga gctgatcgag gcgaatcgtg cgcgccgtga gggttcgctc  
 120  
 ggcgaggctg acttcacgtc gctgctgcag gatcagggtg acggcggtgt gaagcgtcag  
 180  
 gctgagattg gcttgatat cgtcaatgac ggcgagtacg gtcacgcgat gcttgacacg  
 240  
 gttgattacg gcgcgtggtg gacgtattcc atctctcgtt tcggcgggct gtcctttgag  
 300  
 gacgtgcagc gttttgatgt gcgtcccccg gctggccgtg acggtcgcct gtctttctcg  
 360  
 tcgttcgctg agcgcgcga ctggcagcgt ttccggacgc gt  
 402

<210> 1116  
 <211> 134  
 <212> PRT

<213> Homo sapiens

<400> 1116

```

Ser Pro Thr Ala Gln Ile Arg Glu Arg Thr Ala Met Thr Ile Arg Thr
 1              5              10              15
Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Ile Glu Ala Asn
              20              25              30
Arg Ala Arg Arg Glu Gly Ser Leu Gly Glu Ala Asp Phe Thr Ser Leu
              35              40              45
Leu Gln Asp Gln Val Asp Gly Val Val Lys Arg Gln Ala Glu Ile Gly
 50              55              60
Leu Asp Ile Val Asn Asp Gly Glu Tyr Gly His Ala Met Leu Asp Thr
65              70              75              80
Val Asp Tyr Gly Ala Trp Trp Thr Tyr Ser Ile Ser Arg Phe Gly Gly
              85              90              95
Leu Ser Phe Glu Asp Val Gln Arg Phe Asp Val Arg Pro Pro Ala Gly
              100              105              110
Arg Asp Gly Arg Leu Ser Phe Ser Ser Phe Ala Glu Arg Arg Asp Trp
              115              120              125
Gln Arg Phe Arg Thr Arg
              130

```

<210> 1117

<211> 307

<212> DNA

<213> Homo sapiens

<400> 1117

```

ggcgccgggtc ttgccctggc tggaagtggc atgcagacct tggcgcgga cccgctggct
60
gaccctacc tgctaggtgt atcggtggc gcaagtgtgg gagcaaccgc agtcacgct
120
ttggggatgt tcacttcgtg gggaactcac cgactcactc ttggcgccct tgtaggggccc
180
ttggcggcag ctgcattggt ctatctcatt tccatggcgc aaggaggcat gacgccgctt
240
cggttggtgc tgtcgggcgt ggtgtgtgcc tcggcgttct cgcgttggcg agtttcctcg
300
tctttcg
307

```

<210> 1118

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1118

```

Gly Ala Gly Leu Ala Leu Ala Gly Ser Gly Met Gln Thr Leu Val Arg
 1              5              10              15
Asn Pro Leu Ala Asp Pro Tyr Leu Leu Gly Val Ser Ala Gly Ala Ser
              20              25              30
Val Gly Ala Thr Ala Val Ile Ala Leu Gly Met Phe Thr Ser Trp Gly
              35              40              45
Thr His Arg Leu Thr Leu Gly Ala Leu Val Gly Ala Leu Ala Ala Ala

```

```

      50              55              60
Ala Leu Val Tyr Leu Ile Ser Met Ala Gln Gly Gly Met Thr Pro Leu
65              70              75              80
Arg Leu Val Leu Ser Gly Val Val Leu Ser Ser Ala Phe Ser Arg Trp
      85              90              95
Arg Val Ser Ser Ser Phe
      100

```

<210> 1119  
 <211> 353  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1119
cgcgtccttg agatgcttga gcaggctcgg attgaggatc cagccagggt gatggattcc
60
tatccgcata aactgtccgg tggccagcgt caacgggttc tgcttgccat ggcgttggtg
120
aactcgccgg atctgctcat ttgtgacgag ccgacgaccg ccttggaagt cacggtgcag
180
tctcaggtac tggcgactat cgatgagggtg cttgactcgg ttggtgccgc atgcctattt
240
attacccacg atttgccggg tgtctcgcac atctgccggg agcttatcgt gatgacgtcg
300
ggcaagggtcg ttgaagccgg atcagcgcgt gatgtgttat ctcaccctga tca
353

```

<210> 1120  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1120
Arg Val Leu Glu Met Leu Glu Gln Val Gly Ile Glu Asp Pro Ala Arg
1              5              10              15
Val Met Asp Ser Tyr Pro His Gln Leu Ser Gly Gly Gln Arg Gln Arg
      20              25              30
Val Leu Leu Ala Met Ala Leu Val Asn Ser Pro Asp Leu Leu Ile Cys
      35              40              45
Asp Glu Pro Thr Thr Ala Leu Asp Val Thr Val Gln Ser Gln Val Leu
      50              55              60
Ala Thr Ile Asp Glu Val Leu Asp Ser Val Gly Ala Ala Cys Leu Phe
65              70              75              80
Ile Thr His Asp Leu Ala Val Val Ser His Ile Cys Arg Glu Leu Ile
      85              90              95
Val Met Thr Ser Gly Lys Val Val Glu Ala Gly Ser Ala Arg Asp Val
      100              105              110
Leu Ser His Pro Asp
      115

```

<210> 1121  
 <211> 406  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 1121

tgatcaccca tgctccactc gaccgcgcgc tcgacgatgc gacggctgag acgatgctcg  
 60  
 cccagggcac ggtgttcac cgcaccttga cgatgatgaa aggcgtcgcc gcgaatctca  
 120  
 ccgcagcggg cgttccccgt gtgagctatg cacacgcca cgagagcacg cgcgcgatgc  
 180  
 atgccgcggg cgttccggtc ctggccggca ccgacgccta catcgggtcc ttcacacggg  
 240  
 catcgcgcgc atacggcgag agcatgcacg acgaagacgc ctacatcggg ctccctcgaac  
 300  
 gggcaatgcc gccatacggc gagagcatgc acgacgaact cgctctgctc gtggacgccg  
 360  
 gcctgtcaac agccgaagcg ctgcgcgctg ccacctcgac gggcgc  
 406

&lt;210&gt; 1122

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1122

Met Leu Ala Gln Gly Thr Val Phe Ile Pro Thr Leu Thr Met Met Lys  
 1 5 10 15  
 Gly Val Ala Ala Asn Leu Thr Ala Ala Gly Val Pro Gly Val Ser Tyr  
 20 25 30  
 Ala His Ala His Glu Ser Thr Arg Ala Met His Ala Ala Gly Val Pro  
 35 40 45  
 Val Leu Ala Gly Thr Asp Ala Tyr Ile Gly Ser Phe Thr Arg Ala Ser  
 50 55 60  
 Pro Pro Tyr Gly Glu Ser Met His Asp Glu Asp Ala Tyr Ile Gly Leu  
 65 70 75 80  
 Leu Glu Arg Ala Met Pro Pro Tyr Gly Glu Ser Met His Asp Glu Leu  
 85 90 95  
 Ala Leu Leu Val Asp Ala Gly Leu Ser Thr Ala Glu Ala Leu Arg Ala  
 100 105 110  
 Ala Thr Ser Thr Gly  
 115

&lt;210&gt; 1123

&lt;211&gt; 337

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1123

gccggcgatg cgttcattaa ggctaagat gcgcgcgacgc ctccccgctt tctcgcacct  
 60  
 cgcctccacc gcccttgccg cagcggggat ggtgggggtgc tcgtccgagg gggcatcgcc  
 120  
 aagcgaatgc tccccgttg atattgccgc agtgcgcgag gccctgccgc attcgctcgc  
 180  
 taaggcgaag ctgcaccgc actccaccaa cgaggatgaa cactcctttt ccatgctcta  
 240



ccgcgcgcaa gataaggagc aggtcagctt gctggggacg aagtatgagg ccgacggtgc  
300  
accgcgtctgc cccgatgacc ccaatgaggc agcgcgc  
337

<210> 1124  
<211> 110  
<212> PRT  
<213> Homo sapiens

<400> 1124  
Met Arg Ser Leu Arg Pro Lys Met Arg Arg Arg Leu Pro Ala Phe Leu  
1 5 10 15  
Ala Leu Ala Ser Thr Ala Leu Ala Ala Ala Gly Met Val Gly Cys Ser  
20 25 30  
Ser Glu Gly Ala Ser Pro Ser Glu Cys Ser Pro Val Asp Ile Ala Ala  
35 40 45  
Val Arg Glu Ala Leu Pro His Ser Leu Ala Lys Ala Lys Leu Asp Pro  
50 55 60  
His Ser Thr Asn Glu Asp Glu His Ser Phe Ser Met Leu Tyr Arg Ala  
65 70 75 80  
Gln Asp Lys Glu Gln Val Ser Leu Leu Gly Thr Lys Tyr Glu Ala Asp  
85 90 95  
Gly Ala Pro Val Cys Pro Asp Asp Pro Asn Glu Ala Ala Arg  
100 105 110

<210> 1125  
<211> 555  
<212> DNA  
<213> Homo sapiens

<400> 1125  
nncttgaatc gaatcggcat tgcgtctaaa catgacgttg agacactctc tgctaagctc  
60  
gaagagctga cggcattgct agaactgtgc gcgcgtaaac actaaggaga catcgggatg  
120  
gctgttaaaa agactactca gaaagaaggc agctcgtgga tcggggaagt tgaaaaatat  
180  
tcccgtaaaa tctggcttgc tggtttaggc gtgtactcga aggttagcag tgacggcggc  
240  
aaatacttcg agacgttggc caaggacggc gagaaggccg agaagttgac caagagccca  
300  
gtcggtaaaa aagtagaggc ggcaaaagcg agcgcgggtt ctgcgaaatc gagcatttcg  
360  
gatacctggg gcaagttgga agagactttc gacaagcgtc tcaacagtgc tatttcgcga  
420  
ttgggcgtgc ccagcaaagc ggaactgaag acgctgcaca gcaaggtcga taccctgacc  
480  
aagcaaatcg aaaaactcac cggcgccaaa gtggccccgg ctaaaacggc agccgctaaa  
540  
cctgctgcca agctt  
555

<210> 1126

<211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 1126  
 Met Ala Val Lys Lys Thr Thr Gln Lys Glu Gly Ser Ser Trp Ile Gly  
 1 5 10 15  
 Glu Val Glu Lys Tyr Ser Arg Lys Ile Trp Leu Ala Gly Leu Gly Val  
 20 25 30  
 Tyr Ser Lys Val Ser Ser Asp Gly Gly Lys Tyr Phe Glu Thr Leu Val  
 35 40 45  
 Lys Asp Gly Glu Lys Ala Glu Lys Leu Thr Lys Ser Pro Val Gly Lys  
 50 55 60  
 Lys Val Glu Ala Ala Lys Ala Ser Ala Gly Ser Ala Lys Ser Ser Ile  
 65 70 75 80  
 Ser Asp Thr Trp Gly Lys Leu Glu Glu Thr Phe Asp Lys Arg Leu Asn  
 85 90 95  
 Ser Ala Ile Ser Arg Leu Gly Val Pro Ser Lys Ala Glu Leu Lys Thr  
 100 105 110  
 Leu His Ser Lys Val Asp Thr Leu Thr Lys Gln Ile Glu Lys Leu Thr  
 115 120 125  
 Gly Ala Lys Val Ala Pro Ala Lys Thr Ala Ala Ala Lys Pro Ala Ala  
 130 135 140  
 Lys Leu  
 145

<210> 1127  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

<400> 1127  
 cccgaccgcg tactcgtggt cgggtgccgga gtgatgggtg cagcacacgc acacgcgctc  
 60  
 cgcggggtccc tccaggcagt cgtgtgcggc gtggtcgacc tgcaggagcg agcagcgcaa  
 120  
 tcactcgctt cggaagtggg cgtaccggg ttcaccgacc tggatgaaggc gatcgagtcg  
 180  
 accgctccgg acgcccgggt catcgccacg ccggactcgg ctcaccgcca accggtgag  
 240  
 accgccatcg acgcccgcct tgccgtcctg gtcgagaaac cgctcgccac gaccgtcgat  
 300  
 gacgccgaag cgatcgtgct ccgcgtgaa cgggccggcg tccgtctcat ga  
 352

<210> 1128  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 1128  
 Pro Asp Arg Val Leu Val Val Gly Ala Gly Val Met Gly Ala Ala His  
 1 5 10 15  
 Ala His Ala Leu Arg Gly Ser Leu Gln Ala Val Val Cys Gly Val Val

```

      20      25      30
Asp Leu Gln Glu Arg Ala Ala Gln Ser Leu Ala Ser Glu Val Gly Val
      35      40      45
Pro Gly Phe Thr Asp Leu Val Lys Ala Ile Glu Ser Thr Ala Pro Asp
      50      55      60
Ala Ala Val Ile Ala Thr Pro Asp Ser Ala His Arg Gln Pro Ala Glu
65      70      75      80
Thr Ala Ile Asp Ala Gly Leu Ala Val Leu Val Glu Lys Pro Leu Ala
      85      90      95
Thr Thr Val Asp Ala Glu Ala Ile Val Leu Arg Ala Glu Arg Ala
      100      105      110
Gly Val Arg Leu Met
      115

```

&lt;210&gt; 1129

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1129

```

ntggcagccc tggaggagcc gatggtggac ctggacggcg agctgccttt cgtgcggccc
60
ctgccccaca ttgccgtgct ccaggacgag ctgccgcaac tcttcagga tgacgacgtc
120
ggggccgatg aggaagaggc agagttgcgg ggcgaacaca cgctcacaga gaagtttgc
180
tgcttgatg actcctttgg ccatgactgc agcttgacct gtgatgactg caggaacgga
240
gggacctgcc tcttgggcct ggatggctgg gattgccccg agggctggac tgggctcatc
300
tgcaatgaga cttggtcctc gggctgcatg gatatt
336

```

&lt;210&gt; 1130

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1130

```

Xaa Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro
 1      5      10      15
Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro
      20      25      30
Gln Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu
      35      40      45
Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp
      50      55      60
Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly
65      70      75      80
Gly Thr Cys Leu Leu Gly Leu Asp Gly Trp Asp Cys Pro Glu Gly Trp
      85      90      95
Thr Gly Leu Ile Cys Asn Glu Thr Trp Ser Ser Gly Cys Met Asp Ile
      100      105      110

```

<210> 1131  
 <211> 672  
 <212> DNA  
 <213> Homo sapiens

<400> 1131  
 gcgttggtgg tgctcatggc ccgggaaaat ccgctggatc aatacctctt tgagcacccc  
 60  
 gaattattgt tctcgtcctc ggtggaatcg actgtgttgc acccggataa cccgtatgtg  
 120  
 ctcggcccg cgcgtggccgc ggccgcccag gaggcatacc tctcccctgc ggacgaagag  
 180  
 ttttacgggt cggcctttgc cgggatatgc aaaacgctga caggccagaa cgtactgcga  
 240  
 cgtcgcggaa atcggctgtt ctggactcgt ccggaacggg ctgtcgacgc catcgacctg  
 300  
 cgatcggcgg caggcaaagg gattgacatt atcgacgtgt ccaccgggag ggtcatcggg  
 360  
 gtagtcgacg aagccgcccgc agaccgtacc gtgcatccag gcgcggtgta cctgcatcag  
 420  
 ggggatcagt ggctggtcga cgaatacaac ccggtcgagc accacgccct ggtgcaccag  
 480  
 gacctgccgg gatattggac tcaaccgcag tcagcgtcga cggtgagaat ccttcgggag  
 540  
 gagagacgtc gcgcttgtgg tcccggatat gtggcgtgcg ggcaggtgga actgacagag  
 600  
 caagttgttg ggtatctgcy tcgcgacgaa ttcaccaatg atgtgtggta ctcgctggcc  
 660  
 ctcgagatgc cc  
 672

<210> 1132  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 1132  
 Ala Leu Val Val Leu Met Ala Arg Glu Asn Pro Leu Asp Gln Tyr Leu  
 1 5 10 15  
 Phe Glu His Pro Glu Leu Leu Phe Ser Ser Ser Val Glu Ser Thr Val  
 20 25 30  
 Leu His Pro Asp Asn Pro Tyr Val Leu Gly Pro His Val Ala Ala Ala  
 35 40 45  
 Ala Gln Glu Ala Tyr Leu Ser Pro Ala Asp Glu Glu Phe Tyr Gly Ser  
 50 55 60  
 Ala Phe Ala Gly Ile Cys Lys Thr Leu Thr Gly Gln Asn Val Leu Arg  
 65 70 75 80  
 Arg Arg Gly Asn Arg Leu Phe Trp Thr Arg Pro Glu Arg Ala Val Asp  
 85 90 95  
 Ala Ile Asp Leu Arg Ser Ala Ala Gly Lys Gly Ile Asp Ile Ile Asp  
 100 105 110  
 Val Ser Thr Gly Arg Val Ile Gly Val Val Asp Glu Ala Ala Ala Asp  
 115 120 125  
 Arg Thr Val His Pro Gly Ala Val Tyr Leu His Gln Gly Asp Gln Trp

130	135	140
Leu Val Asp Glu Tyr Asn Pro Val Glu His His Ala Leu Val His Gln		
145	150	155
Asp Leu Pro Gly Tyr Trp Thr Gln Pro Gln Ser Ala Ser Thr Val Arg		160
	165	170
Ile Leu Arg Glu Glu Arg Arg Arg Ala Cys Gly Pro Gly Tyr Val Ala		175
	180	185
Cys Gly Gln Val Glu Leu Thr Glu Gln Val Val Gly Tyr Leu Arg Arg		190
	195	200
Asp Glu Phe Thr Asn Asp Val Trp Tyr Ser Leu Ala Leu Glu Met Pro		205
210	215	220

&lt;210&gt; 1133

&lt;211&gt; 796

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1133

acgcgtgaag gggggtccag cgggtgtggc actcgatgac aagacagttt gagagcggct  
60  
tgtctccggg gacctggcgt aggtctcttc tgccttaacc cttggctttt gcacttcttc  
120  
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180  
ccggttcttg tcttaacccc actggcatct tacactctgg gagatagctt ccccttgaga  
240  
ggcgagttag ccacgtaagg ggagggtggc gatggcttcc cttctgtctt gggttggggg  
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agtcaggtag agtatttttt cttttaaaagc atcattgac acataataag gtttgcata  
360  
gtccttaatc acagacctgt gaaatttgga gaattcacgg cacctaggat gggagttagc  
420  
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540  
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600  
gacagagggg ttattagggg tagctctggg acccatcttt tggtagtttc ttctctctct  
660  
ttctctaatg gaataattgt ttctgtctac acttctttat ttctctctct ctacagctgc  
720  
cttctaaaaa tgtgcttttc tgttcttgca gaactgaagc ttgcatggcc tttgttgtag  
780  
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796

&lt;210&gt; 1134

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1134

Met Gly Pro Arg Ala Thr Pro Asn Lys Pro Ser Val Thr Glu Leu Ser

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      1           5           10           15
Cys Met Ser Pro Thr Phe Ser Arg Gly Ser Glu Val Arg Glu Lys Glu
      20           25           30
Gly Gln Thr Lys Ser Val Gln Ser Pro Arg Glu Val Pro Gly Glu Gly
      35           40           45
Pro Asp Thr Gln Gln Gly Ala Cys Lys Arg Ser Phe Leu Glu Val Ser
      50           55           60
Ser Gln Ile Ser Ser Gln Ser Glu Ala His Ser His Pro Arg Cys Arg
      65           70           75           80
Glu Phe Ser Lys Phe His Arg Ser Val Ile Lys Asp Tyr Asp Lys Pro
      85           90           95
Tyr Tyr Val Ile Asn Asp Ala Leu Lys Glu Lys Ile Leu Tyr Leu Thr
      100          105          110
Pro Pro Thr Gln Asp Arg Arg Glu Ala Ile Ala His Leu Pro Leu Arg
      115          120          125
Gly Ser Leu Ala Ser Gln Gly Glu Ala Ile Ser Gln Ser Val Arg Cys
      130          135          140
Gln Trp Gly
145

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&lt;210&gt; 1135

&lt;211&gt; 376

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1135

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gatcaggcca cacaggacaa cttegagaag ggctccatct tcccaccctt caccagcatc
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agaaagatct ctgcgcacat cgctgcagcc gtggctgcaa aagcctacga gctcggtctg
120
gcgacccgctc tgccctcccc cagcgacctg gtgaaatatg cagagaactg catgtacact
180
cccgtctacc gcaactaccg gtagtgctgc ggggatcaat tttgcagtaa taaaaaatct
240
actatcaacg cggatggtac tctgttggtt atagtccttg ctgctaacca cccttggtgc
300
tggtgctgct ggagaggcat tgtacctgct catgcatata tgatatatat atgttgtaac
360
gttgtgaaag caaact
376

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&lt;210&gt; 1136

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1136

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Asp Gln Ala Thr Gln Asp Asn Phe Glu Lys Gly Ser Ile Phe Pro Pro
      1           5           10           15
Phe Thr Ser Ile Arg Lys Ile Ser Ala His Ile Ala Ala Val Ala
      20           25           30
Ala Lys Ala Tyr Glu Leu Gly Leu Ala Thr Arg Leu Pro Pro Ser
      35           40           45
Asp Leu Val Lys Tyr Ala Glu Asn Cys Met Tyr Thr Pro Val Tyr Arg

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Asn Tyr Arg  
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<210> 1137  
<211> 357  
<212> DNA  
<213> Homo sapiens

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atcattgacc tgcaccagtc gctgacctac attgataagg cgtacgcctt cgtcaaggag  
120  
actgtcgcca agggcggcca gattcttttc gtcggcacga agaagcaggc ccaggagtcc  
180  
atcgttgagc aggccactcg cgttggcatg ccctatgtca accagcgttg gcttggggga  
240  
atgctcacta atttcagac catctcgaag cgcattgccc ggctcaagga gctcgaggcc  
300  
atggactttg acaaggtttc cggctccggt ctcaccaaga aggagctgct tatgctc  
357

<210> 1138  
<211> 119  
<212> PRT  
<213> Homo sapiens

<400> 1138  
Thr Arg Arg Trp Asn Pro Lys Met Lys Arg Phe Ile Phe Thr Glu Arg  
1 5 10 15  
Asn Gly Ile Tyr Ile Ile Asp Leu His Gln Ser Leu Thr Tyr Ile Asp  
20 25 30  
Lys Ala Tyr Ala Phe Val Lys Glu Thr Val Ala Lys Gly Gly Gln Ile  
35 40 45  
Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ser Ile Val Glu Gln  
50 55 60  
Ala Thr Arg Val Gly Met Pro Tyr Val Asn Gln Arg Trp Leu Gly Gly  
65 70 75 80  
Met Leu Thr Asn Phe Gln Thr Ile Ser Lys Arg Ile Ala Arg Leu Lys  
85 90 95  
Glu Leu Glu Ala Met Asp Phe Asp Lys Val Ser Gly Ser Gly Leu Thr  
100 105 110  
Lys Lys Glu Leu Leu Met Leu  
115

<210> 1139  
<211> 456  
<212> DNA  
<213> Homo sapiens

<400> 1139  
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ccaatcccggt aggacccgctc tcgtccagca tcgaccaagg cgctgttgag gcgttcggct  
 120  
 tcggtaatga actcgatgcg ctcaatatcc acgggggtag cgaaatcgta gatcttgccc  
 180  
 agactgaggc cttggaggag cgcggccgctc ggggggacgt ggcctgcggc cgggcgttcc  
 240  
 ttgctctcaa ggacttcgctc gtcgcggctg acaaggaata cgtttggtg gtcgcctgca  
 300  
 atgcatgctc gagcgtggtg accatcgagg tgaaggacgg ttccggcata gaggtcatcg  
 360  
 tccacatcgg ccacagttag ttcgacgact cctgagtcga ctagatgacg cgccttctct  
 420  
 gccgcgtctt cgctgacgctc ggccaggacc gctagc  
 456

<210> 1140

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1140

Met	Trp	Thr	Met	Thr	Ser	Met	Pro	Lys	Pro	Ser	Phe	Thr	Ser	Met	Val
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Thr	Thr	Leu	Glu	His	Ala	Leu	Gln	Ala	Thr	Thr	Gln	Thr	Tyr	Ser	Leu
		20					25						30		
Ser	Ala	Ala	Thr	Thr	Lys	Ser	Leu	Arg	Ala	Arg	Asn	Ala	Arg	Pro	Gln
	35					40					45				
Ala	Thr	Ser	Pro	Arg	Arg	Pro	Arg	Ser	Ser	Lys	Ala	Ser	Val	Trp	Pro
	50					55					60				
Arg	Ser	Thr	Ile	Ser	Leu	Pro	Pro	Trp	Ile	Leu	Ser	Ala	Ser	Ser	Ser
65				70					75					80	
Leu	Pro	Lys	Pro	Asn	Ala	Ser	Thr	Ala	Pro	Trp	Ser	Met	Leu	Asp	Glu
			85					90					95		
Thr	Gly	Pro	Thr	Gly	Leu	Val	Lys	Val	Pro	Pro	Tyr	Ser	Asp	Arg	Ser
		100					105						110		
Ser	Ala	Ala	Trp	Pro	Gln	Thr	Thr	Cys	Ala						
	115					120									

<210> 1141

<211> 354

<212> DNA

<213> Homo sapiens

<400> 1141

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 120  
 ccgaccggca ttctggggccg tccggaggtt gagaaagtat gagcagatat cttaaactcg  
 180  
 cgtttttcag cgccctgttg gtgtgggccc tggcctttcc ggtactcggc ctcaagctga  
 240  
 gcattgtcgg gatcaaccac gaagtgcatt gcaccgggtcc cgtgaccttg accatcatcg  
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ccctgtgctc ggtgccgatg ttcttgccg tgetgtttac ccagcaagtc ggtg  
354

<210> 1142  
<211> 53  
<212> PRT  
<213> Homo sapiens

<400> 1142  
Gly Ala Met Leu Gly Gly Leu Val Leu Gly Val Ala Glu Ala Phe Gly  
1 5 10 15  
Ala Asp Ile Phe Gly Asp Gln Tyr Lys Asp Val Val Ala Phe Gly Leu  
20 25 30  
Leu Val Leu Val Leu Leu Phe Arg Pro Thr Gly Ile Leu Gly Arg Pro  
35 40 45  
Glu Val Glu Lys Val  
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<210> 1143  
<211> 353  
<212> DNA  
<213> Homo sapiens

<400> 1143  
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catgcaacgt gaaatgaagt tcgaatcgat caaggcaaag gccaaaggcga tgetcatcgg  
120  
cgagccgac gacacagcaa gcgcaggcgc gaccaaccga gggagggtca acagcgccgc  
180  
attcgaaatc ctggcccacg tggccgtcaa tgcccaacac tacgcgctct ccgagagacc  
240  
ggcgctggag gagttcgcca agagcttcca gccgcgcaac aaccaggact acgtggccgc  
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gatcgccaag aaggccgcga accacacat gcatcccggc aggcagtcga ttt  
353

<210> 1144  
<211> 102  
<212> PRT  
<213> Homo sapiens

<400> 1144  
Met His Gly Val Val Arg Gly Leu Leu Gly Asp Arg Gly His Val Val  
1 5 10 15  
Leu Val Val Ala Arg Leu Glu Ala Leu Gly Glu Leu Leu Gln Arg Arg  
20 25 30  
Ser Leu Gly Glu Arg Val Val Leu Gly Ile Asp Gly His Val Gly Gln  
35 40 45  
Asp Phe Glu Cys Gly Ala Val Glu Pro Pro Ser Val Gly Arg Ala Cys  
50 55 60  
Ala Cys Cys Val Val Gly Cys Ala Asp Glu His Arg Leu Gly Leu Cys  
65 70 75 80  
Leu Asp Arg Phe Glu Leu His Phe Thr Leu His Gly Ile Ser Arg Ser

85  
Met Arg Gln Cys Arg Gly  
100

90

95

<210> 1145  
<211> 360  
<212> DNA  
<213> Homo sapiens

<400> 1145  
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catgaagtgg ccggcacctg ggtactcggg ctgtcggcgg cgatggctct gatgggtgttt  
120  
ttctacgtcc aggtcatcgc caagaagatc aatcctcgac cctccgacga gaaggacgcc  
180  
gaggtgatcg acggggctgg tccggtcggg ttcttcccgc cacagagtat ctggccgttc  
240  
tggtgcgcgc tcgttgctgc catcatgtgc ctcgcccgga tcttcggctg gtggatctct  
300  
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360

<210> 1146  
<211> 120  
<212> PRT  
<213> Homo sapiens

<400> 1146  
Val Phe Gly Gly Leu Gly Leu Phe Tyr Cys Val Met Thr Pro Val Tyr  
1 5 10 15  
Trp Phe Ser Ala His Glu Val Ala Gly Thr Trp Val Leu Gly Leu Ser  
20 25 30  
Ala Ala Met Ala Leu Met Val Phe Phe Tyr Val Gln Val Ile Ala Lys  
35 40 45  
Lys Ile Asn Pro Arg Pro Ser Asp Glu Lys Asp Ala Glu Val Ile Asp  
50 55 60  
Gly Ala Gly Pro Val Gly Phe Phe Pro Pro Gln Ser Ile Trp Pro Phe  
65 70 75 80  
Trp Cys Ala Leu Val Val Ala Ile Met Cys Leu Gly Pro Ile Phe Gly  
85 90 95  
Trp Trp Ile Ser Leu Leu Gly Leu Gly Ile Val Ile Trp Ala Ala Ser  
100 105 110  
Gly Trp Ala Phe Glu Tyr Tyr Arg  
115 120

<210> 1147  
<211> 409  
<212> DNA  
<213> Homo sapiens

<400> 1147  
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gccaaaaagg catccacctt cttcatcaat ccagaattga tcatgctcat gcctgtgggt  
 120  
 ggatcactat gtgctctcca aattgggagg ggaagtctac tctcctctct cctctctctc  
 180  
 ccaccttccc ctctctcttc tctcctttct attcccaggg cagtggaaca tgatgagggt  
 240  
 cttttccctt catggatata ctctttctgc cctccacata aaggggcatt gatggatctt  
 300  
 caagaatggg atgcctttcc ctagaaggc taaatattca tgaggctgaa tgtgaggatc  
 360  
 cagagtacac tgaaatataa ctgggtcatca gtacacatag aatctgath  
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<210> 1148  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 1148  
 Met Gln Ser Gly Leu Leu Lys Val Met Ile Val Ala Lys Asn Ile Glu  
 1 5 10 15  
 Ala Lys Lys Ala Ser Thr Phe Phe Ile Asn Pro Glu Leu Ile Met Leu  
 20 25 30  
 Met Pro Val Gly Gly Ser Leu Cys Ala Leu Gln Ile Gly Arg Gly Ser  
 35 40 45  
 Leu Leu Ser Ser Leu Leu Ser Leu Pro Pro Ser Pro Leu Ser Ser Leu  
 50 55 60  
 Leu Ser Ile Pro Arg Ala Val Glu His Asp Glu Val Leu Phe Pro Ser  
 65 70 75 80  
 Trp Ile Ser Ser Phe Cys Pro Pro His Lys Gly Ala Leu Met Asp Leu  
 85 90 95  
 Gln Glu Trp Asp Ala Phe Pro  
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<210> 1149  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<400> 1149  
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 cgtgaggcgg tatcgcatat cattaccttc ggtaccatgg cggcgaaagc ggttattcgt  
 120  
 gacgtgggcc gtgtactggg tcacccgtat ggcttcgctg atcgcatctc caagctgggtg  
 180  
 ccgcccgatc cgggcatgac gctggaaaaa gcctttgccg ccgaaccgca gttgccggaa  
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 atctacgagg ccgatgagga agtcaaagcg ctgatcgaca tggcgcgcaa gctgggaagg  
 300  
 gtgacgcgg  
 309

<210> 1150

<211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 1150  
 Val Asp Phe Cys Met Glu Lys Arg Asp Leu Val Ile Glu His Val Ala  
 1 5 10 15  
 Glu Met Tyr Gly Arg Glu Ala Val Ser Gln Ile Ile Thr Phe Gly Thr  
 20 25 30  
 Met Ala Ala Lys Ala Val Ile Arg Asp Val Gly Arg Val Leu Gly His  
 35 40 45  
 Pro Tyr Gly Phe Val Asp Arg Ile Ser Lys Leu Val Pro Pro Asp Pro  
 50 55 60  
 Gly Met Thr Leu Glu Lys Ala Phe Ala Ala Glu Pro Gln Leu Pro Glu  
 65 70 75 80  
 Ile Tyr Glu Ala Asp Glu Glu Val Lys Ala Leu Ile Asp Met Ala Arg  
 85 90 95  
 Lys Leu Gly Arg Val Thr Arg  
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<210> 1151  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 1151  
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 gcgctcaata ccttcgcctc gtaccaaact gaggtcattc acgtcgacat ggacgcagac  
 120  
 gggttgggtc cggaatccct gcgtgagaaa gtgactgcag cgcgtaaga cggcaagtcg  
 180  
 gtgaagtcc tttacacggt tccaaactac tcgaaccggt cgggaatctc gcaatccacc  
 240  
 gagcgtcgcc gggagatcct agcgggtggc gacgagctgg atctgttggt ggttgaggac  
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 aaccgtaacg ggttactcaa cctcgatggt gatccactgc cgacgttgaa gtcgatggat  
 360

<210> 1152  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 1152  
 Ala Arg Ile Phe Cys Asn Pro Ser Asp Val Ile Met Ala Glu Ser Pro  
 1 5 10 15  
 Ala Tyr Val Gly Ala Leu Asn Thr Phe Ala Ser Tyr Gln Thr Glu Val  
 20 25 30  
 Ile His Val Asp Met Asp Asp Ser Gly Leu Val Pro Glu Ser Leu Arg  
 35 40 45  
 Glu Lys Val Thr Ala Ala Arg Gln Asp Gly Lys Ser Val Lys Phe Leu  
 50 55 60  
 Tyr Thr Val Pro Asn Tyr Ser Asn Pro Ser Gly Ile Ser Gln Ser Thr

65                                      70                                      75                                      80  
 Glu Arg Arg Arg Glu Ile Leu Ala Val Ala Asp Glu Leu Asp Leu Leu  
    85                                      90                                      95  
 Val Val Glu Asp Asn Pro Tyr Gly Leu Leu Asn Leu Asp Gly Asp Pro  
    100                                      105                                      110  
 Leu Pro Thr Leu Lys Ser Met Asp  
    115                                      120

<210> 1153

<211> 416

<212> DNA

<213> Homo sapiens

<400> 1153

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 120  
 aatccgatct ttaaggcccc cactcagggc attgggttacg ctgatctgtc tacctgtatg  
 180  
 gccctgggag ttactgggtcc tgctctgcgc gctaccggcc tgccgtggga cctgcgcaag  
 240  
 acccagccct attgcgatta cgacacgtat gacttcgacg tcgccacctg ggataacctgt  
 300  
 gactgtttacg ggcgttttcc catccgcctg gaagagatgg accagtcggt gcgcattctc  
 360  
 aagcaatgcc tcaaacgcct cgaggacacc cagggtgacc gtaatatggt cgagga  
 416

<210> 1154

<211> 138

<212> PRT

<213> Homo sapiens

<400> 1154

Ala Trp Ile Arg Pro Gly Gly Val Ala Thr Asp Leu Pro Glu Thr Gly  
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 Leu Asp Gln Leu Arg Asp Leu Ile Lys Arg Met Glu Lys Tyr Leu Pro  
    20                                      25                                      30  
 Glu Ile Gly Gln Phe Cys Asn Glu Asn Pro Ile Phe Lys Ala Arg Thr  
    35                                      40                                      45  
 Gln Gly Ile Gly Tyr Ala Asp Leu Ser Thr Cys Met Ala Leu Gly Val  
    50                                      55                                      60  
 Thr Gly Pro Ala Leu Arg Ala Thr Gly Leu Pro Trp Asp Leu Arg Lys  
 65                                      70                                      75                                      80  
 Thr Gln Pro Tyr Cys Asp Tyr Asp Thr Tyr Asp Phe Asp Val Ala Thr  
    85                                      90                                      95  
 Trp Asp Thr Cys Asp Cys Tyr Gly Arg Phe Arg Ile Arg Leu Glu Glu  
    100                                      105                                      110  
 Met Asp Gln Ser Val Arg Ile Leu Lys Gln Cys Leu Lys Arg Leu Glu  
    115                                      120                                      125  
 Asp Thr Gln Gly Asp Arg Asn Met Val Glu  
    130                                      135

<210> 1155  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<400> 1155  
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 tggcttatgg gacgcttctc agccctaagt aggaaaacag cagtgaaaat ggcaacaaaa  
 120  
 acatcacgca ggactggggg ttttggggaa acagctcact ttagagcagt gcagtgtaga  
 180  
 gctttccgtc ttctaccagg gtccaccttt aacactgttt atctgaaaat tttccccctg  
 240  
 gcttactcgc ttgcagctgc ccactttgca gaaagatggc gctctgatct ctacgctccc  
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 tgttccttca gggactccat agtatttttt ttcacgcgt  
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<210> 1156  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 1156  
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 Thr Lys Thr Ser Arg Arg Thr Gly Gly Phe Gly Glu Thr Ala His Phe  
 20 25 30  
 Arg Ala Val Gln Cys Arg Ala Phe Arg Leu Leu Pro Gly Ser Thr Phe  
 35 40 45  
 Asn Thr Val Tyr Leu Lys Ile Phe Pro Leu Ala Tyr Ser Leu Ala Ala  
 50 55 60  
 Ala His Phe Ala Glu Arg Trp Arg Ser Asp Leu Tyr Ala Pro Cys Ser  
 65 70 75 80  
 Phe Arg Asp Ser Ile Val Phe Phe Phe Thr Arg  
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<210> 1157  
 <211> 426  
 <212> DNA  
 <213> Homo sapiens

<400> 1157  
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 ctggcaaaac tcgtgaccgg acacctgagg gcctatcggt tgcacgttgc cgtcatcatc  
 120  
 gttatgcagg tttgcgcca aatcgcggcc ctgaccttgc caaccatcaa cgcagacatc  
 180  
 atcaacaagg gcgtcgtgac agcggatacc ggatatgtca ccaccactc cctcttcatg  
 240  
 ctggcggtcg ctttagggca ggccatctgc caggtcattg cggtttatct cgccgctcag  
 300

gtggcgatgg gaatgggccc tgacgttcgc gacgccatct tcacccgcac ccttgacttc  
 360  
 tcggccccggg agatcaacaa attcggagca ccatcactca ttacccggac taccaacgac  
 420  
 gtccag  
 426

<210> 1158  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 1158  
 Val Leu Ala Lys Leu Val Thr Arg His Leu Arg Ala Tyr Arg Leu His  
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 Val Ala Val Ile Ile Val Met Gln Val Cys Ala Gln Ile Ala Ala Leu  
 20 25 30  
 Thr Leu Pro Thr Ile Asn Ala Asp Ile Ile Asn Lys Gly Val Val Thr  
 35 40 45  
 Ala Asp Thr Gly Tyr Val Thr Thr His Ser Leu Phe Met Leu Ala Val  
 50 55 60  
 Ala Leu Gly Gln Ala Ile Cys Gln Val Ile Ala Val Tyr Leu Ala Ala  
 65 70 75 80  
 Gln Val Ala Met Gly Met Gly Arg Asp Val Arg Asp Ala Ile Phe Thr  
 85 90 95  
 Arg Thr Leu Asp Phe Ser Ala Arg Glu Ile Asn Lys Phe Gly Ala Pro  
 100 105 110  
 Ser Leu Ile Thr Arg Thr Thr Asn Asp Val Gln  
 115 120

<210> 1159  
 <211> 434  
 <212> DNA  
 <213> Homo sapiens

<400> 1159  
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 ggacgaggca ggagcaggcc gggctctcgc catgggtcac tgcgcctct gccacgggaa  
 120  
 gttttcctcg agaagcctgc gcagcatctc cgagagggcg cctggagcga gcatggagag  
 180  
 gccatccgca gaggagcgcg tgctcgtaag ggacttccag cgcttgcttg gtgtggctgt  
 240  
 ccgccaggac ccaccttgt ctccgtttgt ctgcaagagc tgccacgcc agttctacca  
 300  
 gtgccacagc cttctcaagt ctttctgca gaggggtcaac gcctccccgg ctggtcgccg  
 360  
 gaagccttgt gcaaaggctg gtgcccagcc cccaacaggg gcagaggagg gagegtgtct  
 420  
 ggtggatctg atca  
 434

<210> 1160

<211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 1160  
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 Arg Ser Ile Ser Glu Arg Ala Pro Gly Ala Ser Met Glu Arg Pro Ser  
                   20                  25                  30  
 Ala Glu Glu Arg Val Leu Val Arg Asp Phe Gln Arg Leu Leu Gly Val  
                   35                  40                  45  
 Ala Val Arg Gln Asp Pro Thr Leu Ser Pro Phe Val Cys Lys Ser Cys  
                   50                  55                  60  
 His Ala Gln Phe Tyr Gln Cys His Ser Leu Leu Lys Ser Phe Leu Gln  
   65                  70                  75                  80  
 Arg Val Asn Ala Ser Pro Ala Gly Arg Arg Lys Pro Cys Ala Lys Val  
                   85                  90                  95  
 Gly Ala Gln Pro Pro Thr Gly Ala Glu Glu Gly Ala Cys Leu Val Asp  
                   100                  105                  110  
 Leu Ile

<210> 1161  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<400> 1161  
 ctgcacacac accaggccac gccacgagg acggccagtc agcatgcagc caatacaccc  
   60  
 acagagggat ggggagcagc cctcagtgcc agctccaaca ggcccactgc aggtcctgtc  
   120  
 actgcaccca aggagctgcc ttccatttca cctgacattt ccactaaggc cccagcgttt  
   180  
 atcattccag aagagcagca ggcagaacct tcacctcca agagctgcaa gtgcgctgtg  
   240  
 gcaggaaaag aagatctggc gtctgaagtc agctcctgct ctccaggaaa agagggacga  
   300  
 tgacatagga cttgagcaaa atgagagccc cgtgatggga gagaacacct gatca  
   355

<210> 1162  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 1162  
 Met Gln Pro Ile His Pro Gln Arg Asp Gly Glu Gln Pro Ser Val Pro  
   1                  5                  10                  15  
 Ala Pro Thr Gly Pro Leu Gln Val Leu Ser Leu His Pro Arg Ser Cys  
                   20                  25                  30  
 Leu Pro Phe His Leu Thr Phe Pro Leu Arg Ala Gln Arg Leu Ser Phe  
                   35                  40                  45  
 Gln Lys Ser Ser Arg Gln Asn Leu His Leu Pro Arg Ala Ala Ser Ala



50                      55                      60  
 Leu Trp Gln Glu Lys Lys Ile Trp Arg Leu Lys Ser Ala Pro Ala Leu  
 65                      70                      75                      80  
 Gln Glu Lys Arg Asp Asp Ile Gly Leu Glu Gln Asn Glu Ser Pro  
                     85                      90                      95  
 Val Met Gly Glu Asn Thr  
                     100

<210> 1163  
 <211> 466  
 <212> DNA  
 <213> Homo sapiens

<400> 1163  
 ngcgcgccag gaagcgggag gtcagctgta caccagggt aatagaactt ctaccctcag  
 60  
 aggagtcaaa gagaaggcag aactatggca ggaaagctcc ggaagtccca catccctgga  
 120  
 gtgagcatct ggcagctggg ggaggagatc cctgaaggct gcagcacgcc ggactttgag  
 180  
 cagaagcccg tcacctcggc tctgccagag gggaaaaatg ctgtctttcg ggctgtgggc  
 240  
 tgtggggagc ccaggcccgga ggtgcgttgg cagaactcca aaggtgacct cagtgattcc  
 300  
 agcaagtaca agatctcctc cagccctggc agcaaggagc acgtgctgca gatcaacaag  
 360  
 ctgacaggcg aggacacgga tctgtaccac tgcacagcag taaatgcgta cggagaggcc  
 420  
 gcttgctcag tgagactcac cgtcatcgaa gttggctttc ggaaga  
 466

<210> 1164  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 1164  
 Met Ala Gly Lys Leu Arg Lys Ser His Ile Pro Gly Val Ser Ile Trp  
 1                      5                      10                      15  
 Gln Leu Val Glu Glu Ile Pro Glu Gly Cys Ser Thr Pro Asp Phe Glu  
                     20                      25                      30  
 Gln Lys Pro Val Thr Ser Ala Leu Pro Glu Gly Lys Asn Ala Val Phe  
                     35                      40                      45  
 Arg Ala Val Val Cys Gly Glu Pro Arg Pro Glu Val Arg Trp Gln Asn  
                     50                      55                      60  
 Ser Lys Gly Asp Leu Ser Asp Ser Ser Lys Tyr Lys Ile Ser Ser Ser  
 65                      70                      75                      80  
 Pro Gly Ser Lys Glu His Val Leu Gln Ile Asn Lys Leu Thr Gly Glu  
                     85                      90                      95  
 Asp Thr Asp Leu Tyr His Cys Thr Ala Val Asn Ala Tyr Gly Glu Ala  
                     100                      105                      110  
 Ala Cys Ser Val Arg Leu Thr Val Ile Glu Val Gly Phe Arg Lys  
                     115                      120                      125

<210> 1165  
 <211> 414  
 <212> DNA  
 <213> Homo sapiens

<400> 1165  
 tgggtggttc cggacacana aaatcacgtg ttgaaccgaa tttcaggcat ggtgaaaggc  
 60  
 tgcttttagta aagtccttgt tgagcccggt ctgctcaagc tcaacttgac nattatgtgt  
 120  
 ctgcacattc tgctgatgtc cacgttcgtg gccctgcccg gtcagttggc tgcagcagga  
 180  
 ttccccgccg ctgaacactg gaaagtgtat ctgggtgacga tgctcatctc cttcgtctcc  
 240  
 gttgtccctt tcattatcta tgcagaagtg aaacgccgca tgaagcgcgt attcctgacg  
 300  
 tgtgttgccg tgctgttgat tgccgaaatc gtactatggg gtcgccgtcc acacttctgg  
 360  
 gaactggcca tcggcgatca gcttttcttc ctgccttta atctcatgga agcc  
 414

<210> 1166  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<400> 1166  
 Trp Val Val Pro Asp Thr Xaa Asn His Val Leu Asn Arg Ile Ser Gly  
 1 5 10 15  
 Met Val Lys Gly Cys Phe Ser Lys Val Leu Val Glu Pro Arg Leu Leu  
 20 25 30  
 Lys Leu Asn Leu Thr Ile Met Cys Leu His Ile Leu Leu Met Ser Thr  
 35 40 45  
 Phe Val Ala Leu Pro Gly Gln Leu Ala Ala Ala Gly Phe Pro Ala Ala  
 50 55 60  
 Glu His Trp Lys Val Tyr Leu Val Thr Met Leu Ile Ser Phe Val Ser  
 65 70 75 80  
 Val Val Pro Phe Ile Ile Tyr Ala Glu Val Lys Arg Arg Met Lys Arg  
 85 90 95  
 Val Phe Leu Thr Cys Val Ala Leu Leu Ile Ala Glu Ile Val Leu  
 100 105 110  
 Trp Gly Ser Gly Pro His Phe Trp Glu Leu Val Ile Gly Val Gln Leu  
 115 120 125  
 Phe Phe Leu Ala Phe Asn Leu Met Glu Ala  
 130 135

<210> 1167  
 <211> 464  
 <212> DNA  
 <213> Homo sapiens

<400> 1167  
 gtgcaccccg tgggcaagag tcgcggcccc tgacgataac ttcaccccgcc cggccttgag  
 60

ctgttgggac cggctggcta aggcctgggc accggtagcg gcctggtgga taccctcatg  
 120  
 tagccgggtg acctgcctga ccattctcgg caaaccagtg cgcagttgtg tggatgaactc  
 180  
 attgaccctt cgagacagtc gtgaggaacc gtcagcaagt tcgtcgatgc cgtcgtcgat  
 240  
 gctcttgcca gagttcggat ccttgatcgc catcgccctg acggccaccc ccgaccacgc  
 300  
 ccgcacgccc agggcgtagc catcggtcat cgcgtcgcgg acgatgggta ccaggtcgtg  
 360  
 gcattcctgc gcggtgtggc ttgcacgca tcgacgcagg aagtcagcct cgtcccgagg  
 420  
 cagggcttcc ttactaagtt ccgcgggttt ctttcccgac gcgt  
 464

<210> 1168

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1168

Met	Thr	Asp	Gly	Tyr	Ala	Leu	Gly	Val	Arg	Ala	Gly	Ser	Gly	Val	Ala
1				5					10					15	
Val	Lys	Ala	Met	Ala	Ile	Lys	Asp	Pro	Asn	Ser	Gly	Lys	Ser	Ile	Asp
		20						25					30		
Asp	Gly	Ile	Asp	Glu	Leu	Ala	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Arg	Gly
		35					40					45			
Val	Asn	Glu	Phe	Thr	Thr	Gln	Leu	Arg	Thr	Gly	Leu	Pro	Lys	Met	Val
		50				55				60					
Arg	Gln	Val	Thr	Arg	Leu	His	Glu	Gly	Ile	His	Gln	Ala	Ala	Thr	Gly
65					70				75					80	
Ala	Gln	Ala	Leu	Ala	Ser	Arg	Ser	Gln	Gln	Leu	Lys	Ala	Gly	Gly	Val
			85					90					95		
Lys	Leu	Ser	Ser	Gly	Ala	Ala	Thr	Leu	Ala	His	Gly	Val	Asp		
			100					105					110		

<210> 1169

<211> 486

<212> DNA

<213> Homo sapiens

<400> 1169

nacgcgtgaa gggagcagaa cggacaccag ttactagtgg ctctggtcgg ggacagcctc  
 60  
 cttagcctt tctggccaat gggaacagga atagcccggg gctttctagc tgctatggac  
 120  
 tctgcctgga tgggtccgaag ttggtctcta ggaacgagcc ctttggaagt gctggcagag  
 180  
 agggaaagta ttacaggtt gctgcctcag accaccctg agaatgtgag taagaacttc  
 240  
 agccagtaca gtatcgaccc tgtaactcgg tateccaata tcaacgtcaa cttcctccgg  
 300  
 ccaagccagg tgcgccattt atatgatact ggcgaaacaa aagatattca cctggaaatg  
 360

gagagcctgg tgaattcccg aaccaccccc aaattgactc gcaatgagtc tgtagctcgt  
 420  
 tcaagcaaac tgctgggttg gtgccagagg cagacagatg gctatgcagg ggtaaactgt  
 480  
 acagat  
 486

<210> 1170  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 1170  
 Arg Glu Gln Asn Gly His Gln Leu Leu Val Ala Leu Val Gly Asp Ser  
 1 5 10 15  
 Leu Leu Glu Pro Phe Trp Pro Met Gly Thr Gly Ile Ala Arg Gly Phe  
 20 25 30  
 Leu Ala Ala Met Asp Ser Ala Trp Met Val Arg Ser Trp Ser Leu Gly  
 35 40 45  
 Thr Ser Pro Leu Glu Val Leu Ala Glu Arg Glu Ser Ile Tyr Arg Leu  
 50 55 60  
 Leu Pro Gln Thr Thr Pro Glu Asn Val Ser Lys Asn Phe Ser Gln Tyr  
 65 70 75 80  
 Ser Ile Asp Pro Val Thr Arg Tyr Pro Asn Ile Asn Val Asn Phe Leu  
 85 90 95  
 Arg Pro Ser Gln Val Arg His Leu Tyr Asp Thr Gly Glu Thr Lys Asp  
 100 105 110  
 Ile His Leu Glu Met Glu Ser Leu Val Asn Ser Arg Thr Thr Pro Lys  
 115 120 125  
 Leu Thr Arg Asn Glu Ser Val Ala Arg Ser Ser Lys Leu Leu Gly Trp  
 130 135 140  
 Cys Gln Arg Gln Thr Asp Gly Tyr Ala Gly Val Asn Val Thr Asp  
 145 150 155

<210> 1171  
 <211> 429  
 <212> DNA  
 <213> Homo sapiens

<400> 1171  
 acgcgttcaa caaagcacag aaccggagat gcagtgggag ccgagagcag gaagcgcgga  
 60  
 ggacgcgcca ggtgctggcg ctgcccgagg ccccgtagca agtggggccc atagcagccc  
 120  
 actcgtaga ccctcccaaa acgcacacca cgcgcgacca ggaccgagag gcccgcacgg  
 180  
 ccctgctagg ccacaaacac tccactgtct ccagggtaaa agacaaacac agcctcgctt  
 240  
 gtccctccaa gagtacaacc tctgtctgat gaaaaacaaa cgaccagag agggaggcagc  
 300  
 tgccgggaca ctgcaggctg ggcccgccgc gcccttgag ggcagggtcaa aatcccgga  
 360  
 caggcacagt gttcaggctg attgactgtc ccaggccagg gcggcctcaa ctgccagagc  
 420

acctcctac  
429

<210> 1172  
<211> 118  
<212> PRT  
<213> Homo sapiens

<400> 1172  
Met Gln Trp Glu Pro Arg Ala Gly Ser Ala Glu Ala Ala Pro Gly Ala  
1 5 10 15  
Gly Ala Ala Arg Gly Pro Val Pro Ser Gly Ala His Ser Ser Arg Leu  
20 25 30  
Ala Arg Pro Ser Gln Asn Ala His His Ala Arg Pro Gly Pro Arg Gly  
35 40 45  
Pro His Gly Pro Ala Arg Pro Gln Thr Leu His Cys Leu Gln Gly Lys  
50 55 60  
Arg Gln Thr Gln Pro Arg Leu Ser Leu Gln Glu Tyr Asn Leu Cys Leu  
65 70 75 80  
Met Lys Asn Lys Arg Pro Arg Glu Glu Ala Ala Ala Gly Thr Leu Gln  
85 90 95  
Ala Gly Pro Ala Ala Pro Leu Glu Gly Arg Ser Lys Ser Arg Asn Arg  
100 105 110  
His Ser Val Gln Ala Asp  
115

<210> 1173  
<211> 435  
<212> DNA  
<213> Homo sapiens

<400> 1173  
cgcgctcaatg acgacggcga gcattctgcc gagcagggtga tgcgagccac ccgcggtgct  
60  
ggacttgggg ccgaggccaa gcgtcgcac atcttgggta cctatgcctt gtcggctggg  
120  
tactatgacg cctactacgg ctcggtcag aaagtccgta ccctcatcca acgcgacttc  
180  
gagaaagcat ggcagatgtg cgatgtgtc gtgtcaccgg ccacgccaac gactgccttc  
240  
cggctgggtg agcgtactgc tgacccgatg gcgatgtacc gtcctgatct atgcacggtc  
300  
ccggccaata tggccggaag tcccgcagga tctttcccga tcggtctatc agagaccgac  
360  
ggcatgcccg tcggcatgca ggtgatggcg ccaatcatgg cggacgatcg aatctaccga  
420  
gttggggccg ctcta  
435

<210> 1174  
<211> 145  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 1174

Arg Val Asn Asp Asp Gly Glu His Ser Ala Glu Gln Val Met Arg Ala  
 1 5 10 15  
 Thr Arg Gly Ala Gly Leu Gly Ala Glu Ala Lys Arg Arg Ile Ile Leu  
 20 25 30  
 Gly Thr Tyr Ala Leu Ser Ala Gly Tyr Tyr Asp Ala Tyr Tyr Gly Ser  
 35 40 45  
 Ala Gln Lys Val Arg Thr Leu Ile Gln Arg Asp Phe Glu Lys Ala Trp  
 50 55 60  
 Gln Met Cys Asp Val Leu Val Ser Pro Ala Thr Pro Thr Thr Ala Phe  
 65 70 75 80  
 Arg Leu Gly Glu Arg Thr Ala Asp Pro Met Ala Met Tyr Arg Ser Asp  
 85 90 95  
 Leu Cys Thr Val Pro Ala Asn Met Ala Gly Ser Pro Ala Gly Ser Phe  
 100 105 110  
 Pro Ile Gly Leu Ser Glu Thr Asp Gly Met Pro Val Gly Met Gln Val  
 115 120 125  
 Met Ala Pro Ile Met Ala Asp Asp Arg Ile Tyr Arg Val Gly Ala Ala  
 130 135 140  
 Leu  
 145

&lt;210&gt; 1175

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1175

gatcgactg caatccaccc acatctactt gatatgaaaa ttgggtcaagg caaatatgag  
 60  
 caggggttct ttccaaagtt acagtccgat gtcttggcaa caggaccaac cagtaacaat  
 120  
 cgctgggtaa gtcggagtgc cactgcacag cgcaggaaag gacgccttcg ccagcattct  
 180  
 gagcatgttg ggctggacaa cgacttgagg gagaaatata tgcaagaggc acgaagttaa  
 240  
 ggaaaaaacc tgaggcaacc caaactgtca gacctctctc ctgcagttat tgcacagacc  
 300  
 aactgtaa atcgtagaagg cttattaaaa gaatgtagaa ataagacaaa gcgcatgttg  
 360  
 gtggagaaga tgggacatga agcgggtggaa cttggccatg gagaagcaaa catcaccggc  
 420  
 ctggaggaga acaccttgat cgccagcctt tgtgacctgc tggagaggat atggagccat  
 480  
 ggcttgcagg tcaagcaggg gaagtcggtt ttgtggtcac atttaattcc ttttcaggac  
 540  
 agagaagaga accaagagcc cttgcagaa tcaccagttg ccctcggacc agaaagaaaa  
 600  
 aaatctgact caggagttat gttgccaacg ctcagggtct ctcttattca ggacatgagg  
 660  
 catattcaaa acatgagtga gatcaagact gatgttggac gagctcgggc gtggataaga  
 720  
 ctgtctcta  
 729

<210> 1176  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens

<400> 1176  
 Asp Arg Thr Ala Ile His Pro His Leu Leu Asp Met Lys Ile Gly Gln  
 1 5 10 15  
 Gly Lys Tyr Glu Gln Gly Phe Phe Pro Lys Leu Gln Ser Asp Val Leu  
 20 25 30  
 Ala Thr Gly Pro Thr Ser Asn Asn Arg Trp Val Ser Arg Ser Ala Thr  
 35 40 45  
 Ala Gln Arg Arg Lys Gly Arg Leu Arg Gln His Ser Glu His Val Gly  
 50 55 60  
 Leu Asp Asn Asp Leu Arg Glu Lys Tyr Met Gln Glu Ala Arg Ser Leu  
 65 70 75 80  
 Gly Lys Asn Leu Arg Gln Pro Lys Leu Ser Asp Leu Ser Pro Ala Val  
 85 90 95  
 Ile Ala Gln Thr Asn Cys Lys Phe Val Glu Gly Leu Leu Lys Glu Cys  
 100 105 110  
 Arg Asn Lys Thr Lys Arg Met Leu Val Glu Lys Met Gly His Glu Ala  
 115 120 125  
 Val Glu Leu Gly His Gly Glu Ala Asn Ile Thr Gly Leu Glu Glu Asn  
 130 135 140  
 Thr Leu Ile Ala Ser Leu Cys Asp Leu Leu Glu Arg Ile Trp Ser His  
 145 150 155 160  
 Gly Leu Gln Val Lys Gln Gly Lys Ser Val Leu Trp Ser His Leu Ile  
 165 170 175  
 Pro Phe Gln Asp Arg Glu Glu Asn Gln Glu Pro Leu Ala Glu Ser Pro  
 180 185 190  
 Val Ala Leu Gly Pro Glu Arg Lys Lys Ser Asp Ser Gly Val Met Leu  
 195 200 205  
 Pro Thr Leu Arg Val Ser Leu Ile Gln Asp Met Arg His Ile Gln Asn  
 210 215 220  
 Met Ser Glu Ile Lys Thr Asp Val Gly Arg Ala Arg Ala Trp Ile Arg  
 225 230 235 240  
 Leu Ser Leu

<210> 1177  
 <211> 581  
 <212> DNA  
 <213> Homo sapiens

<400> 1177  
 acgcgtgatg agttgcgcga gaccagcaac tgcagccgaa tacagttttc ttgtgtaccc  
 60  
 cgctgcacag ctgcgagagg tgggcattgc cgagtgaggc aacgatgtct aaggcggaaa  
 120  
 gctcatcctc ggcagacggg aagactttgt cgtcggggat gttgtcaatg agagcgggga  
 180  
 cgctgatctc ggtactgccc atggcgatcat gaaggatcgc gcgatacggg ggcacgaccc  
 240

cgatgagggc gtcgtcgaat ccagcgatga tcgatacctc tctcggtagc acgtccgtgg  
 300  
 ccaacaggtg gtcgacttgg gcgggggcta gccatgtaat tgttccgagc acatggaggg  
 360  
 tggctgccag gaggcggatg gccgggttctg gggcatcttt ggagatcttc agccggacat  
 420  
 cagtgggcag tccggccggg acttggcaga gggcctgggc gggatgggag cgctgggcga  
 480  
 cgacgaaacg ccccgacgcc gtaacgccgt gggcttggag atcgcaggtc cacttctctg  
 540  
 ggctttcacc ggcagagatc atggtgtgga ccaccattgt g  
 581

<210> 1178

<211> 192

<212> PRT

<213> Homo sapiens

<400> 1178

Met	Val	Val	His	Thr	Met	Ile	Ser	Ala	Gly	Glu	Ser	Pro	Glu	Lys	Trp
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Thr	Cys	Asp	Leu	Gln	Ala	His	Gly	Val	Thr	Ala	Ser	Gly	Arg	Phe	Val
			20					25					30		
Val	Ala	Gln	Arg	Ser	His	Pro	Ala	Gln	Ala	Leu	Cys	Gln	Val	Pro	Ala
		35					40					45			
Gly	Leu	Pro	Thr	Asp	Val	Arg	Leu	Lys	Ile	Ser	Lys	Asp	Ala	Pro	Glu
	50					55					60				
Pro	Ala	Ile	Arg	Leu	Leu	Ala	Ala	Thr	Leu	His	Val	Leu	Gly	Thr	Ile
65					70					75				80	
Thr	Trp	Leu	Ala	Pro	Ala	Gln	Val	Asp	His	Leu	Leu	Ala	Thr	Asp	Val
				85				90						95	
Leu	Pro	Arg	Glu	Val	Ser	Ile	Ile	Ala	Gly	Phe	Asp	Asp	Ala	Leu	Ile
			100					105					110		
Gly	Val	Val	Ala	Pro	Tyr	Arg	Ala	Ile	Leu	His	Asp	Ala	Met	Gly	Ser
		115					120					125			
Thr	Glu	Ile	Asp	Val	Pro	Ala	Leu	Ile	Asp	Asn	Ile	Pro	Asp	Asp	Lys
	130					135					140				
Val	Phe	Pro	Ser	Ala	Glu	Asp	Glu	Leu	Ser	Ala	Leu	Asp	Ile	Val	Ala
145					150					155				160	
Ser	Leu	Gly	Asn	Ala	His	Leu	Ser	Gln	Leu	Cys	Asp	Gly	Val	His	Lys
			165					170					175		
Lys	Thr	Val	Phe	Gly	Cys	Ser	Cys	Trp	Ser	Arg	Ala	Thr	His	His	Ala
		180						185					190		

<210> 1179

<211> 597

<212> DNA

<213> Homo sapiens

<400> 1179

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 60  
 gattggggct tctggacatg ctgccacaag atgtctggaa actccagggg gcacctgccg  
 120



agaccctgcc ctgggaacgg ccggaagaat cccaaaacat gagattccgg tgcagctgag  
 180  
 ccccgccaat tcattgtctc tttagtccc ttctgaaggc tgcatttggc aatgtgaccc  
 240  
 tcgggggtggg gaaggcatca gaggaatata ggctatggga cgccagaggc agcgtcctgg  
 300  
 ggacaaagcc cacttcttcc catgcccagg gcttcctcat ggacccagca tgggtggacgt  
 360  
 ggccctcaga cgtccatggg tgggtggggga ggcaagtgtt gtttggccct gtctctgctc  
 420  
 agagtctcat aggaagatgc atggtccaca caacagttag tcggcagggg gtccaggctt  
 480  
 cccctcccaa ccagtgggtg tgagacgctt gggtttataac ccaagatccc ttgtcccatt  
 540  
 ggtgcctcct gaatctccca cctcccggcg cacctgcatg gcctctacct gacgcgt  
 597

<210> 1180

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1180

Met	Gly	Arg	Gln	Arg	Gln	Arg	Pro	Gly	Asp	Lys	Ala	His	Phe	Phe	Pro
1			5					10					15		
Cys	Pro	Gly	Leu	Pro	His	Gly	Pro	Ser	Met	Val	Asp	Val	Ala	Leu	Arg
	20						25					30			
Arg	Pro	Trp	Val	Val	Gly	Glu	Ala	Arg	Ala	Val	Trp	Pro	Cys	Leu	Cys
	35					40					45				
Ser	Glu	Ser	His	Arg	Lys	Met	His	Gly	Pro	His	Asn	Ser	Glu	Ser	Ala
	50				55				60						
Gly	Ser	Pro	Gly	Phe	Pro	Ser	Gln	Pro	Val	Val	Leu	Arg	Arg	Leu	Val
65				70				75					80		
Tyr	Asn	Pro	Arg	Ser	Leu	Val	Pro	Leu	Val	Pro	Pro	Glu	Ser	Pro	Thr
			85				90						95		
Ser	Arg	Gly	Thr	Cys	Met	Ala	Ser	Thr							
			100				105								

<210> 1181

<211> 352

<212> DNA

<213> Homo sapiens

<400> 1181

gtcgactacc tcgatgtttc cccgcgtcag atggtctccg tggctactgc catgattccg  
 60  
 ttctctgagc acgacgacgc taaccgtgcc ctgatgggtg cgaacatgca gcgtcaggct  
 120  
 gtgccgctgc tgcgttcgga ggctccgttc gtcggtaccg gtatggagca gcgtgctgct  
 180  
 tacgacgcgc gcgatgtcat tgctgcttcg gccacagggtg tggctcgagac cgtgtcggca  
 240  
 ggcttcatca ccatcatgga cgatgagggc cagcgcacaca cctacctgct gcgcaagttc  
 300

gagcgacacca accagggcac ctgctacaac cagaagccac tgttgacgag gg  
352

<210> 1182

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1182

Val	Asp	Tyr	Leu	Asp	Val	Ser	Pro	Arg	Gln	Met	Val	Ser	Val	Ala	Thr
1				5					10					15	
Ala	Met	Ile	Pro	Phe	Leu	Glu	His	Asp	Asp	Ala	Asn	Arg	Ala	Leu	Met
			20					25					30		
Gly	Ala	Asn	Met	Gln	Arg	Gln	Ala	Val	Pro	Leu	Leu	Arg	Ser	Glu	Ala
		35				40						45			
Pro	Phe	Val	Gly	Thr	Gly	Met	Glu	Gln	Arg	Ala	Ala	Tyr	Asp	Ala	Gly
		50				55						60			
Asp	Val	Ile	Val	Ala	Ser	Ala	Thr	Gly	Val	Val	Glu	Thr	Val	Ser	Ala
65				70					75					80	
Gly	Phe	Ile	Thr	Ile	Met	Asp	Asp	Glu	Gly	Gln	Arg	His	Thr	Tyr	Leu
				85					90					95	
Leu	Arg	Lys	Phe	Glu	Arg	Thr	Asn	Gln	Gly	Thr	Cys	Tyr	Asn	Gln	Lys
			100					105						110	
Pro	Leu	Leu	Thr	Arg											
															115

<210> 1183

<211> 432

<212> DNA

<213> Homo sapiens

<400> 1183

gataccttctg ggcgctggtc caagcgctg gtgaggccgt cctctcctgc agaaccccg  
60  
cctcttcgcc cctgcccgct cacctgttct gtctctgctca cctcctccag gaagcctgcc  
120  
tgcccttctc catgctgatg ggcgtggccc ttgtccctgc agccatgcat tgacctccgt  
180  
ggctcctgga ggccaggcca cgtcctcatc ccctctgggt gagtgagagg cacagcctgg  
240  
gtgcgtgggg ccgtggcggc tccgaggcgc caccgctgtg tcctctcatg agtgggtgcc  
300  
gtccaggtct gtctctgggt ggctgcgagg aggaggttgg cctcgcgcgg ccatgtgcgt  
360  
gacagtggag acatcgccag cctctgctt gcacagctga cggcagcccc tctctctcca  
420  
gcatgtccc ca  
432

<210> 1184

<211> 141

<212> PRT

<213> Homo sapiens

<400> 1184  
 Met Ala Gly Glu Arg Gly Ala Ala Val Ser Cys Ala Ser Arg Arg Leu  
 1 5 10 15  
 Ala Met Ser Pro Leu Ser Arg Thr Trp Pro Arg Glu Ala Asn Leu Leu  
 20 25 30  
 Leu Ala Ala Ser Pro Gly Gln Thr Trp Thr Ala Pro Thr His Glu Arg  
 35 40 45  
 Thr Gln Arg Trp Arg Leu Gly Ala Ala Thr Ala Pro Arg Thr Gln Ala  
 50 55 60  
 Val Pro Leu Thr His Pro Glu Gly Met Arg Thr Trp Pro Gly Leu Gln  
 65 70 75 80  
 Glu Pro Arg Arg Ser Met His Gly Cys Arg Asp Lys Gly His Ala His  
 85 90 95  
 Gln His Gly Glu Gly Gln Ala Gly Phe Leu Glu Glu Val Ser Arg Thr  
 100 105 110  
 Glu Gln Val Ser Gly Gln Gly Arg Arg Gly Arg Gly Ser Ala Gly Glu  
 115 120 125  
 Asp Gly Leu Thr Thr Arg Leu Asp Gln Arg Pro Glu Gly  
 130 135 140

<210> 1185  
 <211> 423  
 <212> DNA  
 <213> Homo sapiens

<400> 1185  
 accggtgaat ttggccttaa cagcgatgga actcctggcc catcttatga acctggcatg  
 60  
 gaattacgcg gcaaatatgt attgttgggt gaaggtgtac ggggctctct atctaaacaa  
 120  
 gtcatcaata aataccaatt atccgagggt catgaaccac aaaagttcgg ccttggttta  
 180  
 aaagaaattt gggaaataga cccagaaaaa cacaagaag gcagagtcag tcataccatg  
 240  
 ggctggccat taaatggcaa tgctggcggc gggtcttttta tttatcatgc agaaaacaat  
 300  
 caagtcttta tcggctttgt ggtgcatctt aattacgcca acccttacct atccccttac  
 360  
 caagaatttc aacgctttta acaccatccg attatcgagg agctattaac tggcggttaa  
 420  
 cgc  
 423

<210> 1186  
 <211> 141  
 <212> PRT  
 <213> Homo sapiens

<400> 1186  
 Thr Gly Glu Phe Gly Leu Asn Ser Asp Gly Thr Pro Gly Pro Ser Tyr  
 1 5 10 15  
 Glu Pro Gly Met Glu Leu Arg Gly Lys Tyr Val Leu Leu Gly Glu Gly  
 20 25 30  
 Val Arg Gly Ser Leu Ser Lys Gln Val Ile Asn Lys Tyr Gln Leu Ser

```

      35          40          45
Glu Gly His Glu Pro Gln Lys Phe Gly Leu Gly Leu Lys Glu Ile Trp
  50          55          60
Glu Ile Asp Pro Glu Lys His Lys Glu Gly Arg Val Ser His Thr Met
  65          70          75          80
Gly Trp Pro Leu Asn Gly Asn Ala Gly Gly Gly Ser Phe Ile Tyr His
      85          90          95
Ala Glu Asn Asn Gln Val Phe Ile Gly Phe Val Val His Leu Asn Tyr
      100          105          110
Ala Asn Pro Tyr Leu Ser Pro Tyr Gln Glu Phe Gln Arg Phe Lys His
      115          120          125
His Pro Ile Ile Ala Glu Leu Leu Thr Gly Gly Lys Arg
      130          135          140

```

&lt;210&gt; 1187

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1187

```

acgcgtgctg gtgagtttaa attgaatgct gatggtaatt tggtgacgaa ttcaggggct
  60
aagggtccagg gctataatgc aatagatggc atagtcgggtg ggaacttaga agatatggta
  120
gtaccactcg ctcgaatttc tcctcaagca acatcaagtg ttgatttaaa agtgaatctt
  180
aattccgaag gtgaggatgt gccgccttat attcgagcgg actttgatcc agccaatcca
  240
gatacttatg actatactca gacccaaacg gttgcggatg ggagtggtaa taatcattta
  300
attagttatt actatgctaa aagtgatgta gcaaatacct atcagggttta tgccacggta
  360
gatgggaagt cgactgatga taccggt
  387

```

&lt;210&gt; 1188

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1188

```

Thr Arg Ala Gly Glu Phe Lys Leu Asn Ala Asp Gly Asn Leu Val Thr
  1          5          10          15
Asn Ser Gly Ala Lys Val Gln Gly Tyr Asn Ala Ile Asp Gly Ile Val
      20          25          30
Gly Gly Asn Leu Glu Asp Met Val Val Pro Thr Ala Arg Ile Ser Pro
      35          40          45
Gln Ala Thr Ser Ser Val Asp Leu Lys Val Asn Leu Asn Ser Glu Gly
      50          55          60
Glu Asp Val Pro Pro Tyr Ile Arg Ala Asp Phe Asp Pro Ala Asn Pro
  65          70          75          80
Asp Thr Tyr Asp Tyr Thr Gln Thr Gln Thr Val Ala Asp Gly Ser Gly
      85          90          95
Asn Asn His Leu Ile Ser Tyr Tyr Tyr Ala Lys Ser Asp Val Ala Asn

```

100 105 110  
 Thr Tyr Gln Val Tyr Ala Thr Val Asp Gly Lys Ser Thr Asp Asp Thr  
 115 120 125  
 Gly

<210> 1189  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 1189  
 tcgacgccc accgcccggg ccttgccccc ggcacgatcg gtggcctgtt ggccagcacc  
 60  
 ctgggtgctg gtttcattgg cggcatcggt gcagggtttc tggccgggta cagcgccaag  
 120  
 gccattgccc gctgggcacg gctgcccagc agcctggatg cgctcaaacc gattctgac  
 180  
 atttcgctgc tggccagcct gttcactggg ttggtgatga tctacgtggt cggccagccg  
 240  
 gtggcggcca tgctcggagg cctgacacac tttctcgaca gcatgggtac caccaacgcc  
 300  
 attctcctgg gcntgttgct cggcggctag  
 330

<210> 1190  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 1190  
 Ser Ile Ala Asp Arg Pro Gly Leu Ala Pro Gly Met Ile Gly Gly Leu  
 1 5 10 15  
 Leu Ala Ser Thr Leu Gly Ala Gly Phe Ile Gly Gly Ile Val Ala Gly  
 20 25 30  
 Phe Leu Ala Gly Tyr Ser Ala Lys Ala Ile Ala Arg Trp Ala Arg Leu  
 35 40 45  
 Pro Ser Ser Leu Asp Ala Leu Lys Pro Ile Leu Ile Ile Ser Leu Leu  
 50 55 60  
 Ala Ser Leu Phe Thr Gly Leu Val Met Ile Tyr Val Val Gly Gln Pro  
 65 70 75 80  
 Val Ala Ala Met Leu Gly Gly Leu Thr His Phe Leu Asp Ser Met Gly  
 85 90 95  
 Thr Thr Asn Ala Ile Leu Leu Gly Xaa Leu Leu Gly Gly  
 100 105

<210> 1191  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 1191  
 cggccgacga tgtgcggtga gcaagagatt tggagagcca tgatgacgtc agcagacaaa  
 60

gcagggacta acggacagac catgcagaca ccgccggtgg tgctgccgca ggactgggag  
 120  
 gcagcccgtc agcaactgct cgtgaaggaa aaggcgcata cccgtgcccg cgacgcactc  
 180  
 gccgccgaac ggaggcgcac gccgtggatg gaagtgacaa aaacctacgc attcgaggcg  
 240  
 ccctcggggca aggccagtct gctcgatctg ttccagggcc ggaagcagct gatcctgtac  
 300  
 cgggccttct tcgagccggg cgtgttcggc tggcccgaac atgcctgccg c  
 351

<210> 1192

<211> 114

<212> PRT

<213> Homo sapiens

<400> 1192

Met	Cys	Gly	Glu	Gln	Glu	Ile	Trp	Arg	Ala	Met	Met	Thr	Ser	Ala	Asp
1				5					10					15	
Lys	Ala	Gly	Thr	Asn	Gly	Gln	Thr	Met	Gln	Thr	Pro	Pro	Val	Val	Ser
			20					25					30		
Pro	Gln	Asp	Trp	Glu	Ala	Ala	Arg	Gln	Gln	Leu	Leu	Val	Lys	Glu	Lys
		35					40					45			
Ala	His	Thr	Arg	Ala	Arg	Asp	Ala	Leu	Ala	Ala	Glu	Arg	Arg	Arg	Met
	50					55					60				
Pro	Trp	Met	Glu	Val	Thr	Lys	Thr	Tyr	Ala	Phe	Glu	Ala	Pro	Ser	Gly
65					70					75				80	
Lys	Ala	Ser	Leu	Leu	Asp	Leu	Phe	Gln	Gly	Arg	Lys	Gln	Leu	Ile	Leu
			85					90					95		
Tyr	Arg	Ala	Phe	Phe	Glu	Pro	Gly	Val	Phe	Gly	Trp	Pro	Asp	His	Ala
			100					105					110		
Cys	Arg														

<210> 1193

<211> 722

<212> DNA

<213> Homo sapiens

<400> 1193

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 cgacttagga cgcccagttt gtactcagtg tttgctcttt tatggcagag cctctgcact  
 120  
 cccagcctcc tggccccttc tgtacatgat tttccttggt gccactccat gcatttttct  
 180  
 tggctcagga cttagtgggc ctccatggga cttggtacct ctacttggtc ccttctggaa  
 240  
 tctgtaactt tgtgttcccc accattcttt cctttatgaa ccgatggtgc aacagcatga  
 300  
 ctacctgaaa ttcttagtca ctcccagctg ctttagtgga gggaaaatgc ccacagcaca  
 360  
 ggaaatagtc ctgcccttcg agagaggcca ggggatggga gcgtgtccag agaaggcgca  
 420

tgggttgatg aaggggtggcc acagcgcccg ggaggaaggg gccagaacgc tctctgttct  
 480  
 gttccatgag gaggattatg ttggtgtgtg tagtcccctg gttcagagtt gtccagaaat  
 540  
 agctcagtgt aaggaacaat tttccaaaga tcaaaagagc tgtctcaaga tagcagtgcg  
 600  
 ttcccagccc ctacaggtgt atacagcaca aaggaggagg ccccttagtg tggctgtcac  
 660  
 agaggggaagt ggacgtcctg tggtttgacc ccaccagatg gcttttagaga tctgggccccg  
 720  
 ag  
 722

<210> 1194  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 1194  
 Met Val Gln Gln His Asp Tyr Leu Lys Phe Leu Val Thr Pro Ser Cys  
 1 5 10 15  
 Phe Ser Gly Gly Lys Met Pro Thr Ala Gln Glu Ile Val Leu Pro Phe  
 20 25 30  
 Glu Arg Gly Gln Gly Met Gly Ala Cys Pro Glu Lys Gly Asp Gly Leu  
 35 40 45  
 Met Lys Gly Gly His Ser Ala Arg Glu Glu Gly Ala Arg Thr Leu Ser  
 50 55 60  
 Val Leu Phe His Glu Glu Asp Tyr Val Gly Val Cys Ser Pro Leu Val  
 65 70 75 80  
 Gln Ser Cys Pro Glu Ile Ala Gln Cys Lys Glu Gln Phe Ser Lys Asp  
 85 90 95  
 Gln Lys Ser Cys Leu Lys Ile Ala Val Arg Ser Gln Pro Leu Gln Val  
 100 105 110  
 Tyr Thr Ala Gln Arg Glu Gly Pro Pro Ser Val Ala Val Thr Glu Gly  
 115 120 125  
 Ser Gly Arg Pro Val Val  
 130

<210> 1195  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 1195  
 tctagagcat gatattccgc gggcgcggcc ggggtggactt tggttcgaga gtggaactaa  
 60  
 gtgagtaatg ggggcgggcg gccagacgc gctcccagcc tcttggcgag agtgctgccc  
 120  
 gggtttcccgg gggcacggga gtgtgtctag gaggggaggc caggatcctt cctcgagtcc  
 180  
 tgtcctgaac aaaagaaaac gaggtgggtg gtgcttgaac ggccctgttt actctgcaga  
 240  
 tagccgaact ggtaggactc cggcgcgccc tatttatctt gattggctct gctgaaggc  
 300

aagcgttaat cccgtccaac ctgtatcact gcgaagagct cgttcgggag cgctttttgg  
 360  
 aaatgcagat tcttagcccc caccagatc t  
 391

<210> 1196  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 1196  
 Met Gly Ala Ala Arg Pro Asp Ala Leu Pro Ala Ser Trp Arg Glu Cys  
 1 5 10 15  
 Cys Pro Val Ser Arg Gly His Gly Ser Val Ser Arg Arg Gly Gly Gln  
 20 25 30  
 Asp Pro Ser Ser Ser Pro Val Leu Asn Lys Arg Lys Arg Gly Gly Trp  
 35 40 45  
 Cys Leu Asn Gly Pro Val Tyr Ser Ala Asp Ser Arg Thr Gly Arg Thr  
 50 55 60  
 Pro Ala Arg Pro Ile Tyr Leu Asp Trp Leu Cys Leu Lys Ala Ser Val  
 65 70 75 80  
 Asn Pro Val Gln Pro Val Ser Leu Arg Arg Ala Arg Ser Gly Ala Leu  
 85 90 95  
 Phe Gly Asn Ala Asp Ser  
 100

<210> 1197  
 <211> 386  
 <212> DNA  
 <213> Homo sapiens

<400> 1197  
 acgcgtgatg atcatgaaaa tggtagagag cgtctagcag aagtcgcctc tgtgatgggc  
 60  
 tggcagcaag atgaaatcat cgtaaagta caaggggatg aaccctttct gcctgttgca  
 120  
 cttattcatg ccacgggttaa agcgtagcc gatgatgctg aatctgaaat ggccacgatt  
 180  
 gcctgtgcga ttgataacgt agcagagctg ttaacccaa atgtagttaa agtcgtttgt  
 240  
 gatgaaaaac agcgcgcctt gtatttcagt cgtgcgccta tgccatggga ccgtaatggt  
 300  
 tttatggaaa aaacagacga tcaagcgta ccagcggatt ttcctgcgtt gcgtcatatt  
 360  
 ggtccgtatg tttaccgcac gacatn  
 386

<210> 1198  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 1198  
 Thr Arg Asp Asp His Glu Asn Gly Thr Glu Arg Leu Ala Glu Val Ala



```

      1           5           10           15
Ser Val Met Gly Trp Gln Gln Asp Glu Ile Ile Val Asn Val Gln Gly
      20           25           30
Asp Glu Pro Phe Leu Pro Val Ala Leu Ile His Ala Thr Val Lys Ala
      35           40           45
Leu Ala Asp Asp Ala Glu Ser Glu Met Ala Thr Ile Ala Cys Ala Ile
      50           55           60
Asp Asn Val Ala Glu Leu Phe Asn Pro Asn Val Val Lys Val Val Cys
      65           70           75           80
Asp Glu Lys Gln Arg Ala Leu Tyr Phe Ser Arg Ala Pro Met Pro Trp
      85           90           95
Asp Arg Asn Gly Phe Met Glu Lys Thr Asp Asp Gln Ala Leu Pro Ala
      100          105          110
Asp Phe Pro Ala Leu Arg His Ile Gly Pro Tyr Val Tyr Arg Thr Thr
      115          120          125

```

&lt;210&gt; 1199

&lt;211&gt; 318

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1199

```

acgcgttcag cgtcatgtac agccccgggc cgggtcaattt gatgggcctc aatgccgggc
60
ttacgggcaa attgcgtcgc tccagcgggt tctacatcgg cgtgggggtgc gcgatgctgc
120
tgatggtcgg gctggttggg ctcaccggcg aagcgatcat ctcccaggcg gcgctgccgt
180
atatttcttt gattggcggg gtgtacacgc tgtacctcgc ctaccaggtg ttcaccgcac
240
gtaccgaagt ggatgacgcc ccaagcgcg ctcgccaagac cttgaccttc tggaatggcc
300
tggtgatcca gttgctcc
318

```

&lt;210&gt; 1200

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1200

```

Met Tyr Ser Pro Gly Pro Val Asn Leu Met Gly Leu Asn Ala Gly Leu
  1           5           10           15
Thr Gly Lys Leu Arg Arg Ser Ser Gly Phe Tyr Ile Gly Val Gly Cys
      20           25           30
Ala Met Leu Leu Met Val Gly Leu Val Gly Leu Thr Gly Glu Ala Ile
      35           40           45
Ile Ser Gln Ala Ala Leu Pro Tyr Ile Ser Leu Ile Gly Gly Val Tyr
      50           55           60
Thr Leu Tyr Leu Ala Tyr Gln Val Phe Thr Ala Arg Thr Glu Val Asp
      65           70           75           80
Asp Ala Pro Ser Ala Pro Ala Lys Thr Leu Thr Phe Trp Asn Gly Leu
      85           90           95
Val Ile Gln Leu Leu

```

100

<210> 1201  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 1201  
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 60  
 atgatacctca ccgtgctgcg catggccaag gatgaccgca accgttggaa tgcaaaaatc  
 120  
 acgctgcagg cgatccgcga gctggataac gccttcgcg tgctggaaca gttcaagggc  
 180  
 cgccgcaagg tcacggtggt tggctcgcg cgacgcgg tcgaaagccc gctgtacgcc  
 240  
 ttggcaaggg aagtcggcac gctgctggcg caatccgacc tgatggtgat caccggcggt  
 300  
 ggcgcgaggca tcatggccgc tgcccacgag ggcgcaaggt ctggaacaca gcctgggggt  
 360

<210> 1202  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 1202  
 Val Asp Ala Gln Leu Gln Leu Val Ala Pro Asn Ser Pro Asn Ile Pro  
 1 5 10 15  
 Leu Tyr Arg Asp Met Ile Leu Thr Val Leu Arg Met Ala Lys Asp Asp  
 20 25 30  
 Arg Asn Arg Trp Asn Ala Lys Ile Thr Leu Gln Ala Ile Arg Glu Leu  
 35 40 45  
 Asp Asn Ala Phe Arg Val Leu Glu Gln Phe Lys Gly Arg Arg Lys Val  
 50 55 60  
 Thr Val Phe Gly Ser Ala Arg Thr Pro Val Glu Ser Pro Leu Tyr Ala  
 65 70 75 80  
 Leu Ala Arg Glu Val Gly Thr Leu Leu Ala Gln Ser Asp Leu Met Val  
 85 90 95  
 Ile Thr Gly Gly Gly Gly Ile Met Ala Ala Ala His Glu Gly Ala  
 100 105 110  
 Arg Ser Gly Thr Gln Pro Gly Gly  
 115 120

<210> 1203  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

<400> 1203  
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 60  
 cctgagtatg caatgactgg acaacttagc tctaagagtg acgtttacag ttttgaggt  
 120

ggtcttctgg agctcctgac tggaagaaag cctgtggatc ttccattacc aagaggacag  
 180  
 caaagtcttg tgacatgggc aactccacgg ctttgtgaag ataaagttag gcaatgcgtt  
 240  
 gattcaagac ttggagtaga atatcctcct aaatccgttg caaagtttgc agctgttgct  
 300  
 gcactgtgtg tgcaatatga agctgacttt cgacccaaca tgagcatcgt ggtgaaggcg  
 360  
 cttcagcccc tgctgaatgc acgtgcatcc aacaaccctg gatgaatgaa tgaatgactg  
 420  
 ccgttgcttt tccctgacga gagtatctga atcagacaat catgtagcat tgaattc  
 477

<210> 1204

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1204

Pro	Asp	Met	Ala	Ala	Arg	Leu	His	Ser	Thr	Arg	Val	Leu	Gly	Thr	Phe
1				5					10					15	
Gly	Tyr	His	Ala	Pro	Glu	Tyr	Ala	Met	Thr	Gly	Gln	Leu	Ser	Ser	Lys
		20						25				30			
Ser	Asp	Val	Tyr	Ser	Phe	Gly	Val	Gly	Leu	Leu	Glu	Leu	Leu	Thr	Gly
		35				40					45				
Arg	Lys	Pro	Val	Asp	Leu	Pro	Leu	Pro	Arg	Gly	Gln	Gln	Ser	Leu	Val
	50				55				60						
Thr	Trp	Ala	Thr	Pro	Arg	Leu	Cys	Glu	Asp	Lys	Val	Arg	Gln	Cys	Val
65				70					75					80	
Asp	Ser	Arg	Leu	Gly	Val	Glu	Tyr	Pro	Pro	Lys	Ser	Val	Ala	Lys	Phe
			85					90					95		
Ala	Ala	Val	Ala	Ala	Leu	Cys	Val	Gln	Tyr	Glu	Ala	Asp	Phe	Arg	Pro
		100						105					110		
Asn	Met	Ser	Ile	Val	Val	Lys	Ala	Leu	Gln	Pro	Leu	Leu	Asn	Ala	Arg
	115						120					125			
Ala	Ser	Asn	Asn	Pro	Gly										
	130														

<210> 1205

<211> 407

<212> DNA

<213> Homo sapiens

<400> 1205

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 tgtgcacagg gaaacactag ctaccgtgca gcaggaaatg atgggagaaa tcagccatgg  
 120  
 taacaagaac caagccatcc tggacacaga cggccgggggt tgtgcgaacg gaacgttagt  
 180  
 ctatcaatgt gttgcggaac gattcaaggg atgctggccc ccccatcac ttgcccaatc  
 240  
 aagatgtgga gggaatctgt ctgcgcagaa cctggatctc gtggttgtag gacgttgctc  
 300

ccttctcgct cggacgccgc tcatgctccg ccacgtcgct gagcgagtga caaggatatcc  
 360  
 tgggaccatg cgtatgggtt caactgaagc gctggcgaat cgtaaan  
 407

<210> 1206  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 1206  
 Met Met Gly Glu Ile Ser His Gly Asn Lys Asn Gln Ala Ile Leu Asp  
 1 5 10 15  
 Thr Asp Gly Arg Gly Cys Ala Asn Gly Thr Leu Val Tyr Gln Cys Val  
 20 25 30  
 Ala Glu Arg Phe Lys Gly Cys Trp Pro Pro Pro Ser Leu Ala Gln Ser  
 35 40 45  
 Arg Cys Gly Gly Asn Leu Ser Ala Gln Asn Leu Asp Leu Val Val Val  
 50 55 60  
 Arg Arg Cys Pro Leu Leu Ala Arg Thr Pro Leu Met Leu Arg His Val  
 65 70 75 80  
 Ala Glu Arg Val Thr Arg Tyr Pro Gly Thr Met Arg Met Val Ser Thr  
 85 90 95  
 Glu Ala Leu Ala Asn Arg Lys  
 100

<210> 1207  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens

<400> 1207  
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 gcttgccctc attcctatgt gctttcccgt ccttgcttct ccagccatgt gtgggacaac  
 120  
 caggggtgct caccacctag tgagtttcag ggacactcca catgtcccag caagtcttat  
 180  
 cagcatctta gctggcttct caacaagact cagtggcacc cctgtggatg tctcccatca  
 240  
 agtttcatta gtgccccagg gggagactcc cagaaagttt cagcagcacc ac  
 292

<210> 1208  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 1208  
 Met Ser Leu Phe Ser Ser Val Asp Gly Thr Gly Glu Thr Leu Gln Asp  
 1 5 10 15  
 Glu Glu Ala Cys Leu His Ser Tyr Val Leu Ser Arg Pro Cys Phe Ser  
 20 25 30  
 Ser His Val Trp Asp Asn Gln Gly Cys Ser Pro Pro Ser Glu Phe Gln

```

      35              40              45
Gly His Ser Thr Cys Pro Ser Lys Ser Tyr Gln His Leu Ser Trp Leu
      50              55              60
Leu Asn Lys Thr Gln Trp His Pro Cys Gly Cys Leu Pro Ser Ser Phe
65              70              75              80
Ile Ser Ala Pro Gly Gly Asp Ser Gln Lys Val Ser Ala Ala Pro
      85              90              95

```

&lt;210&gt; 1209

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1209

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ttggttccta taatggcggg agcttacatt tttgctggta tcattatattt gtaaatgcat
60
gccagtgaag ttattccggc aatatcaact attgtcgagt atgcctttac gccagcttct
120
gcgcagggtg gttttgctgg tgcaacggta tggatggcga ttcgttttgg tgttgcccgt
180
ggtgtatttt caaatgaggg aggtttaggt tcggcgccga tcgctcatgc cagtgcacaa
240
actaatgaac cggttcgcca agggttgggtg gcgatgttag gtactttcct tgatacactt
300
attatttgta caggtttagt gattgttatt tctggtgctt ggacagaagg attgtcgggt
360
gctgcgtaaa catctgctgc atttaatctg gcgttacctg gttggggggg atacttagtc
420
gctatcagct g
431

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&lt;210&gt; 1210

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1210

```

Leu Val Pro Ile Met Ala Val Ala Tyr Ile Phe Ala Gly Ile Ile Ile
 1              5              10              15
Leu Leu Met His Ala Ser Glu Val Ile Pro Ala Ile Ser Thr Ile Val
      20              25              30
Glu Tyr Ala Phe Thr Pro Ala Ser Ala Gln Gly Gly Phe Ala Gly Ala
      35              40              45
Thr Val Trp Met Ala Ile Arg Phe Gly Val Ala Arg Gly Val Phe Ser
      50              55              60
Asn Glu Ala Gly Leu Gly Ser Ala Pro Ile Ala His Ala Ser Ala Gln
65              70              75              80
Thr Asn Glu Pro Val Arg Gln Gly Leu Val Ala Met Leu Gly Thr Phe
      85              90              95
Leu Asp Thr Leu Ile Ile Cys Thr Gly Leu Val Ile Val Ile Ser Gly
      100              105              110
Ala Trp Thr Glu Gly Leu Ser Gly Ala Ala Leu Thr Ser Ala Ala Phe
      115              120              125
Asn Leu Ala Leu Pro Gly Trp Gly Gly Tyr Leu Val Ala Ile Ser

```

130 135 140

<210> 1211  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<400> 1211  
 gaggagggac gagaggctgg tgagatggag tccagcaccc tgcaggagag cccaggggcc  
 60  
 agagccgaag ctgtgcttct ccatgagatg gatgaagatg atctggccaa tgccctgac  
 120  
 tggcctgaga ttcaacagga gctgaaaatc attgaatctg aggaggagct ctcatcgctg  
 180  
 ccacctctcg ctctgaagac cagcccaatt cagcctattc tgcagtcgag tctggggccc  
 240  
 tttattccct cagagcctcc tgggagcttg ccttgtggct ccttcctgc tccagtctcc  
 300  
 acccctctgg aggtgtggac tagggatcca gccaatcaga gcacacaggg ggcttcaca  
 360  
 gcagccagca gagagaagcc ggaacctgag cagggcctgc acccagacct cgccagcctg  
 420  
 gctcctctgg aaatagttcc ttttgagaag gcatctccag aggctggagt gtgctcgaga  
 480

<210> 1212  
 <211> 160  
 <212> PRT  
 <213> Homo sapiens

<400> 1212  
 Glu Glu Gly Arg Glu Ala Gly Glu Met Glu Ser Ser Thr Leu Gln Glu  
 1 5 10 15  
 Ser Pro Arg Ala Arg Ala Glu Ala Val Leu Leu His Glu Met Asp Glu  
 20 25 30  
 Asp Asp Leu Ala Asn Ala Leu Ile Trp Pro Glu Ile Gln Gln Glu Leu  
 35 40 45  
 Lys Ile Ile Glu Ser Glu Glu Leu Ser Ser Leu Pro Pro Pro Ala  
 50 55 60  
 Leu Lys Thr Ser Pro Ile Gln Pro Ile Leu Glu Ser Ser Leu Gly Pro  
 65 70 75 80  
 Phe Ile Pro Ser Glu Pro Pro Gly Ser Leu Pro Cys Gly Ser Phe Pro  
 85 90 95  
 Ala Pro Val Ser Thr Pro Leu Glu Val Trp Thr Arg Asp Pro Ala Asn  
 100 105 110  
 Gln Ser Thr Gln Gly Ala Ser Thr Ala Ala Ser Arg Glu Lys Pro Glu  
 115 120 125  
 Pro Glu Gln Gly Leu His Pro Asp Leu Ala Ser Leu Ala Pro Leu Glu  
 130 135 140  
 Ile Val Pro Phe Glu Lys Ala Ser Pro Glu Ala Gly Val Cys Ser Arg  
 145 150 155 160

<210> 1213  
 <211> 1141

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1213

```

nntcatgatg gcggcctggt gtgtgggtat gtccacgatg ggcgcgtcac gcgtgtcgcc
60
cgtgatgctc aggggcgggt taccgggata gaggggccat cagggcggtg gagttacggc
120
tacaacgagg ctgggtcact catcagcgcg acggggcccc gcacacaaca taactggact
180
cacgacgcct atggccggct caccagccac gccacatccg gaaccgacac caccttcgcc
240
tgggaccagg aagggcacct ggcgagacg tgtacgcgtg cacacgggca tgccactgcc
300
accagtatc gctatgacgc agcgggacgg cgcgtcagtg cgaccagctc agacggccag
360
gaggagcggt actcctggga tggacgggggt tggctgtctg acatcaccac cgacgccacg
420
accgtatcga ctcacgtcga tgcattgggg cgcgccagtc gtatcaccac taagggccag
480
caggtaacgag tggactggga cctcgtgacc ggagcccca cctcgattga tggtcgtcct
540
gtgcttcccc tgcccgagg acgcatcctc ggcgccacac ccacgaggca taccaacctc
600
tggcgtgagg tcatgccac cgaccctgac aacccttacc agcccgccac ggccactatt
660
gagggtgtcc ccgagacgat caggatggcc gggaacacgc tagtggttga tggtcaccct
720
tgggtgggggc gcgcctctac gacccaacta ccaccacctt cttgtctcct gaccggttaa
780
ccccgcccgc cggcgcgcta tgggccaaca acccctacga ctacgccaac aacaaccccc
840
tcaccttcac cgatcctctc gggaccacc cgcgcaccga cgaccaactg gcactcctca
900
cccaccccat cggcacactc gcacactacg tcgccaactc cgtcagcaca ctcgtgcac
960
acatcacgga tccgatcagc cactggtggg ccaccacaa agaccggatc ctctcccg
1020
acttctgat cgggtgccggc ctcgtcatcg gcggtatcgc gtagcggcca cgggcgtagg
1080
aggaccctc ctagccgagg ccatttccgg gggactcatc tcaggcgggt tttccgtag
1140
c
1141

```

&lt;210&gt; 1214

&lt;211&gt; 259

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1214

```

Xaa His Asp Gly Gly Leu Val Cys Gly Tyr Val His Asp Gly Arg Val
1           5           10          15
Thr Arg Val Ala Arg Asp Ala Gln Gly Arg Val Thr Gly Ile Glu Gly

```

	20		25		30										
Pro	Ser	Gly	Arg	Trp	Ser	Tyr	Gly	Tyr	Asn	Glu	Ala	Gly	Ser	Leu	Ile
	35		40		45										
Ser	Ala	Thr	Gly	Pro	Arg	Thr	Gln	His	Asn	Trp	Thr	His	Asp	Ala	Tyr
	50		55		60										
Gly	Arg	Leu	Thr	Ser	His	Ala	Thr	Ser	Gly	Thr	Asp	Thr	Thr	Phe	Ala
65			70		75		80								
Trp	Asp	Gln	Glu	Gly	His	Leu	Ala	Gln	Thr	Cys	Thr	Arg	Ala	His	Gly
		85			90		95								
His	Ala	Thr	Ala	Thr	Gln	Tyr	Arg	Tyr	Asp	Ala	Ala	Gly	Arg	Arg	Val
	100		105		110										
Ser	Ala	Thr	Ser	Ser	Asp	Gly	Gln	Glu	Glu	Arg	Tyr	Ser	Trp	Asp	Gly
	115		120		125										
Arg	Gly	Trp	Leu	Ser	Asp	Ile	Thr	Thr	Asp	Ala	Thr	Thr	Val	Ser	Thr
	130		135		140										
His	Val	Asp	Ala	Leu	Gly	Arg	Ala	Ser	Arg	Ile	Thr	Thr	Lys	Gly	Gln
145			150		155		160								
Gln	Val	Arg	Val	Asp	Trp	Asp	Leu	Val	Thr	Gly	Ala	Pro	Thr	Ser	Ile
		165			170		175								
Asp	Gly	Arg	Pro	Val	Leu	Pro	Leu	Pro	Gly	Gly	Arg	Ile	Leu	Gly	Ala
	180		185		190										
Thr	Pro	Ile	Gly	Asp	Thr	Asn	Leu	Trp	Arg	Glu	Val	Met	Pro	Thr	Asp
	195		200		205										
Pro	Asp	Asn	Pro	Tyr	Gln	Pro	Ala	Thr	Ala	Thr	Ile	Glu	Gly	Val	Pro
	210		215		220										
Glu	Thr	Ile	Arg	Met	Ala	Gly	Asn	Thr	Leu	Val	Val	Asp	Gly	His	Pro
225			230		235		240								
Trp	Trp	Gly	Arg	Ala	Ser	Thr	Thr	Gln	Leu	Pro	Pro	Pro	Ser	Cys	Leu
		245			250		255								

Leu Thr Arg

&lt;210&gt; 1215

&lt;211&gt; 317

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1215

acgcgttcgc tgcagatcga gtcgccggtg agctcgatct acctgtggat gtactacgtg

60

ggcgtgccga catccggcat cgggggggat cccaacctgc ttacctttta ttggaaccgc

120

ccccggggtc aaccgggcca tcaccgggag aacgccgctc ctcggagggg gtgttctcgc

180

agtcgccggc gtgggtgcgt ggaagaagta ccgcggcacg accttcggcg ggctgctccc

240

gtcgtgtccc ctcggcctcg tgctcgcgtt catcgtgctg aacaaggctg gtcgccgca

300

gtacatcgcc tggatcn

317

&lt;210&gt; 1216

&lt;211&gt; 102

&lt;212&gt; PRT



<213> Homo sapiens

<400> 1216

```

Met Tyr Cys Gly Glu Pro Thr Leu Phe Ser Thr Met Asn Ala Ser Thr
 1           5           10           15
Arg Pro Arg Asp Ser Asp Gly Ser Ser Pro Pro Lys Val Val Pro Arg
      20           25           30
Tyr Phe Phe His Ala Pro Thr Pro Ala Thr Ala Arg Thr Pro Pro Pro
      35           40           45
Arg Ser Gly Val Leu Pro Val Met Ala Gly Leu Thr Pro Gly Ala Val
      50           55           60
Pro Ile Lys Gly Lys Gln Val Gly Ile Pro Pro Asp Ala Gly Cys Arg
      65           70           75           80
His Ala His Val Val His Pro Gln Val Asp Arg Ala His Arg Arg Leu
      85           90           95
Asp Leu Gln Arg Thr Arg
      100

```

<210> 1217

<211> 548

<212> DNA

<213> Homo sapiens

<400> 1217

```

naccgctggg ttgacgcgct attaaacgat aagagcaaaa aaacatttcc tcattttatta
60
cgttgtcggg tgaatgatgt ttctggtgat agtcagtgga tagagatgcg aggcagtgtg
120
acagggtggg acagccgtca tcgagctcag atggtgagag ggacattcga gcgtattaac
180
catcttattg acgctgaaaa tgaattaatt gcggcccggtg aagatgctca gcgacgagag
240
cttattttat cggctttgct aaataatatt ccagaccctg tttggtctaa agatgaaagc
300
ggtcgttatt tggactgtaa ccatgcgttt tgtctgttta atgggtttaga gcagagtgat
360
gttcaggggc aaaaagacag tgaattaaac ttagataata atgggtcaata ttatcaagat
420
atgggcgggtg aggtattagc gcgaggggag atttttcatg aacattgttg gggtacgcct
480
gcagatggaa gtgacaaccg cttgtttgaa gtatatcgag tccctatcaa agagcctacc
540
gtgaattc
548

```

<210> 1218

<211> 182

<212> PRT

<213> Homo sapiens

<400> 1218

```

Xaa Ala Trp Val Asp Ala Leu Leu Asn Asp Lys Ser Lys Lys Thr Phe
 1           5           10           15
Pro His Leu Leu Arg Cys Arg Val Asn Asp Val Ser Gly Asp Ser Gln

```

```

      20      25      30
Trp Ile Glu Met Arg Gly Ser Val Thr Gly Trp Asp Ser Arg His Arg
      35      40      45
Ala Gln Met Val Arg Gly Thr Phe Glu Arg Ile Asn His Leu Ile Asp
      50      55      60
Ala Glu Asn Glu Leu Ile Ala Ala Arg Glu Asp Ala Gln Arg Arg Glu
65      70      75      80
Leu Ile Leu Ser Ala Leu Leu Asn Asn Ile Pro Asp Pro Val Trp Ser
      85      90      95
Lys Asp Glu Ser Gly Arg Tyr Leu Asp Cys Asn His Ala Phe Cys Leu
      100      105      110
Phe Asn Gly Leu Glu Gln Ser Asp Val Gln Gly Gln Lys Asp Ser Glu
      115      120      125
Leu Asn Leu Asp Asn Asn Gly Gln Tyr Tyr Gln Asp Met Gly Gly Glu
      130      135      140
Val Leu Ala Arg Gly Glu Ile Phe His Glu His Cys Trp Gly Thr Pro
145      150      155      160
Ala Asp Gly Ser Asp Asn Arg Leu Phe Glu Val Tyr Arg Val Pro Ile
      165      170      175
Lys Glu Pro Thr Val Asn
      180

```

&lt;210&gt; 1219

&lt;211&gt; 308

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1219

```

acgcgtgaag ggaggaatac agatggagaa atgggtccac caaaaaatga tgagggtacc
60
tccagagaaa attaccaaga ccattctgtt agtattttcc agtccacag gcctttggaa
120
gttccagac caccctccct cttttcaaac taaaacaggg atggctctta accaccaccc
180
aaaggcaagg ggggtcttaa aacccaaacc aagtggggca ggggccagcc tcttcaggag
240
ggcccaaccc tgcagcctct gccatttgg gaaagaccgt gagttggaat tatgggtcgg
300
tggggggc
308

```

&lt;210&gt; 1220

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1220

```

Met Glu Lys Trp Val His Gln Lys Met Met Arg Val Pro Pro Glu Lys
1      5      10      15
Ile Thr Lys Thr Ile Leu Leu Val Phe Ser Ser Ser Thr Gly Leu Trp
      20      25      30
Lys Phe Pro Asp His Pro Pro Ser Phe Gln Thr Lys Thr Gly Met Ala
      35      40      45
Leu Asn His His Pro Lys Ala Arg Gly Val Leu Lys Pro Lys Pro Ser

```

50                      55                      60  
 Gly Ala Gly Ala Ser Leu Phe Arg Arg Ala Gln Pro Cys Ser Leu Cys  
 65                      70                      75                      80  
 Pro Phe Gly Lys Asp Arg Glu Leu Glu Leu Trp Val Gly Gly Gly  
                     85                      90                      95

<210> 1221  
 <211> 569  
 <212> DNA  
 <213> Homo sapiens

<400> 1221  
 gcgcgccagg ggcaggtagc ctgtggcagg tgaggctgcg tgtgggggtgt gctcccagag  
 60  
 gcccgctccag gaaagctgca cctcagagaa gcagtttctt tccttacctg ggaagtttct  
 120  
 tctgtaacac gttaagcccc acaggtaagg cctgatcccc cctggacggc tccccctctc  
 180  
 agtgttccca gtctggaggt antcttttct aagccatcct ctcagaatgt gatgggtacc  
 240  
 aggatgcaca cccggtggcc ctgtggtgtg aggcctcagc aaacacggtc agaagatgaa  
 300  
 cacacagaga cccgcccgtc ggaaggagag gagggagcgg atacggaggc ccacgtgcca  
 360  
 gaaggggtccc ttgcagtggg gtggttatgt gcctgcaatc ccagagtgtc ctcgaaggac  
 420  
 ctcagatcta acgagctcag ccggcagctg cacgtgggac cagccctctg agcttcactt  
 480  
 gttttcctct gtgccatcag aaaccaatac gaagataaaa tgggaaaaaa aaaaatccca  
 540  
 ttcacggcac agcctgccga gaaacgcgt  
 569

<210> 1222  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 1222  
 Met Asn Thr Gln Arg Pro Ala Arg Arg Lys Glu Arg Arg Glu Arg Ile  
 1                      5                      10                      15  
 Arg Arg Pro Thr Cys Gln Lys Gly Pro Leu Gln Trp Cys Gly Tyr Val  
                     20                      25                      30  
 Pro Ala Ile Pro Glu Cys Pro Arg Arg Thr Ser Asp Leu Thr Ser Ser  
                     35                      40                      45  
 Ala Gly Ser Cys Thr Trp Asp Gln Pro Ser Glu Leu His Leu Phe Ser  
                     50                      55                      60  
 Ser Val Pro Ser Glu Thr Asn Thr Lys Ile Lys Trp Glu Lys Lys Lys  
 65                      70                      75                      80  
 Ser His Ser Arg His Ser Leu Pro Arg Asn Ala  
                     85                      90

<210> 1223  
 <211> 450

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1223

```

aagcttgctc aggctagtgc cgacgctgct gctctcaaac tcgtcgatgc ccaccggttg
60
ttgtgcgctc accgagaggg gccatacggg gtagacgagt ggtctcagcg catggttact
120
gtactttcag atgtgttgcc tgggtgtggc caaggccggt gggttctcgg cgaaactgca
180
atagtaacgc ataacctcgc acaattggga gtcaataacg gtgattgcgg ggtcatcggt
240
gaaacaaggc ccgtccccac gatagctcta cggggacccg gtggagtccc cagacggttg
300
ccctgttccc tcatcccatc gctgcaaccc ttacaggcga tgacgattca caaagcgcag
360
ggcagccaat tcacggacgt aacggtggtc ctgccaccac ccgactcgcc cctcctctct
420
cgtgagttgc tctataaccg catcacgcgt
450

```

&lt;210&gt; 1224

&lt;211&gt; 150

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1224

```

Lys Leu Ala Gln Ala Ser Ala Asp Ala Ala Ala Leu Lys Leu Val Asp
1      5      10      15
Ala His Arg Leu Leu Cys Ala His Arg Glu Gly Pro Tyr Gly Val Asp
20     25     30
Glu Trp Ser Gln Arg Met Val Thr Val Leu Ser Asp Val Leu Pro Gly
35     40     45
Val Gly Gln Gly Arg Trp Val Leu Gly Glu Thr Ala Ile Val Thr His
50     55     60
Asn Leu Ala Gln Leu Gly Val Asn Asn Gly Asp Cys Gly Val Ile Val
65     70     75     80
Glu Thr Arg Pro Val Pro Thr Ile Ala Leu Pro Gly Pro Gly Gly Val
85     90     95
Pro Arg Arg Leu Pro Cys Ser Leu Ile Pro Ser Leu Gln Pro Leu Gln
100    105    110
Ala Met Thr Ile His Lys Ala Gln Gly Ser Gln Phe Thr Asp Val Thr
115    120    125
Val Val Leu Pro Pro Pro Asp Ser Pro Leu Leu Ser Arg Glu Leu Leu
130    135    140
Tyr Thr Ala Ile Thr Arg
145    150

```

&lt;210&gt; 1225

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1225

ncccatcccc caccgggat ggtgaacact gggatggcca cttgggagct caaagtgttg  
 60  
 tcagtgggag gacaagggtcc tcaattcctg gcacattggc ccagagaagt catgaaaacc  
 120  
 caaagccccc cgaaagtaag aagtagaaaa aaacccgacc ccgaccagat gaagggaccc  
 180  
 gggaagtttt tggaaaagag actgctgaag tgtctccttg caggcatcac cgtgagctgg  
 240  
 ggctttgcac acagcatctt catggctttc cacaatgata ccagaactga tccagagaaa  
 300  
 cccagggatc aggggttgac ccgaccctgt catcatccca ttctacaaat gaggacactg  
 360  
 aggcctgggtg aaaagggagg ggtggatgga accaggtggc ctggctctaa gaccagagg  
 420  
 ctggagtgtg ctcatg  
 436

&lt;210&gt; 1226

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1226

Met	Val	Asn	Thr	Gly	Met	Ala	Thr	Trp	Glu	Leu	Lys	Val	Leu	Ser	Val
1				5				10					15		
Gly	Gly	Gln	Gly	Pro	Gln	Phe	Leu	Ala	His	Trp	Pro	Arg	Glu	Val	Met
		20					25					30			
Lys	Thr	Gln	Ser	Pro	Pro	Lys	Val	Arg	Ser	Arg	Lys	Lys	Pro	Asp	Pro
		35				40						45			
Asp	Gln	Met	Lys	Gly	Pro	Gly	Lys	Phe	Leu	Glu	Lys	Arg	Leu	Leu	Lys
		50				55					60				
Cys	Leu	Leu	Ala	Gly	Ile	Thr	Val	Ser	Trp	Gly	Phe	Ala	His	Ser	Ile
65					70					75				80	
Phe	Met	Ala	Phe	His	Asn	Asp	Pro	Arg	Thr	Asp	Pro	Glu	Lys	Pro	Arg
				85					90					95	
Asp	Gln	Gly	Leu	Thr	Arg	Pro	Cys	His	His	Pro	Ile	Leu	Gln	Met	Arg
			100					105					110		
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Gly	Gly	Val	Asp	Gly	Thr	Arg	Trp	Pro
		115					120					125			
Gly	Ser	Lys	Thr	Gln	Arg	Leu	Glu	Cys	Ala	His					
		130				135									

&lt;210&gt; 1227

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1227

gttgagttcc acgtgaaaca aaatgcactt tacaatagaa tgacgattcg tatcaaagat  
 60  
 aatggtattg gaataccgat taacaaggta gataaaatct ttgatagatt ctaccgtgtc  
 120  
 gacaaagcac gtacacgtaa gatgggagggt acaggactag gtctagctat ttccaaagag  
 180

attgtcgaag cacataatgg ccgtatttgg gcaaatagtg tcgaaggaca aggtacatct  
 240  
 atcttcatta ccctaccatg tgaaattatt gaagatgggtg attgggatga atagtaaaga  
 300  
 atacatcaaa acgattatcc tgatactact tgtattaatg agtatcgtct taacctacat  
 360  
 ggtatggaac ttctcacctg atctatcaaa tgctgatagt acgtcatcag ataataagaa  
 420  
 agataattct aaacctattg gaaaaccaat gagtgcgaaa acggataaaa ccatcacacc  
 480  
 atttcaaadc gttcaatcta atggcgaaaa aacaaaagggt atgccagcaa cagggtcatgc  
 540  
 agtatctcaa attttaagcc cattaagaaga taaaaatggt gattcagtac aacatttaaa  
 600  
 acgaaatcat aacttaatta ttctgaatt aagtataaac tttatcgttc ttgatttcac  
 660  
 atatgattta ccgttatcaa ttacttaag ccaagtatta aacatagatg ctaagacacc  
 720  
 taatcatttt aactttaatc gactactgat tgatca  
 756

<210> 1228

<211> 97

<212> PRT

<213> Homo sapiens

<400> 1228

Val	Glu	Phe	His	Val	Lys	Gln	Asn	Ala	Leu	Tyr	Asn	Arg	Met	Thr	Ile
1				5					10					15	
Arg	Ile	Lys	Asp	Asn	Gly	Ile	Gly	Ile	Pro	Ile	Asn	Lys	Val	Asp	Lys
		20					25					30			
Ile	Phe	Asp	Arg	Phe	Tyr	Arg	Val	Asp	Lys	Ala	Arg	Thr	Arg	Lys	Met
		35					40					45			
Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ala	Ile	Ser	Lys	Glu	Ile	Val	Glu	Ala
		50					55				60				
His	Asn	Gly	Arg	Ile	Trp	Ala	Asn	Ser	Val	Glu	Gly	Gln	Gly	Thr	Ser
65					70					75				80	
Ile	Phe	Ile	Thr	Leu	Pro	Cys	Glu	Ile	Ile	Glu	Asp	Gly	Asp	Trp	Asp
				85					90					95	

Glu

<210> 1229

<211> 377

<212> DNA

<213> Homo sapiens

<400> 1229

nacgcgtcgt gaacgcggcg tcaacagctt ttcggatata cctctgagga gcccaagatg  
 60  
 cttgtcgccc ccatggcaaa ccaggggggtc gagggcactg gagcgatggg aaccgacacc  
 120  
 ccgctggccg tgctatctaa ctgtccgcgg atgctctggg actatttcag tcagcttttc  
 180

gctcaggtaa ccaatccgcc cttggacgct atccgcgagg agcttgtcac ctccctgacg  
 240  
 ggcaccatcg gcccgaggc gaacttgctt gagcctggcc cggaatcatg tcggcaagtg  
 300  
 gtcgtcaact acccgatcat cgattccgac cagcttgcca agatcattca catcgacgct  
 360  
 gacggggagc atccgga  
 377

<210> 1230

<211> 121

<212> PRT

<213> Homo sapiens

<400> 1230

Thr	Arg	Arg	Gln	Gln	Leu	Phe	Gly	Tyr	Thr	Ser	Glu	Glu	Pro	Lys	Met
1			5					10					15		
Leu	Val	Ala	Pro	Met	Ala	Asn	Gln	Gly	Val	Glu	Ala	Thr	Gly	Ala	Met
			20					25					30		
Gly	Thr	Asp	Thr	Pro	Leu	Ala	Val	Leu	Ser	Asn	Cys	Pro	Arg	Met	Leu
		35					40					45			
Trp	Asp	Tyr	Phe	Ser	Gln	Leu	Phe	Ala	Gln	Val	Thr	Asn	Pro	Pro	Leu
		50				55					60				
Asp	Ala	Ile	Arg	Glu	Glu	Leu	Val	Thr	Ser	Leu	Thr	Gly	Thr	Ile	Gly
65				70					75					80	
Pro	Glu	Ala	Asn	Leu	Leu	Glu	Pro	Gly	Pro	Glu	Ser	Cys	Arg	Gln	Val
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<210> 1231

<211> 351

<212> DNA

<213> Homo sapiens

<400> 1231

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<211> 91

<212> PRT

<213> Homo sapiens

<400> 1232

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Leu Ser Asn Ser Ser Asp Glu Ser Leu Arg Arg Val Glu Lys Leu Ala
      35           40           45
Gly Arg Ser Ala Gln Phe Tyr Gln Gly Asp Ile Leu Asp Ala Glu Cys
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<212> DNA

<213> Homo sapiens

<400> 1233

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<210> 1234

<211> 708

<212> PRT

<213> Homo sapiens

<400> 1234

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			20					25					30		
Ser	Gly	Thr	Ile	Ile	Thr	Glu	Asp	Pro	Phe	Lys	Ser	Gly	Ser	Ser	Asp
			35					40					45		
Val	Gly	Arg	Asp	Trp	Asp	Pro	Ser	Ser	Thr	Glu	Gly	Gly	Ser	Ser	Pro
			50					55				60			
Leu	Ile	Cys	Pro	Asp	Ser	Ser	Ala	Arg	Pro	Arg	Val	Lys	Ser	Ser	Tyr
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Ser	Met	Glu	Asn	Ala	Asn	Lys	Trp	Ser	Cys	His	Met	Cys	Thr	Tyr	Leu
					85				90					95	
Asn	Trp	Pro	Arg	Ala	Ile	Arg	Cys	Thr	Gln	Cys	Leu	Ser	Gln	Arg	Arg
			100					105					110		
Thr	Arg	Ser	Pro	Thr	Glu	Ser	Pro	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Arg
			115					120					125		
Pro	Val	Ala	Phe	Ser	Val	Asp	Pro	Cys	Glu	Glu	Tyr	Asn	Asp	Arg	Asn
			130					135					140		
Lys	Leu	Asn	Thr	Arg	Thr	Gln	His	Trp	Thr	Cys	Ser	Val	Cys	Thr	Tyr

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Ser Ile Ile Asn Glu Gln Asp Arg Ala Arg Trp Arg Gly Ser Cys Ser
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Ser Gly Asn Ser Gln Arg Arg Ser Pro Pro Ala Thr Lys Arg Asp Ser
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Glu Val Lys Met Asp Phe Gln Arg Ile Glu Leu Ala Gly Ala Val Gly
225          230          235          240
Ser Lys Glu Glu Leu Glu Val Asp Phe Lys Lys Leu Lys Gln Ile Lys
          245          250          255
Asn Arg Met Lys Lys Thr Asp Trp Leu Phe Leu Asn Ala Cys Val Gly
          260          265          270
Val Val Glu Gly Asp Leu Ala Ala Ile Glu Ala Tyr Lys Ser Ser Gly
          275          280          285
Gly Asp Ile Ala Arg Gln Leu Thr Ala Asp Glu Val Arg Leu Leu Asn
          290          295          300
Arg Pro Ser Ala Phe Asp Val Gly Tyr Thr Leu Val His Leu Ala Ile
305          310          315          320
Arg Phe Gln Arg Gln Asp Met Leu Ala Ile Leu Leu Thr Glu Val Ser
          325          330          335
Gln Gln Ala Ala Lys Cys Ile Pro Ala Met Val Cys Pro Glu Leu Thr
          340          345          350
Glu Gln Ile Arg Arg Glu Ile Ala Ala Ser Leu His Gln Arg Lys Gly
          355          360          365
Asp Phe Ala Cys Tyr Phe Leu Thr Asp Leu Val Thr Phe Thr Leu Pro
          370          375          380
Ala Asp Ile Glu Asp Leu Pro Pro Thr Val Gln Glu Lys Leu Phe Asp
385          390          395          400
Glu Val Leu Asp Arg Asp Val Gln Lys Glu Leu Glu Glu Glu Ser Pro
          405          410          415
Ile Ile Asn Trp Ser Leu Glu Leu Ala Thr Arg Leu Asp Ser Arg Leu
          420          425          430
Tyr Ala Leu Trp Asn Arg Thr Ala Gly Asp Cys Leu Leu Asp Ser Val
          435          440          445
Leu Gln Ala Thr Trp Gly Ile Tyr Asp Lys Asp Ser Val Leu Arg Lys
          450          455          460
Ala Leu His Asp Ser Leu His Asp Cys Ser His Trp Phe Tyr Thr Arg
465          470          475          480
Trp Lys Asp Trp Glu Ser Trp Tyr Ser Gln Ser Phe Gly Leu His Phe
          485          490          495
Ser Leu Arg Glu Glu Gln Trp Gln Glu Asp Trp Ala Phe Ile Leu Ser
          500          505          510
Leu Ala Ser Gln Pro Gly Ala Ser Leu Glu Gln Thr His Ile Phe Val
          515          520          525
Leu Ala His Ile Leu Arg Arg Pro Ile Ile Val Tyr Gly Val Lys Tyr
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Tyr Lys Ser Phe Arg Gly Glu Thr Leu Gly Tyr Thr Arg Phe Gln Gly
545          550          555          560
Val Tyr Leu Pro Leu Leu Trp Glu Gln Ser Phe Cys Trp Lys Ser Pro
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Ile Ala Leu Gly Tyr Thr Arg Gly His Phe Ser Ala Leu Val Ala Met

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 Lys Leu Leu His Val His Phe Leu Ser Ala Gln Glu Leu Gly Asn Glu  
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 Glu Gly Gly Val Leu Val Ala Met Gln Lys Ser Ser Arg Arg Arg Asn  
 660 665 670  
 His Pro Leu Val Thr Gln Met Val Glu Lys Trp Leu Asp Arg Tyr Arg  
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<210> 1235

<211> 383

<212> DNA

<213> Homo sapiens

<400> 1235

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<210> 1236

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1236

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 35 40 45  
 Phe Leu Gly Gly Gly Glu Met Ile Glu Val Val Arg Met Glu Gly Ser  
 50 55 60  
 Thr Tyr Ala Glu Pro Pro His Arg Phe Glu Ala Gly Thr Pro Pro Ile

65		70		75		80									
Ala	Gln	Leu	Ala	Ala	Leu	Gly	Val	Ala	Ala	Asp	Tyr	Leu	Asp	Gly	Ile
			85					90						95	
Gly	Met	Gln	Ala	Ile	Ala	Glu	His	Glu	His	Glu	Leu	Ala	Ala	Arg	Met
			100					105						110	
Leu	Glu	Asp	Tyr	Gln	Thr	Val	Lys	Gly	Val	Gln	Pro	Glu	Arg	Gly	
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&lt;210&gt; 1237

&lt;211&gt; 1608

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1237

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<210> 1238

<211> 458

<212> PRT

<213> Homo sapiens

<400> 1238

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		20						25					30		
Phe	Pro	Glu	Leu	Gln	Leu	Pro	Val	Ser	Pro	Ser	Val	Cys	Leu	Asp	Gln
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Lys	Pro	Arg	Val	Trp	Lys	Pro	Gly	Asp	Trp	Ser	Arg	Glu	Gln	Leu	Asn
	65				70					75				80	
Glu	Thr	Thr	Val	Leu	Ala	Pro	His	Glu	Thr	Ile	Phe	Arg	Ala	Lys	Asp
			85					90						95	
Leu	Ser	Val	Ile	Leu	Lys	Ala	Tyr	Val	Leu	Val	Thr	Ser	Leu	Thr	Pro
		100						105					110		
Leu	Arg	Ala	Phe	Ile	His	Ser	Thr	Gly	Thr	Val	Trp	Asn	Pro	Pro	Lys
		115					120					125			
Lys	Lys	Arg	Phe	Thr	Val	Lys	Leu	Gln	Thr	Phe	Phe	Glu	Thr	Phe	Leu
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	195						200					205			
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Gln	Asn	Thr	Glu	Glu	Phe	Leu	Leu	Asn	Asp	Thr	Phe	Asn	Phe	Leu	Phe
	225				230					235					240
Pro	Asn	Glu	Ser	Ser	Leu	Ser	Ile	Phe	Ser	Glu	Ile	Phe	Gln	Arg	Leu
			245					250						255	
Tyr	Arg	Ser	Asp	Val	Phe	Lys	Gly	Glu	Asn	Tyr	Gln	Lys	Glu	Leu	Asn

	260		265		270										
Gln	Cys	Leu	Ser	Leu	Glu	Glu	Ile	Asn	Ser	Ile	Met	Thr	Phe	Ile	Lys
	275				280						285				
Glu	Leu	Gly	Ser	Leu	Gly	Gln	Phe	Gln	Leu	Leu	Phe	Pro	Ser	Thr	Thr
	290				295						300				
Pro	Gly	Ile	Gln	Ser	Leu	Met	His	Glu	Phe	Tyr	Asp	Val	Ala	Asn	Pro
305					310					315				320	
Val	Gly	Asn	Pro	Gly	Ser	Val	Leu	Thr	Gln	Tyr	Trp	Ser	Leu	Leu	Asn
				325					330					335	
Val	Phe	Glu	Gln	Phe	Gln	Phe	Met	Asn	Lys	Lys	Thr	Gln	Pro	His	Pro
	340							345				350			
Leu	Glu	Trp	Asn	Ser	Phe	Thr	Glu	Asp	Lys	Asn	Ile	Glu	Lys	Pro	Gln
	355						360					365			
Val	Pro	Phe	Asp	Ala	Ile	Glu	Asn	Lys	Lys	Ala	Ala	Val	Pro	Gln	Ile
	370					375						380			
Lys	Asn	Glu	Asn	Lys	Glu	Ile	His	Cys	Ser	Asp	Asp	Glu	Asn	Thr	Pro
385					390					395				400	
Cys	His	Ile	Lys	Gln	Ile	Phe	Thr	His	Pro	His	Leu	Glu	Leu	Asn	Pro
				405					410					415	
Asp	Phe	His	Pro	Lys	Ile	Lys	Asp	Tyr	Tyr	Cys	Glu	Val	Pro	Phe	Asp
	420						425					430			
Val	Val	Thr	Val	Thr	Ile	Gly	Val	Glu	Thr	Pro	Lys	Cys	Leu	Cys	Lys
	435						440					445			
Val	His	Leu	Tyr	Glu	Gln	Ala	Gly	Pro	Ser						
	450					455									

&lt;210&gt; 1239

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1239

atacctactg aacgtgaacg aacagaaagg ctaattaaaa ccaaattaag ggagatcatg  
60

atgcagaagg atttgagagaa tattacatcc aaagagataa gaacagagtt ggaaatgcaa  
120

atggtgtgca acttgcgagg attcaaggaa tttatagaca atgaaatgat agtgatcctt  
180

ggcctcaact tagaggactt acagaaccga ggggtacggt atatcttgaa tgtcactcga  
240

gagatagata actttttccc aggagtcttt gagtatcata acattcgggt atatgatgaa  
300

gaggcaacgg atctcctggc gtactggaat gacacttaca aattcatctc taaagcaaag  
360

aaacatggat ctaaatgcct tgtgcac  
420

aaacatggat ctaaatgcct tgtgcac  
447

&lt;210&gt; 1240

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens



&lt;400&gt; 1240

```

Ile Pro Thr Glu Arg Glu Arg Thr Glu Arg Leu Ile Lys Thr Lys Leu
 1           5           10           15
Arg Glu Ile Met Met Gln Lys Asp Leu Glu Asn Ile Thr Ser Lys Glu
          20           25           30
Ile Arg Thr Glu Leu Glu Met Gln Met Val Cys Asn Leu Arg Glu Phe
          35           40           45
Lys Glu Phe Ile Asp Asn Glu Met Ile Val Ile Leu Gly Gln Met Asp
          50           55           60
Ser Pro Thr Gln Ile Phe Glu His Val Phe Leu Gly Ser Glu Trp Asn
65           70           75           80
Ala Ser Asn Leu Glu Asp Leu Gln Asn Arg Gly Val Arg Tyr Ile Leu
          85           90           95
Asn Val Thr Arg Glu Ile Asp Asn Phe Phe Pro Gly Val Phe Glu Tyr
          100          105          110
His Asn Ile Arg Val Tyr Asp Glu Glu Ala Thr Asp Leu Leu Ala Tyr
          115          120          125
Trp Asn Asp Thr Tyr Lys Phe Ile Ser Lys Ala Lys Lys His Gly Ser
          130          135          140
Lys Cys Leu Val His
145

```

&lt;210&gt; 1241

&lt;211&gt; 489

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1241

```

acgcgtgtgc agcgtatcca gcaccgtcct cagaataata gctgtgaaaa ggaggaaggg
60
aactaggcag acagaccgac agataggggg aaaccgggat gtttaatgtg tccgaacaag
120
taggaagatc aatgaggcgc gagtgtgtgt gtgtacgtgt gcgcgtgtgt gtgtgagaga
180
gagagaaaaga aagaagaaag gtcccgattg caacgtgtca gatcttgcaa ccttcccccc
240
acccaacaca acaaccctca gacacaaaaa caccattgct gactgatacc ccaggtcttc
300
agggttaaag gaaccgtgtg ttggcagcgc aattgtgcag acgctgtaag gccaaaacga
360
ggatttgtgt tgtgaggtcg gtggtgcgtt cttttctttc tcttctcgcc tgttttcccg
420
gagtgcttgg gttgcgagaa aggcgcacgc caggctgtgc agccgaatcg cttcgcaatt
480
attcatgct
489

```

&lt;210&gt; 1242

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1242

```

Met Asn Asn Cys Glu Ala Ile Arg Leu His Ser Leu Arg Cys Ala Phe

```

```

      1           5           10           15
Leu Ala Thr Gln Ala Leu Arg Glu Asn Arg Arg Glu Glu Lys Glu Lys
      20           25           30
Asn Ala Pro Pro Thr Ser Gln His Lys Ser Ser Phe Trp Pro Tyr Ser
      35           40           45
Val Cys Thr Ile Ala Leu Pro Thr His Gly Ser Phe Asn Pro Glu Asp
      50           55           60
Leu Gly Tyr Gln Ser Ala Met Val Phe Leu Cys Leu Arg Val Val Val
      65           70           75           80
Leu Gly Gly Gly Lys Val Ala Arg Ser Asp Thr Leu Gln Ser Gly Pro
      85           90           95
Phe Phe Phe Leu Ser Leu Ser Leu Thr His Thr Arg Ala His Val His
      100          105          110
Thr His Thr Arg Ala Ser Leu Ile Phe Leu Leu Val Arg Thr His
      115          120          125

```

&lt;210&gt; 1243

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1243

```

ntagactccg tcgatcccct catggagaat ccagtgtgcc aggtcccttc ggcgtactgg
60
gagatgatat acctaccggg aatgttcact gtctacttcg atggccagtt ctgggtcgga
120
gtcctagaga ggcgcgacga ggggttggtg cgtgccgtaa aagtcacgtt tggcgccgaa
180
ccgtctgaca cggaattgta cgggtgggtt agccgtcatg gcaacgcact tatagagcga
240
ttggagtcta ccgtgctgt cctaccacc cgcagtcctc gagccaagcg actgaacccc
300
aagagggcgt tacgagatgc agcgcgagct gcccaagcac accgtgccag cagcnccgca
360
caggccgca ttaaggcca tcaggaagct
390

```

&lt;210&gt; 1244

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1244

```

Xaa Asp Ser Val Asp Pro Leu Met Glu Asn Pro Val Cys Gln Val Pro
1           5           10           15
Ser Ala Tyr Trp Glu Met Ile Tyr Leu Pro Gly Met Phe Thr Val Tyr
      20           25           30
Phe Asp Gly Gln Phe Trp Val Gly Val Leu Glu Arg Arg Asp Glu Gly
      35           40           45
Leu Val Arg Ala Val Lys Val Thr Phe Gly Ala Glu Pro Ser Asp Thr
      50           55           60
Glu Leu Tyr Gly Trp Val Ser Arg His Gly Asn Ala Leu Ile Glu Arg
      65           70           75           80
Leu Glu Ser Thr Ala Ala Val Pro Thr Thr Arg Ser Pro Arg Ala Lys

```

```

      85              90              95
Arg Leu Asn Pro Lys Arg Ala Leu Arg Asp Ala Ala Arg Ala Ala Gln
      100              105              110
Ala His Arg Ala Ser Thr Xaa Ala Gln Ala Ala Ile Lys Ala Asp Gln
      115              120              125
Glu Ala
      130

```

<210> 1245  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1245
gccaaagcagc aaaaaccaca gatcattgct atgggaaatg tgcattttc ttgttcacaa
60
ccacaatcta tgcccgtgac tttctgagc tccaggagtt ttttagcact gccagacttc
120
tctggagagg aggaggtttc tgccactttt caatttcgaa cttggaataa ggcagggctt
180
ctgctgttca gtgaacttca gctgatttca gggggatatcc tcctctttct gagtgatgga
240
aaacttaagt cgaatctcta ccagccaaga aaattaccca gtgacatcac agcaggtgtc
300
gaattaaatg atgggcagtg gcattctgtc tctttatct
339

```

<210> 1246  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1246
Ala Lys Gln Gln Lys Pro Gln Ile Ile Ala Met Gly Asn Val Ser Phe
1      5      10      15
Ser Cys Ser Gln Pro Gln Ser Met Pro Val Thr Phe Leu Ser Ser Arg
      20      25      30
Ser Phe Leu Ala Leu Pro Asp Phe Ser Gly Glu Glu Glu Val Ser Ala
      35      40      45
Thr Phe Gln Phe Arg Thr Trp Asn Lys Ala Gly Leu Leu Leu Phe Ser
      50      55      60
Glu Leu Gln Leu Ile Ser Gly Gly Ile Leu Leu Phe Leu Ser Asp Gly
65      70      75      80
Lys Leu Lys Ser Asn Leu Tyr Gln Pro Arg Lys Leu Pro Ser Asp Ile
      85      90      95
Thr Ala Gly Val Glu Leu Asn Asp Gly Gln Trp His Ser Val Ser Leu
      100      105      110
Ser

```

<210> 1247  
 <211> 366  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 1247

ttgacctcca acccgggcac gcgcacctcg cccagatcc cgatggatgg gcatgacctc  
 60  
 aacccgggtgt ggcgggacgt cggcctgata gtgcacccgc cgatgctcta catgggctac  
 120  
 gtcggtttct ccggtggcctt tgcgtttgcc atcgccgcct tgcctggcgg gcgcctcgat  
 180  
 gcggcctggg cgcgctggtc gcggccatgg accattgtgg cctgggcgtt cctcggtatc  
 240  
 ggtatcacc cgggttcgtg gtgggcctac tacgaactcg gctggngcgg ctgggtggtc  
 300  
 tgggaccccg gggaaaaccc cttcttcata ccctggctgg ggggcacccc gctgattcac  
 360  
 tcgctg  
 366

&lt;210&gt; 1248

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1248

Leu Thr Ser Asn Pro Gly Thr Arg Ile Leu Pro Gln Ile Pro Met Asp  
 1 5 10 15  
 Gly His Asp Leu Asn Pro Val Trp Arg Asp Val Gly Leu Ile Val His  
 20 25 30  
 Pro Pro Met Leu Tyr Met Gly Tyr Val Gly Phe Ser Val Ala Phe Ala  
 35 40 45  
 Phe Ala Ile Ala Ala Leu Leu Gly Gly Arg Leu Asp Ala Ala Trp Ala  
 50 55 60  
 Arg Trp Ser Arg Pro Trp Thr Ile Val Ala Trp Ala Phe Leu Gly Ile  
 65 70 75 80  
 Gly Ile Thr Leu Gly Ser Trp Trp Ala Tyr Tyr Glu Leu Gly Trp Xaa  
 85 90 95  
 Gly Trp Trp Phe Trp Asp Pro Gly Glu Asn Pro Phe Phe Met Pro Trp  
 100 105 110  
 Leu Gly Gly Thr Pro Leu Ile His Ser Leu  
 115 120

&lt;210&gt; 1249

&lt;211&gt; 374

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1249

acgcgtgtcc tcaacaccct ggcgcccacg ctgattgccg tggaaccggt gccggcaatg  
 60  
 ggcgcgagct tgagcaagct gctgccgat gtgcacctgg tcaatggcac tgccgagggc  
 120  
 attccactgg aaagcgccgt ggcggtatgc gtggtgtgcg cacaagcctt ccattggttt  
 180  
 tccagcgagg cggccctggc ggaaatccat cgggtactca aaccggatgg gcgcctgggg  
 240

ctggtgtgga atgtgcgcga cgagtcggtg gattgggtcg ccgccattac tcaaatacatc  
 300  
 acgccttatg aaggcgacac gccgcgcttt cataccggcc gttggcgga agccttcact  
 360  
 ggcgagtatt ttg  
 374

<210> 1250

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1250

Thr	Arg	Val	Leu	Asn	Thr	Leu	Ala	Pro	Thr	Leu	Ile	Ala	Val	Glu	Pro
1				5					10					15	
Val	Pro	Ala	Met	Gly	Ala	Gln	Leu	Ser	Lys	Leu	Leu	Pro	Asp	Val	His
			20					25					30		
Leu	Val	Asn	Gly	Thr	Ala	Glu	Ala	Ile	Pro	Leu	Glu	Ser	Ala	Val	Ala
		35					40					45			
Asp	Ala	Val	Val	Cys	Ala	Gln	Ala	Phe	His	Trp	Phe	Ser	Ser	Glu	Ala
	50					55					60				
Ala	Leu	Ala	Glu	Ile	His	Arg	Val	Leu	Lys	Pro	Asp	Gly	Arg	Leu	Gly
65					70					75				80	
Leu	Val	Trp	Asn	Val	Arg	Asp	Glu	Ser	Val	Asp	Trp	Val	Ala	Ala	Ile
			85						90					95	
Thr	Gln	Ile	Ile	Thr	Pro	Tyr	Glu	Gly	Asp	Thr	Pro	Arg	Phe	His	Thr
			100					105					110		
Gly	Arg	Trp	Arg	Glu	Ala	Phe	Thr	Gly	Glu	Tyr	Phe				
		115					120								

<210> 1251

<211> 742

<212> DNA

<213> Homo sapiens

<400> 1251

accggtctct tcctcgga aa ggcagggccg aggggcttgc ggggcagcca tggaggcgac  
 60  
 gcggaggcgg cagcacgtgg gagcgacggg cggcccaggc gcgcagttgg gcgcctcctt  
 120  
 ccctgcaggc caggcatggc tctgtgagcg ctgatgaggc tgcccgcacg gctcccttcc  
 180  
 acctcgacct ctggttctac ttcacactgc agaactgggt tctggacttt gggcgcccc  
 240  
 ttgccatgct ggtattccct ctcgagtggg ttccactcaa caagcccagt gttggggact  
 300  
 atttccacat ggctacaac gtcatacgc cctttctctt gctcaagctc atcgagcggg  
 360  
 cccccgcac cctgctacgc tccatcacgt acgtgagcat catcatcttc atcatgggtg  
 420  
 ccagcatcca cctgggtggg gactctgtca accaccgct gctcttcagt ggctaccagc  
 480  
 accacctgtc tgtccgtgag aacccatca tcaagaatct caagccggag acgctgatcg  
 540

actcctttga gctgctctac tattatgatg agtacctggg tcaactgcatg tggtagatcc  
 600  
 ccttcttcct catcctcttc atgtacttca gcggctgctn ttactgcctc taaagctgag  
 660  
 agcttgattc cagggcctgc cctgctcctg gtggcaccca gtggcctgta ctactggtac  
 720  
 ctggtcacccg agggccagat ct  
 742

<210> 1252

<211> 80

<212> PRT

<213> Homo sapiens

<400> 1252

Met	Arg	Leu	Pro	Ala	Arg	Leu	Pro	Ser	Thr	Ser	Thr	Ser	Gly	Ser	Thr
1				5				10					15		
Ser	His	Cys	Arg	Thr	Gly	Phe	Trp	Thr	Leu	Gly	Val	Pro	Leu	Pro	Cys
			20					25				30			
Trp	Tyr	Ser	Leu	Ser	Ser	Gly	Phe	His	Ser	Thr	Ser	Pro	Val	Leu	Gly
			35				40					45			
Thr	Thr	Ser	Thr	Trp	Pro	Thr	Thr	Ser	Ser	Arg	Pro	Phe	Ser	Cys	Ser
	50					55				60					
Ser	Ser	Ser	Ser	Gly	Pro	Pro	Ala	Pro	Cys	Tyr	Ala	Pro	Ser	Arg	Thr
65					70					75					80

<210> 1253

<211> 675

<212> DNA

<213> Homo sapiens

<400> 1253

gggccccctc ccaggcgctt tctgggagct tttagaactg cgctctgaag tttccagaga  
 60  
 gcgaggagct tttgcggcag gcagagacaa tggaagaaaa tgaaagccag aaatgtgagc  
 120  
 cgtgccttcc ttactcagca gacagaagac agatgcagga acaaggcaaa ggcaatctgc  
 180  
 atgtaacatc accagaagat gcagaatgcc gcagaaccaa ggaacgcctt tctaattggaa  
 240  
 acagtctgtg ttcagtcttc aagtcttccc gcaatatccc aaggagacac accctagggg  
 300  
 ggccccgaag ttccaaggaa atactgggaa tgcaaacatc tgagatggat cggaagagag  
 360  
 gaaaaagcgt tcctagaaca tctgaagcag aagtaccccc accacgcctc tgcaatcatg  
 420  
 ggtcaccaag agaggctgag agaccagaca aggatcccca aactgtctca cagtctctca  
 480  
 ccaccagtg tgggtgaccc ggtcgagcat ttatcagaga cgtccgctga ttctttggaa  
 540  
 gccatgtctg agggggatgc tccaaccctt ttttccagag gcagccggac tcgtgcgagc  
 600  
 cttcctgtgg tgaggtaaac caaccagacg aaagaaagat ctctgggggt tctctatctc  
 660

cagtatggag atgaa  
675

<210> 1254

<211> 86

<212> PRT

<213> Homo sapiens

<400> 1254

Met Gly His Gln Glu Arg Leu Arg Asp Gln Thr Arg Ile Pro Lys Leu  
1 5 10 15  
Ser His Ser Pro Gln Pro Pro Ser Val Gly Asp Pro Val Glu His Leu  
20 25 30  
Ser Glu Thr Ser Ala Asp Ser Leu Glu Ala Met Ser Glu Gly Asp Ala  
35 40 45  
Pro Thr Pro Phe Ser Arg Gly Ser Arg Thr Arg Ala Ser Leu Pro Val  
50 55 60  
Val Arg Ser Thr Asn Gln Thr Lys Glu Arg Ser Leu Gly Val Leu Tyr  
65 70 75 80  
Leu Gln Tyr Gly Asp Glu  
85

<210> 1255

<211> 401

<212> DNA

<213> Homo sapiens

<400> 1255

ncgccgatta ccaaggetat ggatgtgtgg gccttgggcg taacgtata ctgtctgctg  
60  
ttcggtcgag tgccatttga tgcagagacg gactacttgc tgctggaaag taccctgcat  
120  
gacgattatg ccgtcccgac gcacatgggt agcgaccgcg tgttggtagg cccgcgacca  
180  
gcacgttggc cctcgctcgca agagacgccc aacgtgccgc tgtccggcga ggcgcgatga  
240  
gtacgccatc tgctcgatgc ccttctcgac aaggatccag cgacgcgcct cactctcgat  
300  
cgtgttataa cacacccatg gctcgtggca gagtcatggt aatagtagca attgtatata  
360  
ccctcatcac caagatggcc aaagcggtag aaggcccgcg g  
401

<210> 1256

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1256

Xaa Pro Ile Thr Lys Ala Met Asp Val Trp Ala Leu Gly Val Thr Leu  
1 5 10 15  
Tyr Cys Leu Leu Phe Gly Arg Val Pro Phe Asp Ala Glu Thr Glu Tyr  
20 25 30  
Leu Leu Leu Glu Ser Ile Leu His Asp Asp Tyr Ala Val Pro Thr His

```

      35              40              45
Met Gly Ser Asp Arg Val Leu Val Gly Pro Arg Pro Ala Arg Trp Pro
   50              55              60
Ser Ser Gln Glu Thr Pro Asn Val Pro Leu Ser Gly Glu Ala His Ala
65              70              75              80
Val Arg His Leu Leu Asp Ala Leu Leu Asp Lys Asp Pro Ala Thr Arg
      85              90              95
Leu Thr Leu Asp Arg Val Ile Thr His Pro Trp Leu Val Ala Glu Ser
      100              105              110
Trp

```

&lt;210&gt; 1257

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1257

```

cgcgtagcagc tgattgaagg tgatgtcgcc aacgccgacc tgggtggcgca agccgccatc
60
ggcgccacgg cggtgggtgca tttggcagcg gtggcttcgg tgcaagcctc ggtggatgac
120
ccggtcagca cgcgccagag caatcttctgc ggcaccttga atgtctgcga agccatgcgc
180
aaggccgggtg tgaagcgtgt ggtatttctgc tccagcgttg cggtgtatgg caacaatggc
240
gaggggcgctt cgattgacga agagaccatc aaggccccgc tgacgcctta cgcg
294

```

&lt;210&gt; 1258

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1258

```

Arg Val Gln Leu Ile Glu Gly Asp Val Ala Asn Ala Asp Leu Val Ala
 1              5              10              15
Gln Ala Ala Ile Gly Ala Thr Ala Val Val His Leu Ala Ala Val Ala
      20              25              30
Ser Val Gln Ala Ser Val Asp Asp Pro Val Ser Thr Arg Gln Ser Asn
      35              40              45
Phe Val Gly Thr Leu Asn Val Cys Glu Ala Met Arg Lys Ala Gly Val
      50              55              60
Lys Arg Val Val Phe Ala Ser Ser Val Ala Val Tyr Gly Asn Asn Gly
65              70              75              80
Glu Gly Ala Ser Ile Asp Glu Glu Thr Ile Lys Ala Pro Leu Thr Pro
      85              90              95
Tyr Ala

```

&lt;210&gt; 1259

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;400&gt; 1259

nnacactcta gcctctgact caaggaagct gccacgggtc ttgcccttcg gtttgggggg  
 60  
 atcccgtctc cttctgctcg gagcagacat agtgagaacg tgagaagctg caggcgtggc  
 120  
 ctcaccgtgg tgtgttccaa gatgtccagg gccaaaggatg cctgtctctc cggggtggcc  
 180  
 agcgtgggtg acgtggctaa gggagtgggtc caggaggaggc tggacaccac tcggtctgca  
 240  
 cttacgggca ccaaggaggc ggtgtccagc ggggtcacag gggccatgga catggctaag  
 300  
 ggggccgtcc aaggggggtct ggacacctcg aaggctgtcc tcaccggcac caaggacacg  
 360  
 gtgtccactg ggctcacggg ggcagtgaat gtggccaaag ggcccgtaca ggccggc  
 417

&lt;210&gt; 1260

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1260

Leu Lys Glu Ala Ala Gln Gly Leu Ala Leu Arg Phe Gly Gly Ile Pro  
 1 5 10 15  
 Ser Pro Phe Val Trp Ser Arg His Ser Glu Asn Val Arg Ser Cys Arg  
 20 25 30  
 Arg Gly Leu Thr Val Val Cys Ser Lys Met Ser Arg Ala Lys Asp Ala  
 35 40 45  
 Val Ser Ser Gly Val Ala Ser Val Val Asp Val Ala Lys Gly Val Val  
 50 55 60  
 Gln Gly Gly Leu Asp Thr Thr Arg Ser Ala Leu Thr Gly Thr Lys Glu  
 65 70 75 80  
 Ala Val Ser Ser Gly Val Thr Gly Ala Met Asp Met Ala Lys Gly Ala  
 85 90 95  
 Val Gln Gly Gly Leu Asp Thr Ser Lys Ala Val Leu Thr Gly Thr Lys  
 100 105 110  
 Asp Thr Val Ser Thr Gly Leu Thr Gly Ala Val Asn Val Ala Lys Gly  
 115 120 125  
 Pro Val Gln Ala Gly  
 130

&lt;210&gt; 1261

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1261

ngtgcacgtg ccgttcggca tcaggagatg aacatggatt tgaacgctga agtcgatcag  
 60  
 ctgggtccgcc aatcccagac ctggatcccc ttgatcatgg agtacggcag ccgcctgctg  
 120tgaccctggc ggtcggctgg tggatcgaca acaaggctcag cgcccgcctg 180  
 ggcaaaactgg taggcctgcg caacgccgac ctggcactgc aaggctttat cagcaccttg  
 240

tcgaacatcg ggctgaaagt gctgctgttc gtcagtgtgg cgtcgatgat cggcattgag  
 300  
 accacctcgt tcgtcgcgga catcgggtgct  
 330

<210> 1262  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 1262  
 Xaa Ala Arg Ala Val Arg His Gln Glu Met Asn Met Asp Leu Asn Ala  
 1 5 10 15  
 Glu Val Asp Gln Leu Val Arg Gln Ser Gln Thr Trp Ile Pro Leu Ile  
 20 25 30  
 Met Glu Tyr Gly Ser Arg Leu Leu Leu Ala Leu Leu Thr Leu Ala Val  
 35 40 45  
 Gly Trp Trp Ile Asp Asn Lys Val Ser Ala Arg Leu Gly Lys Leu Val  
 50 55 60  
 Gly Leu Arg Asn Ala Asp Leu Ala Leu Gln Gly Phe Ile Ser Thr Leu  
 65 70 75 80  
 Ser Asn Ile Gly Leu Lys Val Leu Leu Phe Val Ser Val Ala Ser Met  
 85 90 95  
 Ile Gly Ile Glu Thr Thr Ser Phe Val Ala Asp Ile Gly Ala  
 100 105 110

<210> 1263  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 1263  
 acgcgtggac gatggacttc gtcggctctgc ggtacgacga agggctcaac attgccggtg  
 60  
 gcatcgatga tgagtttgct cgctgggca acacctagca gcaatggcat cgatagtccc  
 120  
 tgcccagcct gctccatttc gacgacgatg gtcgccgggt tcagtttctt ctcgctccac  
 180  
 gtcaacagac cgtcaccgtg gttgacgatc tcgccggtgg aggcgtcctt gacgacgatc  
 240  
 tggccacgcy ccaggaata catctcccca tccacccaaa agaacgcccc caagctgggc  
 300  
 atcttgcca gcccgatgat cgagagggtt tcaacaagcg actcgggatc c  
 351

<210> 1264  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 1264  
 Met Pro Ser Leu Gly Ala Phe Phe Trp Val Asp Gly Glu Met Tyr Ser  
 1 5 10 15  
 Leu Ala Arg Gly Gln Ile Val Val Lys Asp Ala Ser Thr Gly Glu Ile

```

      20      25      30
Val Asn His Gly Asp Gly Leu Leu Thr Trp Ser Glu Lys Lys Leu Asn
      35      40      45
Pro Ala Thr Ile Val Val Glu Met Glu Gln Ala Gly Gln Gly Leu Ser
      50      55      60
Met Pro Leu Leu Leu Gly Val Ala Gln Ala Ser Lys Leu Ile Ile Asp
65      70      75      80
Ala Thr Gly Asn Val Glu Pro Phe Val Val Pro Gln Thr Asp Glu Val
      85      90      95
His Arg Pro Arg
      100

```

&lt;210&gt; 1265

&lt;211&gt; 318

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1265

```

accggtgtat gcaactgaaa tgctgtccga tatgcctgcg ctccagctcg tgaatcgaaa
60
gttggataac gctcgcttgg tggaatcgtc gctacggaag cttatcaagg atacggatgc
120
tgctgcaccg ccaaaattat ggacgcccc cgacccact cgctctgacg ataccattgc
180
acagccgaaa gtgcaaccag cccaagcagt gggagatgac tcgatcatgt cggtcgatga
240
gcctgatgca accgtccatg acatgccact caccacgaca ctcgacaacg tgggtcgctc
300
agatccatcg cgacgcgt
318

```

&lt;210&gt; 1266

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1266

```

Met Leu Ser Asp Met Pro Ala Leu Gln Leu Val Asn Arg Lys Leu Asp
1      5      10      15
Asn Ala Arg Leu Val Glu Ser Ser Leu Arg Lys Leu Ile Lys Asp Thr
      20      25      30
Asp Ala Ala Ala Pro Pro Lys Leu Trp Thr Pro Pro Asp Pro Thr Arg
      35      40      45
Ser Asp Asp Thr Ile Ala Gln Pro Lys Val Gln Pro Ala Gln Ala Val
50      55      60
Gly Asp Asp Ser Ile Met Ser Val Asp Glu Pro Asp Ala Thr Val His
65      70      75      80
Asp Met Pro Leu Thr Thr Leu Asp Asn Val Gly Arg Ser Asp Pro
      85      90      95
Ser Arg Arg

```

&lt;210&gt; 1267

&lt;211&gt; 343

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1267

nggacacttg tgggaaatgc cccacagcct gtgtttttat tccccttggtg aacacttggtg  
 60  
 ggaactgtcc cacggcccgt gtttctgtgc gcctgcagac actcgtggga aatgccccac  
 120  
 aacctgtgtt tttgttcccc ttgtgaacac tcgtgggaaa tgccccacaa cctgtgtttt  
 180  
 tattcccctt gtgaacactc gtgggaaatg tcccatggcc cgtgtttccg tgcacctgag  
 240  
 gatactcatc aaacaccagg ctgtcattgg ggacagggtg agctctggct gttggtgcag  
 300  
 catggttaga agagcaccaa gtcctggact ctgttgattt ata  
 343

&lt;210&gt; 1268

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1268

Met	Pro	His	Ser	Leu	Cys	Phe	Tyr	Ser	Pro	Cys	Glu	His	Leu	Trp	Glu
1				5				10					15		
Leu	Ser	His	Gly	Pro	Cys	Phe	Cys	Ala	Pro	Ala	Asp	Thr	Arg	Gly	Lys
			20					25					30		
Cys	Pro	Thr	Thr	Cys	Val	Phe	Val	Pro	Leu	Val	Asn	Thr	Arg	Gly	Lys
		35				40					45				
Cys	Pro	Thr	Thr	Cys	Val	Phe	Ile	Pro	Leu	Val	Asn	Thr	Arg	Gly	Lys
	50				55					60					
Cys	Pro	Met	Ala	Arg	Val	Ser	Val	His	Leu	Arg	Ile	Leu	Ile	Lys	His
65				70				75					80		
Gln	Ala	Val	Ile	Gly	Asp	Arg	Val	Ser	Ser	Gly	Cys	Trp	Cys	Ser	Met
			85					90					95		
Val	Gly	Arg	Ala	Pro	Ser	Pro	Gly	Leu	Cys						
			100					105							

&lt;210&gt; 1269

&lt;211&gt; 391

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1269

tcgcatccg gagcgatcgg tgctgcagat ggctggcgac gccctgcggg gcgcattgag  
 60  
 ggacgccgac ctggagccgg ccgccctaga cgggctgacg gtccagggtg ggtccccccg  
 120  
 cggcgcggac tacgacaccg tgtccgaaac ctttgggtctt tcgccacaat tctgcagcca  
 180  
 gacctggggc gcacggccgg ttaccgcaa cggatgacct ggcagcggcc atggcgggtg  
 240  
 ccagcggcct cgcgcggcgg gtggcttgcc tcatgggcat gaagaattcg gacctcgggc  
 300

ggttgggtga ggcggacaat ccctttcatc atgagcaatt ccgggagaat ggcggggccgc  
360

acggggaaga gggttggatc ggcattgcct c  
391

<210> 1270

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1270

Met	Met	Lys	Gly	Ile	Val	Arg	Leu	Thr	Gln	Pro	Pro	Glu	Val	Arg	Ile
1				5					10					15	
Leu	His	Ala	His	Glu	Ala	Ser	His	Pro	Pro	Arg	Glu	Ala	Ala	Gly	His
			20					25					30		
Arg	His	Gly	Arg	Cys	Gln	Asp	His	Arg	Cys	Gly	Glu	Pro	Ala	Val	Arg
		35					40				45				
Pro	Arg	Ser	Gly	Cys	Arg	Ile	Val	Ala	Lys	Asp	Gln	Arg	Phe	Arg	Thr
	50				55					60					
Arg	Cys	Arg	Ser	Pro	Arg	Arg	Gly	Gly	Thr	Pro	Pro	Gly	Arg	Ser	Ala
65				70					75					80	
Arg	Leu	Gly	Arg	Pro	Ala	Pro	Gly	Arg	Arg	Pro	Ala	Met	Arg	Pro	Ala
			85				90						95		
Gly	Arg	Arg	Gln	Pro	Ser	Ala	Ala	Pro	Ile	Ala	Pro	Asp	Arg		
			100					105					110		

<210> 1271

<211> 661

<212> DNA

<213> Homo sapiens

<400> 1271

acgcgtcggtt actggccacc tgcgagcgca ccagggtagg cagcactcgg tctccgtcga  
60  
accagaaagc gtcattcgggg tggatgaacga gaacggggcga tggatgtggg ggacggataa  
120  
cccccggttg cgtcaccata tggcccaacta aagagttcac cagggttgat ttaccagccc  
180  
cggtcgaccc tctaccacc gccagaagcg gcgcatcaat agtctctaag cgcggcaaaa  
240  
tatagtcggtt aagctgggta gcgatgcgct gtgccagccc ggctgagta atagcctccg  
300  
gcaaatccaa ggggaactgg gcctgacgca ggtgtgtgcc cagatcggtc aacgacagca  
360  
gtatctgctc agtggttcatt gtgacccctc ctgggtcactc gtcaggcctg tggcggcgcc  
420  
cactgcaact cgttggtgac cggttggttg cgacgtcgct tgaggaatgc gggcagtcctc  
480  
ggcttcgaca atttggcacc tcggggcgac gtgatagccg ccggggcgag cacgttcata  
540  
cgggtgatga gctcgatctg aagcggacca ggatcatcgt ccaaccacg cacaatggcg  
600  
tcacgaagat aagcaagatc tgtcccaacg cgcaggaact ctaacgtgtg ccaccaccgg  
660

t  
661

<210> 1272  
<211> 126  
<212> PRT  
<213> Homo sapiens

<400> 1272  
Met Asn Thr Glu Gln Ile Leu Leu Ser Leu Thr Asp Leu Arg His Asn  
1 5 10 15  
Leu Arg Gln Ala Gln Phe Pro Leu Asp Leu Pro Glu Ala Ile Thr Gln  
20 25 30  
Ala Gly Leu Ala Arg Arg Ile Ala Asn Gln Leu Asn Asp Tyr Ile Leu  
35 40 45  
Pro Arg Leu Glu Thr Ile Asp Ala Pro Leu Leu Ala Val Val Gly Gly  
50 55 60  
Ser Thr Gly Ala Gly Lys Ser Thr Leu Val Asn Ser Leu Val Gly His  
65 70 75 80  
Met Val Thr Gln Pro Gly Val Ile Arg Pro Thr Thr Thr Ser Pro Val  
85 90 95  
Leu Val His His Pro Asp Asp Ala Phe Trp Phe Asp Gly Asp Arg Val  
100 105 110  
Leu Pro Thr Leu Val Arg Ser Gln Val Ala Ser Asn Asp Ala  
115 120 125

<210> 1273  
<211> 489  
<212> DNA  
<213> Homo sapiens

<400> 1273  
gccggcgaga ccgggtgccgg aaagaccatg gtggtcaccg gtattgggtt gctgctcggc  
60  
gacaaggctg acaactggatt ggtccggcat ggctgcgac gtgccgtcgt cgaagccgtt  
120  
ctcgacacgc ctgatgccgg tcgcgtcagc gagcttggcg gaacagtcga ggatgggtgag  
180  
gttatctgcg ctcgacacat cacgagtcgt cgctctcgag cgctgcttgg aggagctcaa  
240  
gttaccgcta gtcagctggc ccacatcggt ggggatcagg tgaccatcca tggccaatct  
300  
gaacaagtga gggtggtcga cgcagcgcg cagctcgacg tcgttgaccg ggctgccgga  
360  
gatgagctgg caggctacct aagtcgacat gcacagctgt ggtcggagtt tcgtgctgca  
420  
tcccagcgtc ttcagcgcct caacgaggat cgcgctgggg ccgagatgga acgcgaggtg  
480  
cttacgcgt  
489

<210> 1274  
<211> 163  
<212> PRT

<213> Homo sapiens

<400> 1274

Ala Gly Glu Thr Gly Ala Gly Lys Thr Met Val Val Thr Gly Ile Gly  
 1 5 10 15  
 Leu Leu Leu Gly Asp Lys Ala Asp Thr Gly Leu Val Arg His Gly Cys  
 20 25 30  
 Asp Arg Ala Val Val Glu Ala Val Leu Asp Thr Pro Asp Ala Gly Arg  
 35 40 45  
 Val Ser Glu Leu Gly Gly Thr Val Glu Asp Gly Glu Val Ile Cys Ala  
 50 55 60  
 Arg His Ile Thr Ser Arg Arg Ser Arg Ala Leu Leu Gly Gly Ala Gln  
 65 70 75 80  
 Val Thr Ala Ser Gln Leu Ala His Ile Val Gly Asp Gln Val Thr Ile  
 85 90 95  
 His Gly Gln Ser Glu Gln Val Arg Leu Val Asp Ala Ala Arg Gln Leu  
 100 105 110  
 Asp Val Val Asp Arg Ala Ala Gly Asp Glu Leu Ala Gly Tyr Leu Ser  
 115 120 125  
 Arg His Ala Gln Leu Trp Ser Glu Phe Arg Ala Ala Ser Gln Arg Leu  
 130 135 140  
 Gln Arg Leu Asn Glu Asp Arg Ala Gly Ala Glu Met Glu Arg Glu Val  
 145 150 155 160  
 Leu Thr Arg

<210> 1275

<211> 384

<212> DNA

<213> Homo sapiens

<400> 1275

nngctagcaa gtgcaagtac gagcaaaagt tatcagcaac agcgggagggc tgaacttctc  
 60  
 gtcgcacggc tagaggggga aatgcacgca cacagcgacc cgaccccgtc gccacaacca  
 120  
 cccgaggatg caggggtgat tgatgttgcc ctgaaagagg cgaagaaagc ctttgatgaa  
 180  
 ggcaaggctg atctaattga taaactcaat caggagatac ttcgcctggc aaacgaattc  
 240  
 ggtgcgctcg ggcttgaatc tattgagctt ggctccgacg cgaagatggc agtacgcaaa  
 300  
 ggcaatcaga aatcagcggt cagcaggctg actcccgggtg aacgtctcag gctgcgcatt  
 360  
 gctacagcca tcgcgttggtt acgc  
 384

<210> 1276

<211> 128

<212> PRT

<213> Homo sapiens

<400> 1276

Xaa Leu Ala Ser Ala Ser Thr Ser Lys Ser Tyr Gln Gln Gln Arg Glu

```

      1             5             10             15
Ala Glu Leu Leu Val Ala Arg Leu Glu Gly Glu Met His Ala His Ser
      20             25             30
Asp Pro Thr Pro Ser Pro Gln Pro Pro Glu Asp Ala Gly Leu Ile Asp
      35             40             45
Val Ala Leu Lys Glu Ala Lys Lys Ala Phe Asp Glu Gly Lys Val Asp
      50             55             60
Leu Met Asp Lys Leu Asn Gln Glu Ile Leu Arg Leu Ala Asn Glu Phe
65      70             75             80
Gly Ala Leu Gly Leu Glu Ser Ile Glu Leu Gly Ser Asp Ala Lys Met
      85             90             95
Ala Val Arg Lys Gly Asn Gln Lys Ser Ala Phe Ser Arg Leu Thr Pro
      100            105            110
Gly Glu Arg Leu Arg Leu Arg Ile Ala Thr Ala Ile Ala Leu Leu Arg
      115            120            125

```

&lt;210&gt; 1277

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1277

```

cagtttcagc cccgctgtgt gtccccaatt cctgtctctc ctaccagccg gattcagaac
60
ccagtggctt tcctcagctc tggtctgcct tctctcctg ccatcccacc cacaaatgcc
120
atggggctgc ctagaagtgc accatccatg ccatcccagg gattagcgaa gaaaaatata
180
aagtctcttc aaccagtga tgaatgataac attcgtgaaa ctaagaacgc agtgattcga
240
gacttgggga aaaaaataac tttcagtgat gtcagaccaa accagcagga gtacaaaatt
300
tcaagctttg agcagaggct gatgaatgaa atagagtttc gcttggaacg tactcctgtt
360
gatgaatcac atgatgaaat tcaacatgat gg
392

```

&lt;210&gt; 1278

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1278

```

Gln Phe Gln Pro Arg Cys Val Ser Pro Ile Pro Val Ser Pro Thr Ser
1             5             10             15
Arg Ile Gln Asn Pro Val Ala Phe Leu Ser Ser Val Leu Pro Ser Leu
      20             25             30
Pro Ala Ile Pro Pro Thr Asn Ala Met Gly Leu Pro Arg Ser Ala Pro
      35             40             45
Ser Met Pro Ser Gln Gly Leu Ala Lys Lys Asn Thr Lys Ser Pro Gln
      50             55             60
Pro Val Asn Asp Asp Asn Ile Arg Glu Thr Lys Asn Ala Val Ile Arg
65      70             75             80
Asp Leu Gly Lys Lys Ile Thr Phe Ser Asp Val Arg Pro Asn Gln Gln

```



85 90 95  
 Glu Tyr Lys Ile Ser Ser Phe Glu Gln Arg Leu Met Asn Glu Ile Glu  
 100 105 110  
 Phe Arg Leu Glu Arg Thr Pro Val Asp Glu Ser His Asp Glu Ile Gln  
 115 120 125  
 His Asp  
 130

<210> 1279

<211> 297

<212> DNA

<213> Homo sapiens

<400> 1279

atggagtcgc agactctccg ccacatgacg gaggacgact gcgccgacaa cggcatccca  
 60  
 ctccccaaacg tcaactccag gatcctctct aaggatcatcg agtactgcaa cagtcacgtc  
 120  
 cagccgcgcg ccaaaccgcg tgactccgct gcctccgagg gcggcgagga cctcaagagc  
 180  
 tgggacgcga agttcgtaaa ggtggaccag gctacgctct tcgacctcat cctggctgcc  
 240  
 aactatctga acatcaaggg attgctggac ctgacctgcc agacgggtgc tgacatg  
 297

<210> 1280

<211> 99

<212> PRT

<213> Homo sapiens

<400> 1280

Met Glu Ser Gln Thr Leu Arg His Met Ile Glu Asp Asp Cys Ala Asp  
 1 5 10 15  
 Asn Gly Ile Pro Leu Pro Asn Val Asn Ser Arg Ile Leu Ser Lys Val  
 20 25 30  
 Ile Glu Tyr Cys Asn Ser His Val His Ala Ala Ala Lys Pro Ala Asp  
 35 40 45  
 Ser Ala Ala Ser Glu Gly Gly Glu Asp Leu Lys Ser Trp Asp Ala Lys  
 50 55 60  
 Phe Val Lys Val Asp Gln Ala Thr Leu Phe Asp Leu Ile Leu Ala Ala  
 65 70 75 80  
 Asn Tyr Leu Asn Ile Lys Gly Leu Leu Asp Leu Thr Cys Gln Thr Gly  
 85 90 95  
 Ala Asp Met

<210> 1281

<211> 515

<212> DNA

<213> Homo sapiens

<400> 1281

acgcgtgaag ggggctttgg aggggatggc ttctggactg cacgatgggt gaacacagtt  
 60

ttttaaactc tttccacat ctgtataggt ttgaaaatta tcaacaactc atggggaggg  
 120  
 tggcgtgcc a ggtcatggct gcctggagcc cttctgagga gggccggctc aaccgaggac  
 180  
 gccctcccca ctaccaagta ggcactgcgg gcaggagtcg ccacccccac cccaaggaag  
 240  
 ttcagaacag gcaacaggag gagcctgact ccaacagagt tgggtgtcatc cggcgcacgc  
 300  
 ctaaggacgt cacaacacat caactctggg agcccaaggg ggtgtgtggg ccactcaagg  
 360  
 ggaagatgat ccagaagctc tgctccctcc ctttgccttt gaagaacaca ggagtgcac  
 420  
 gtgggggaatc taccggctta atttcttctt agtaacaggc atagtaggat caaaaaattt  
 480  
 ttgcttctaa tttttaaaaa cattcaatgt gtaca  
 515

<210> 1282

<211> 135

<212> PRT

<213> Homo sapiens

<400> 1282

Met	Gly	Glu	His	Ser	Phe	Leu	Asn	Ser	Phe	Pro	His	Leu	Tyr	Arg	Phe
1				5					10					15	
Glu	Asn	Tyr	Gln	Gln	Leu	Met	Gly	Arg	Val	Ala	Cys	Gln	Val	Met	Ala
			20					25					30		
Ala	Trp	Ser	Pro	Ser	Glu	Glu	Gly	Arg	Leu	Asn	Arg	Gly	Arg	Pro	Pro
		35					40					45			
His	Tyr	Gln	Val	Gly	Thr	Ala	Gly	Arg	Ser	Arg	His	Pro	His	Pro	Lys
	50					55					60				
Glu	Val	Gln	Asn	Arg	Gln	Gln	Glu	Glu	Pro	Asp	Ser	Asn	Arg	Val	Gly
65					70					75				80	
Val	Ile	Arg	Arg	Ile	Ala	Lys	Asp	Val	Thr	Thr	His	Gln	Leu	Trp	Glu
			85					90					95		
Pro	Lys	Gly	Val	Cys	Gly	Pro	Leu	Lys	Gly	Lys	Met	Ile	Gln	Lys	Leu
			100					105					110		
Cys	Ser	Leu	Pro	Leu	Leu	Leu	Lys	Asn	Thr	Gly	Val	Thr	Arg	Gly	Glu
		115					120					125			
Ser	Thr	Gly	Leu	Ile	Ser	Ser									
	130					135									

<210> 1283

<211> 296

<212> DNA

<213> Homo sapiens

<400> 1283

gaattcctca caatgaactg cagtgtcttg aggaccagtt gggtagcctt actccgggtc  
 60  
 tccactgcag aacttataca tatatgcttt gtgcacacaa agaaaaacag cagcccaaaa  
 120  
 gaatccccgc tggggctctt aggagggagg aaagttccca caggtaactc actggttaat  
 180

tttaaagagc tcaggaaagg aaggaaggat ggctttttct cttgtgagtc aagacaaggt  
 240  
 cctgatgata accctcccag atcagaacgt aactttcaac ccacgagtgc tgctcn  
 296

<210> 1284  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 1284  
 Met Asn Cys Ser Val Trp Arg Thr Ser Trp Val Ala Leu Leu Arg Val  
 1 5 10 15  
 Ser Thr Ala Glu Leu Ile His Ile Cys Phe Val His Thr Lys Lys Asn  
 20 25 30  
 Ser Ser Pro Lys Glu Ser Arg Leu Gly Leu Leu Gly Gly Arg Lys Val  
 35 40 45  
 Pro Thr Gly Asn Ser Leu Val Asn Phe Lys Glu Leu Arg Lys Gly Arg  
 50 55 60  
 Lys Asp Gly Phe Phe Ser Cys Glu Ser Arg Gln Gly Pro Asp Asp Asn  
 65 70 75 80  
 Pro Pro Arg Ser Glu Arg Asn Phe Gln Pro Thr Ser Ala Ala  
 85 90

<210> 1285  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<400> 1285  
 gggccccttc ttacctgccc cttccccgtg ccaccaaccc gtagacaggg agggcaagca  
 60  
 gtgaaaggtc catctagagg aggtaaaaga cagggctgag ggaaaacgcc ttgtacagtc  
 120  
 aggatggcag atgtactctg tcagggaaga cagccccaca gaaaaggctc ggcttgccca  
 180  
 agaagcaaca aaagggattc tacacctcag accaggaggagg gggaatgtgt acaaagattg  
 240  
 gatttactaa attcagagcc acagactttc aggtacttcg gtgaagatca gtgctctttc  
 300  
 aaacccacac ttcagaggca ggctttaaaa cgctgactt ctgtcagggc cacaggctgg  
 360  
 gctgccc aaa gctcctacgg ggctggggga tccgagagag gacttcccac tagtccaaga  
 420  
 tgtggtgact agtttcaagc cagagattga ggagcagacc tgatgccctt tcgggcccct  
 480  
 gctaagaacc tgattcgagg aaaaggaagt gaagacagta acgcgt  
 526

<210> 1286  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 1286

```

Met Ala Asp Val Leu Cys Gln Gly Arg Gln Pro His Arg Lys Gly Ser
 1           5           10           15
Ala Trp Pro Arg Ser Asn Lys Arg Asp Ser Thr Pro Gln Thr Arg Glu
          20           25           30
Gly Glu Cys Val Gln Arg Leu Asp Leu Leu Asn Ser Glu Pro Gln Thr
          35           40           45
Phe Arg Tyr Phe Gly Glu Asp Gln Cys Ser Phe Lys Pro Thr Leu Gln
          50           55           60
Arg Gln Ala Leu Lys Arg Leu Thr Ser Val Arg Ala Thr Gly Trp Ala
65           70           75           80
Ala Gln Ser Ser Tyr Gly Ala Gly Gly Ser Glu Arg Gly Leu Pro Thr
          85           90           95
Ser Pro Arg Cys Gly Asp
          100

```

&lt;210&gt; 1287

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1287

```

acgcgtgaag gggagaggca gctccaggtg gaggggaagtg catgaggaag cagagaggca
60
ggcgacagggc agcgtggctg gggctgggca ggccttccag tttgattgca gccagaggtt
120
caggtgagaa gaaggtacaa caagcaagga agggccccagg aagccactgg ggggtgttga
180
gccattgaat attctggatt ttaggacatt tctgtggctg actccactgc catcagagtt
240
catccacccc aactccagcc tgagagtgtc ggggcactgg gcactccgga attcttcaaa
300
gctctgatgc aacatgtccc caggggtgtct gac
333

```

&lt;210&gt; 1288

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1288

```

Met Leu His Gln Ser Phe Glu Glu Phe Arg Ser Ala Gln Cys Pro Ser
 1           5           10           15
Thr Leu Arg Leu Glu Leu Gly Trp Met Asn Ser Asp Gly Ser Gly Val
          20           25           30
Ser His Arg Asn Val Leu Lys Ser Arg Ile Phe Asn Gly Ser Asn Thr
          35           40           45
Pro Ser Gly Phe Leu Gly Pro Ser Leu Leu Val Val Pro Ser Ser His
          50           55           60
Leu Thr Ser Gly Leu Gln Ser Asn Trp Lys Ala Cys Pro Ala Pro Ala
65           70           75           80
Thr Leu Pro Val Ala Cys Leu Ser Ala Ser Ser Cys Thr Ser Leu His
          85           90           95
Leu Glu Leu Pro Leu Pro Phe Thr Arg

```

100

105

<210> 1289  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

<400> 1289  
 acgcgtgtct gtgtacaggt ggaaggggat gggatatgaga tgggtgcagcg tgtgcatggg  
 60  
 cacggcgat ggtgtgtgag tgcactcgtg tgccggagag ctgtaagctg ctggctgagt  
 120  
 cctgcacggg ggaggaggca aggtggcccc tgccctgtggg cacagagccc accttccggg  
 180  
 ccagcccagag gcccctttcc cagagcccc tcccaagggg ccataccacc tgcattcccca  
 240  
 agatggcgtg gggcgctcct ggtgcaggag caggggacag tcagggaggc gtgtggcgga  
 300  
 cagtagcagc cccccagccc ccctcccccc accggg  
 336

<210> 1290  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 1290  
 Met Val Cys Glu Cys Thr Arg Val Pro Glu Ser Cys Lys Leu Leu Ala  
 1 5 10 15  
 Glu Ser Cys Thr Val Glu Glu Ala Arg Trp Pro Leu Pro Val Gly Thr  
 20 25 30  
 Glu Pro Thr Phe Arg Ser Ser Pro Arg Pro Leu Ser Gln Ser Pro Leu  
 35 40 45  
 Pro Arg Gly His Thr Thr Cys Ile Pro Lys Met Ala Trp Gly Val Pro  
 50 55 60  
 Gly Ala Gly Ala Gly Asp Ser Gln Gly Gly Val Trp Arg Thr Val Ala  
 65 70 75 80  
 Ala Pro Gln Pro Pro Ser Pro His Arg  
 85

<210> 1291  
 <211> 379  
 <212> DNA  
 <213> Homo sapiens

<400> 1291  
 tggccatcca cctctgtcag ctgttccggc aaccattca gatcattgtg gtagtaacga  
 60  
 atcttctgca acggcccggc accgtccacg cgagccagag gttgatagcc ttcattcctca  
 120  
 taaacgtaca ggcttgtctg gctgtgttta tgctcctgca ataaccgcaa accatcccag  
 180  
 gttaaaccggg tttcccccaa cggataccca tcaactgccat gctcggtttt ttcttatccga  
 240

cgccccagcg ggtcatacac catcctgacc acgctaccat cgtcattacg cacttcaacc  
 300  
 agccggcttt cagcgtcata cgcaaaccgc tgcacgccac gcttggcact gcgcttctcg  
 360  
 accatccgcc caaacgcgt  
 379

<210> 1292  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 1292  
 Met Val Glu Lys Arg Ser Ala Lys Arg Gly Val Gln Arg Phe Ala Tyr  
 1 5 10 15  
 Asp Ala Glu Ser Arg Leu Val Glu Val Arg Asn Asp Asp Gly Ser Val  
 20 25 30  
 Val Arg Met Val Tyr Asp Pro Leu Gly Arg Arg Ile Glu Lys Thr Glu  
 35 40 45  
 His Gly Ser Asp Gly Tyr Pro Leu Gly Glu Thr Arg Phe Thr Trp Asp  
 50 55 60  
 Gly Leu Arg Leu Leu Gln Glu His Lys His Ser Gln Thr Ser Leu Tyr  
 65 70 75 80  
 Val Tyr Glu Asp Glu Gly Tyr Gln Pro Leu Ala Arg Val Asp Gly Ala  
 85 90 95  
 Gly Pro Leu Gln Lys Ile Arg Tyr Tyr His Asn Asp Leu Asn Gly Leu  
 100 105 110  
 Pro Glu Gln Leu Thr Glu Val Asp Gly  
 115 120

<210> 1293  
 <211> 340  
 <212> DNA  
 <213> Homo sapiens

<400> 1293  
 nngccggccg cccgagagct gttcgaggcg tgccgcaacg gggacgtgga acgagtcaag  
 60  
 aggctggtga cgcctgagaa ggtgaacagc cgcgacacgg cgggcaggaa atccaccccg  
 120  
 ctgcacttcg ccgcaggttt tgggcggaaa gacgtagttg aatatttgct tcagaatggt  
 180  
 gcaaagtcc aagcacgtga tgatgggggc cttattcctc ttcataatgc atgctctttt  
 240  
 ggtcatgctg aagtagtcaa tctccttttg cgacatggtg cagaccccaa tgcttgagat  
 300  
 aattggaatt atactcctag aggggtggagt gtgctcgcga  
 340

<210> 1294  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 1294

Xaa Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys Arg Asn Gly Asp Val  
 1 5 10 15  
 Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys Val Asn Ser Arg Asp  
 20 25 30  
 Thr Ala Gly Arg Lys Ser Thr Pro Leu His Phe Ala Ala Gly Phe Gly  
 35 40 45  
 Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala Asn Val Gln  
 50 55 60  
 Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala Cys Ser Phe  
 65 70 75 80  
 Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly Ala Asp Pro  
 85 90 95  
 Asn Ala

&lt;210&gt; 1295

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1295

ggatcccgga gacctcgctcg gcgaacgtca cctcgctccag ggccgaggcg cggaacaccg  
 60  
 acgtgtcgat gccctcgccc tcgatgcagt cggtcagcgg tacgacggcg ccgcgaggag  
 120  
 cgaagggtgcc gatctggctg cgctcggcgt agaccagcga cggcgggttcg cccgacgcca  
 180  
 cggaggagag gaactgctgg atgtcgaggt caccctcgat cagcttgacc ttggcgctcg  
 240  
 cgagctcctc cttegcccg tgcagccgca ccgtcgcgat ctcgtcgccg gcaccgaagc  
 300  
 ccatcacctc gacctcgccg gagagcttcg ccccgctgtc gaaagacgcg t  
 351

&lt;210&gt; 1296

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1296

Gly Ser Arg Arg Pro Arg Arg Arg Thr Ser Pro Arg Pro Gly Pro Arg  
 1 5 10 15  
 Arg Gly Thr Pro Thr Cys Arg Cys Pro Arg Pro Arg Cys Ser Arg Ser  
 20 25 30  
 Ala Val Arg Arg Arg Gly Arg Arg Arg Cys Arg Ser Gly Cys Ala  
 35 40 45  
 Arg Arg Arg Pro Ala Thr Ala Val Arg Pro Thr Pro Arg Arg Arg Gly  
 50 55 60  
 Thr Ala Gly Cys Arg Gly His Pro Arg Ser Ala  
 65 70 75

&lt;210&gt; 1297

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1297

gtgcacccgg attccattg ccaccgactt cgagtaaact ccagtcccgga ggacacgaga  
 60  
 gacacccagg cctcaggccc catgggcacg ctccacgcca cggctcctac cagagggaca  
 120  
 gatacactct acaaactctg gggccaccca caccaagaag acacggagga gccaacaaaa  
 180  
 gaaggaccat acgaaatgca ccccaaagc aaccaaccaa tccaagaaaa aatacgtctc  
 240  
 agggttctgt gggccctctt gcatgggctg ccctgcccc ctgttctggc ctggctcaag  
 300  
 caccttacc cagcctgctc gaaagagccc tggctaccag agcagagcac tggcct  
 356

&lt;210&gt; 1298

&lt;211&gt; 91

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1298

Met	Gly	Thr	Leu	His	Ala	Thr	Ala	Pro	Thr	Arg	Gly	Thr	Asp	Thr	Leu
1				5					10					15	
Tyr	Lys	Ser	Arg	Gly	Pro	Pro	His	Gln	Glu	Asp	Thr	Glu	Glu	Pro	Thr
			20					25					30		
Lys	Glu	Gly	Pro	Tyr	Glu	Met	His	Pro	Gln	Ser	Asn	Gln	Pro	Ile	Gln
			35				40					45			
Glu	Lys	Ile	Arg	Leu	Arg	Val	Leu	Trp	Ala	Leu	Leu	His	Gly	Leu	Pro
	50					55				60					
Cys	Pro	Pro	Val	Leu	Ala	Trp	Leu	Lys	His	Leu	Thr	Pro	Ala	Cys	Ser
65				70						75				80	
Lys	Glu	Pro	Trp	Leu	Pro	Glu	Gln	Ser	Thr	Gly					
				85						90					

&lt;210&gt; 1299

&lt;211&gt; 307

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1299

ggatccactt ctaagatgtc tcaactcacgt ggtgatggca gcaggcctca gactctgggtg  
 60  
 gttgttggca ggatgtctca gttccttgcc atgtgggtct ctacacaggg cagcttctctg  
 120  
 tgtctttgcc atatggcaac tgagaatgat cttggctacc ttctccagcc cgggagtcgg  
 180  
 gagttttctg ggggtggggc acgggtcttg cccggagttc gccctggcaa aggcctgtgc  
 240  
 cagtgatcct ggagcggagc gaagtgtttc cgtgactctg cagccgcagt tcttagggct  
 300  
 tccttag  
 307



<210> 1300  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 1300  
 Met Ala Ala Gly Leu Arg Leu Trp Trp Leu Leu Ala Gly Cys Leu Ser  
 1 5 10 15  
 Ser Leu Pro Cys Gly Ser Leu His Arg Ala Ala Ser Cys Val Phe Ala  
 20 25 30  
 Ile Trp Gln Leu Arg Met Ile Leu Ala Thr Phe Ser Ser Pro Gly Val  
 35 40 45  
 Gly Ser Phe Leu Gly Trp Gly His Gly Ser Cys Pro Glu Phe Ala Leu  
 50 55 60  
 Ala Lys Ala Cys Ala Ser Asp Pro Gly Ala Glu Arg Ser Val Ser Val  
 65 70 75 80  
 Thr Leu Gln Pro Gln Phe Leu Gly Leu Pro  
 85 90

<210> 1301  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

<400> 1301  
 ctgagcaagt taaaagaagt tcttgaattt tataacttta ttttgacaaa ctattataaa  
 60  
 gttgagccta tttcctttga tgcagtatac gctgaagggt tggaaatggc tgagttcttg  
 120  
 cgcctatgg tgtcagatac gattacactt ttgcatgacc ttagaagggtc tggcgcaaac  
 180  
 atcatgtttg aaggcgcgca agggctcttg ttggatgttg atcatggtac ttaccggtat  
 240  
 gtgacttcat ctaatacgac tgcgggcgga gcgccagcgg gaacagggtt tggtcctttg  
 300  
 tacttagatt atgtattagg tatcactaag gcttatacga ctgcggttgg ttctggacct  
 360  
 ttccctactg agttgtttga cgaagatggt gagcgtcttg gtacgcgt  
 408

<210> 1302  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

<400> 1302  
 Leu Ser Lys Leu Lys Glu Val Leu Glu Phe Tyr Asn Phe Ile Leu Thr  
 1 5 10 15  
 Asn Tyr Tyr Lys Val Glu Pro Ile Ser Phe Asp Ala Val Tyr Ala Glu  
 20 25 30  
 Gly Leu Glu Met Ala Glu Phe Leu Arg Pro Met Val Ser Asp Thr Ile  
 35 40 45  
 Thr Leu Leu His Asp Leu Arg Arg Ser Gly Ala Asn Ile Met Phe Glu

50                      55                      60  
 Gly Ala Gln Gly Ser Leu Leu Asp Val Asp His Gly Thr Tyr Pro Tyr  
 65                      70                      75                      80  
 Val Thr Ser Ser Asn Thr Thr Ala Gly Gly Ala Pro Ala Gly Thr Gly  
                     85                      90                      95  
 Phe Gly Pro Leu Tyr Leu Asp Tyr Val Leu Gly Ile Thr Lys Ala Tyr  
                     100                      105                      110  
 Thr Thr Arg Val Gly Ser Gly Pro Phe Pro Thr Glu Leu Phe Asp Glu  
                     115                      120                      125  
 Asp Gly Glu Arg Leu Gly Thr Arg  
                     130                      135

<210> 1303  
 <211> 1037  
 <212> DNA  
 <213> Homo sapiens

<400> 1303  
 gccggggggg ggatgctatc taacatcttc atgttcaacc cagagaagaa acatcccgcc  
 60  
 gtttgccctg gggccctctc atcccacatc attttttcaa cccttcccca nccttttnga  
 120  
 aatagggccca accccttaaa aancaaatnt tcanataaac ccttttccct ccaccctttt  
 180  
 cccatcccat cctttttccc tcacaaacac aaacaaaang cctctttcct ttgccatttc  
 240  
 cactcctttt ggaagaaaca ggccctgttc cctccctgct caccacttca cccagctcag  
 300  
 ctggcacaaa aatactgccca ccacaccttc accctgccta gcccacctg gcagggcctc  
 360  
 ggagtagcct gccagctaaa atacgggttg cccagataac tgtgaatgtc agataagaat  
 420  
 cttctgggac aagtatgtcc catgccatat ttgggacata cttacactaa taaatttctg  
 480  
 tttatctgaa actcaaattt gcctgggcgt cctgtacttt tcttaactaa atttggtgcc  
 540  
 tctacacaca aggtccctgg ggtggggggg cacaggagca agccccttcc caggctgggt  
 600  
 ccctgccggc atctcccaca ggccaggact ggccaccag atggagcccg tgccaggcag  
 660  
 ccggcgacag acggacaaaag gctgctcagg agacactgca caccttctc tttcttgtct  
 720  
 gggggctcaa gaatccagac gccacctcc ccgagcgagc accaagacag gaagccaacc  
 780  
 tgcaatgcc agcccactgc gaccacaggg ctctgccggg gtccctgccg aaccagggt  
 840  
 tccggtccag aagccaggga taaatgccgc ttctcctata gggacgggtca gagtagagag  
 900  
 ggggaggcct acagtctcac ctgcaggag aggaagtcct cggggcgggc acgtgggggg  
 960  
 cctgacagct ccgagcacac ccggccacag tgaccacgga ctgcacacgc agaagcagtc  
 1020  
 tggatccac gcgtggc  
 1037

<210> 1304  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 1304  
 Met Glu Pro Val Pro Gly Ser Arg Arg Gln Thr Asp Lys Gly Cys Ser  
 1 5 10 15  
 Gly Asp Thr Ala His Leu Pro Leu Ser Cys Leu Gly Ala Gln Glu Ser  
 20 25 30  
 Arg Arg Pro Pro Arg Ala Ser Thr Lys Thr Gly Ser Gln Pro Ala  
 35 40 45  
 Met Pro Ser Pro Leu Arg Pro Gln Gly Ser Ala Gly Val Leu Pro Glu  
 50 55 60  
 Pro Arg Val Pro Val Gln Lys Pro Gly Ile Asn Ala Ala Ser Pro Ile  
 65 70 75 80  
 Gly Thr Val Arg Val Glu Arg Gly Arg Pro Thr Val Ser Pro Ala Gly  
 85 90 95  
 Arg Gly Ser Pro Arg Gly Gly His Val Gly Gly Leu Thr Ala Pro Ser  
 100 105 110  
 Thr Pro Gly His Ser Asp His Gly Leu His Thr Gln Lys Gln Ser Gly  
 115 120 125  
 Ser His Ala Trp  
 130

<210> 1305  
 <211> 775  
 <212> DNA  
 <213> Homo sapiens

<400> 1305  
 nacgcgttct gcgaggccat gcgggtctat gccccgcggc cgttgacctc gccacactc  
 60  
 ccggccccgc tgcgggtgga gagacgtcgg gccctctacg ggtcctggta cgagtttttc  
 120  
 ccgcgctctc aggggtgctta tgtcgatgcg gacgggtcact gggtttcagg tactttcgac  
 180  
 acctcctggg agcgcttgga cgccgcgct gcgatgggat ttgacgttgt ttacctgccc  
 240  
 gcgatccatc ccatgggcca agccttcgc aagggaagg acaacaccct gacccaggt  
 300  
 ccggacgac cgggatcgcc gtgggccatc ggatcgctcg atggcggcca tgacaccatt  
 360  
 caccgcgacc taggcacctt cgacgacctc gaccgtttcg tggcccacgc tcatgacctc  
 420  
 ggcattggagg tggccctaga ttttgccttg caagcctcac cagaccaccc gtgggtacac  
 480  
 cagcaccgg agtgggtcac gaccgcggt gatggcacca tcgcctatgc agaaaattca  
 540  
 cccaaaaagt atcaggacat ctaccgatc aacttcgaca atgaccctga cggatatctac  
 600  
 caggaatgct tgcggctgct ggagttatgg atctccacg gcgtgacgat tttccgcgtc  
 660

gataatccac ataccaagcc tctgaatttc tgggcctggc tcatggaaca ggttcacgt  
 720  
 cgtcaccccg aggtcatctt cctggcagag gccttcaccc gtcccagat gatca  
 775

<210> 1306

<211> 258

<212> PRT

<213> Homo sapiens

<400> 1306

Xaa	Ala	Phe	Cys	Glu	Ala	Met	Arg	Val	Tyr	Ala	Pro	Arg	Pro	Leu	Thr
1				5					10					15	
Ser	Pro	Thr	Leu	Pro	Ala	Pro	Leu	Arg	Val	Glu	Arg	Arg	Arg	Ala	Leu
			20					25					30		
Tyr	Gly	Ser	Trp	Tyr	Glu	Phe	Phe	Pro	Arg	Ser	Gln	Gly	Ala	Tyr	Val
		35					40					45			
Asp	Ala	Asp	Gly	His	Trp	Val	Ser	Gly	Thr	Phe	Asp	Thr	Ser	Trp	Glu
	50					55					60				
Arg	Leu	Asp	Ala	Ala	Ala	Ala	Met	Gly	Phe	Asp	Val	Val	Tyr	Leu	Pro
65					70					75				80	
Ala	Ile	His	Pro	Met	Gly	Gln	Ala	Phe	Arg	Lys	Gly	Lys	Asp	Asn	Thr
			85						90					95	
Leu	Thr	Pro	Gly	Pro	Asp	Asp	Pro	Gly	Ser	Pro	Trp	Ala	Ile	Gly	Ser
		100						105					110		
Ser	Asp	Gly	Gly	His	Asp	Thr	Ile	His	Pro	Asp	Leu	Gly	Thr	Phe	Asp
	115					120						125			
Asp	Leu	Asp	Arg	Phe	Val	Ala	His	Ala	His	Asp	Leu	Gly	Met	Glu	Val
	130					135					140				
Ala	Leu	Asp	Phe	Ala	Leu	Gln	Ala	Ser	Pro	Asp	His	Pro	Trp	Val	His
145					150					155				160	
Gln	His	Pro	Glu	Trp	Phe	Thr	Thr	Arg	Val	Asp	Gly	Thr	Ile	Ala	Tyr
			165						170					175	
Ala	Glu	Asn	Ser	Pro	Lys	Lys	Tyr	Gln	Asp	Ile	Tyr	Pro	Ile	Asn	Phe
		180						185					190		
Asp	Asn	Asp	Pro	Asp	Gly	Ile	Tyr	Gln	Glu	Cys	Leu	Arg	Leu	Leu	Glu
	195					200						205			
Leu	Trp	Ile	Ser	His	Gly	Val	Thr	Ile	Phe	Arg	Val	Asp	Asn	Pro	His
	210					215						220			
Thr	Lys	Pro	Leu	Asn	Phe	Trp	Ala	Trp	Leu	Met	Glu	Gln	Val	His	Arg
225					230					235				240	
Arg	His	Pro	Glu	Val	Ile	Phe	Leu	Ala	Glu	Ala	Phe	Thr	Arg	Pro	Glu
			245						250					255	

Met Ile

<210> 1307

<211> 624

<212> DNA

<213> Homo sapiens

<400> 1307

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 60

atgctgggca catgcggtca gggccctgtg cctgagccgt ggaactccac agccattcca  
 120  
 catgttcagt cccacaccct gaggccaagg caccctgagt cctgagggga gcaaggccct  
 180  
 gccacccgag gctgccgctg cagaggcaaa cagccccgag caaggcccgg caaccccagg  
 240  
 ctgtggctgc atggggcaaa cacagcctgg cctgaggctg ccggccagtc ggggtggcca  
 300  
 taggctaacy agaagccagg gcctccctcc cactggggtt ttccacaaaa acctgactaa  
 360  
 tgtccagggg cagccaaagg ccttgaggtc agctgggtgg aacacctttc ccctaccatc  
 420  
 ccgagatatt gtcttcttgg atggagtttt caaagccctc catgtggagg tctcgggatg  
 480  
 agaggcctcg gctgagctct gtgcagagga gcaggaagct gcagaatggg caccgcctc  
 540  
 cctcccagca cctccagtcg ctgccacgcc ccaagctcct gagctgctct gcccaagacc  
 600  
 tcccccaacc ttggtctgac gcgt  
 624

<210> 1308

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1308

Met	Ala	Thr	Pro	Thr	Gly	Arg	Gln	Pro	Gln	Ala	Arg	Leu	Cys	Leu	Pro
1				5				10					15		
His	Ala	Ala	Thr	Ala	Trp	Gly	Cys	Arg	Ala	Leu	Leu	Gly	Ala	Val	Cys
			20				25					30			
Leu	Cys	Ser	Gly	Ser	Leu	Gly	Trp	Gln	Gly	Leu	Ala	Pro	Ser	Gly	Thr
		35				40					45				
Arg	Gly	Ala	Leu	Ala	Ser	Gly	Cys	Gly	Thr	Glu	His	Val	Glu	Trp	Leu
	50				55				60						
Trp	Ser	Ser	Thr	Ala	Gln	Ala	Gln	Gly	Pro	Asp	Arg	Met	Cys	Pro	Ala
65				70				75				80			
Ser	Leu	Thr	Ser	Pro	Glu	Val	Gly	Cys	Arg	Glu	Pro	Gly	Ala	Trp	His
			85				90					95			
Ser	Pro	Pro	Ala												
			100												

<210> 1309

<211> 563

<212> DNA

<213> Homo sapiens

<400> 1309

ntgatcatcg ccaaccacca gtccaactat gacctgttcg tgtttggcac gggagtgcc  
 60  
 taccgtactg tgtgtatcgg caaaaagagc ctgaaatggg tgccgctgtt cggtcagtgt  
 120  
 ttctggctgg cgggcaatgt gttgattgac cggggcaacg cgcacaaggc gcgcccgtca  
 180

atgtcacca ccaccacac cttgcagcat aaagacacat cgatctgggt atttgccgaa  
 240  
 ggtacacgca acttcggtga aaccttgctg ccgttcaaga aaggtgcgtt ccagatggcg  
 300  
 attgccgcag gtgtgccgat cgtgcagggtg tgtgtcagca cgtatgtgaa gcacatgaag  
 360  
 ctcaatcgtt gggacagtgg cgatatttta attcgctcgt tgccgccaat tcctacgacc  
 420  
 ggactgacgt tggatgacat gccacggttg atggagacct gccgtcaaca aatgcgcgag  
 480  
 tgcattgagg caatggaccg cgagctggaa atcgccctt gtaggaacga attggctcgc  
 540  
 gaagggcgtt aacgactacg cgt  
 563

<210> 1310

<211> 183

<212> PRT

<213> Homo sapiens

<400> 1310

Xaa	Ile	Ile	Ala	Asn	His	Gln	Ser	Asn	Tyr	Asp	Leu	Phe	Val	Phe	Gly
1				5				10						15	
Thr	Gly	Val	Pro	Tyr	Arg	Thr	Val	Cys	Ile	Gly	Lys	Lys	Ser	Leu	Lys
			20					25					30		
Trp	Val	Pro	Leu	Phe	Gly	Gln	Leu	Phe	Trp	Leu	Ala	Gly	Asn	Val	Leu
		35				40					45				
Ile	Asp	Arg	Gly	Asn	Ala	His	Lys	Ala	Arg	Arg	Ser	Met	Leu	Thr	Thr
	50					55					60				
Thr	His	Thr	Leu	Gln	His	Lys	Asp	Thr	Ser	Ile	Trp	Val	Phe	Ala	Glu
65					70					75					80
Gly	Thr	Arg	Asn	Phe	Gly	Glu	Thr	Leu	Leu	Pro	Phe	Lys	Lys	Gly	Ala
			85					90						95	
Phe	Gln	Met	Ala	Ile	Ala	Ala	Gly	Val	Pro	Ile	Val	Gln	Val	Cys	Val
		100						105						110	
Ser	Thr	Tyr	Val	Lys	His	Met	Lys	Leu	Asn	Arg	Trp	Asp	Ser	Gly	Asp
		115					120					125			
Ile	Leu	Ile	Arg	Ser	Leu	Pro	Pro	Ile	Pro	Thr	Thr	Gly	Leu	Thr	Leu
"	130					135						140			
Asp	Asp	Met	Pro	Arg	Leu	Met	Glu	Thr	Cys	Arg	Gln	Gln	Met	Arg	Glu
145					150					155					160
Cys	Ile	Glu	Ala	Met	Asp	Arg	Glu	Leu	Glu	Ile	Val	Pro	Cys	Arg	Asn
			165					170						175	
Glu	Leu	Ala	Arg	Glu	Gly	Arg									
			180												

<210> 1311

<211> 674

<212> DNA

<213> Homo sapiens

<400> 1311

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 60

tccagggccg acccggcaca caccgtcggg ctgacggatg atctgagctg ggtcaagcgc  
 120  
 atctccccgc cgccgaaagc cggaatacca cgaggcgctg gatcggcgat tctgttcaca  
 180  
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<212> PRT

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<400> 1312

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<212> PRT

<213> Homo sapiens

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Leu	Asn	Ile	Pro	His	Val	Val	Ala	Trp	Ala	Gln	Ile	Pro	Glu	Glu	Thr
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Val	His	Leu	Arg	Met	Lys	Leu	Glu	Glu	Lys	Arg	Arg	Ala	Ile	Glu	Ala
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&lt;210&gt; 1317

&lt;211&gt; 1123

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1317

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<211> 285

<212> PRT

<213> Homo sapiens

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Gly	Glu	Glu	Leu	Asp	Gly	Ser	Asp	Met	Ser	Ala	Ile	Ile	Tyr	Glu	Ile
			100					105					110		
Pro	Lys	Glu	Pro	Glu	Lys	Arg	Arg	Ser	Lys	Arg	Ser	Arg	Val	Met	
	115						120				125				
Asp	Ala	Asp	Gly	Leu	Leu	Glu	Met	Phe	His	Cys	Pro	Tyr	Glu	Gly	Cys
	130					135					140				
Ser	Gln	Val	Tyr	Val	Ala	Leu	Ser	Ser	Phe	Gln	Asn	His	Val	Asn	Leu
145					150					155				160	
Val	His	Arg	Lys	Gly	Lys	Thr	Lys	Val	Cys	Pro	His	Pro	Gly	Cys	Gly
			165						170				175		
Lys	Lys	Phe	Tyr	Leu	Ser	Asn	His	Leu	Arg	Arg	His	Met	Ile	Ile	His
		180						185				190			
Ser	Gly	Val	Arg	Glu	Phe	Thr	Cys	Glu	Thr	Cys	Gly	Lys	Ser	Phe	Lys
	195						200				205				
Arg	Lys	Asn	His	Leu	Glu	Val	His	Arg	Arg	Thr	His	Thr	Gly	Glu	Thr
	210					215					220				
Pro	Leu	Gln	Cys	Val	Ile	Cys	Gly	Tyr	Gln	Cys	Arg	Gln	Arg	Ala	Ser
225					230					235				240	
Leu	Asn	Trp	His	Met	Lys	Lys	His	Thr	Ala	Glu	Val	Gln	Tyr	Asn	Phe
			245						250				255		
Thr	Cys	Asp	Ala	Cys	Gly	Lys	Arg	Phe	Glu	Lys	Leu	Asp	Ser	Val	Lys
		260						265				270			
Phe	His	Thr	Leu	Lys	Ser	His	Pro	Asp	His	Lys	Pro	Thr			
	275						280					285			

&lt;210&gt; 1319

&lt;211&gt; 538

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1319

cgggagcgga gccagctct tggctggtga tgagggcctg gaagcagatg gcctctcagt  
 60  
 cctccatttg ggaggactcc caaaatagtg caggctcgag ggggtgggga atggctcctg  
 120  
 ctgaatgtgt gaatgggtcc ctgggtgctt tccttcctct gggagctccg tgggagagtg  
 180  
 gagtcgatgc caagtcagag agcagttggg gaggaacca gaagccctgg gatggtgtct  
 240  
 gcatgggaat gtgtaggag gcagccacaa tgggcctggg ccttcctttc tctccttct  
 300  
 gtccccctcc cccatcccc tctctctctc ctctcttctg gaaacccagt actgggggaa  
 360  
 acacacacag gtgggatgca ggtatccggg aagctcatag aagctgccac gctgctggag  
 420  
 tttgcctcat acaggagcgt gggcatgccc cgcgtggagt tgtgctgtgt gtgtgcatat  
 480  
 gtatggttgt gtgtgcatgg ggggtgggga ttctgacctg gggtcactcc caaagctt  
 538

&lt;210&gt; 1320

&lt;211&gt; 169

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1320

Met	Arg	Ala	Trp	Lys	Gln	Met	Ala	Ser	Gln	Ser	Ser	Ile	Trp	Glu	Asp
1				5					10					15	
Ser	Gln	Asn	Ser	Ala	Gly	Ser	Arg	Gly	Trp	Gly	Met	Ala	Pro	Ala	Glu
		20					25					30			
Cys	Val	Asn	Gly	Ser	Leu	Gly	Ala	Phe	Leu	Pro	Leu	Gly	Ala	Pro	Trp
		35				40					45				
Glu	Ser	Gly	Val	Asp	Ala	Lys	Ser	Glu	Ser	Ser	Trp	Gly	Gly	Thr	Gln
	50					55				60					
Lys	Pro	Trp	Asp	Gly	Val	Cys	Met	Gly	Met	Cys	Arg	Glu	Ala	Ala	Thr
65					70					75				80	
Met	Gly	Leu	Gly	Leu	Pro	Phe	Ser	Pro	Ser	Cys	Pro	Pro	Pro	Pro	Ser
				85					90					95	
Pro	Ser	Leu	Leu	Pro	Ser	Phe	Trp	Lys	Pro	Ser	Thr	Gly	Gly	Asn	Thr
		100						105					110		
His	Arg	Trp	Asp	Ala	Gly	Ile	Arg	Glu	Ala	His	Arg	Ser	Cys	His	Ala
		115					120					125			
Ala	Gly	Val	Cys	Leu	Ile	Gln	Glu	Arg	Gly	His	Ala	Pro	Arg	Gly	Val
		130				135					140				
Val	Leu	Cys	Val	Cys	Ile	Cys	Met	Val	Val	Cys	Ala	Trp	Gly	Trp	Gly
145					150					155				160	
Ile	Leu	Thr	Trp	Gly	His	Ser	Gln	Ser							
					165										



<210> 1321  
<211> 1292  
<212> DNA  
<213> Homo sapiens

<400> 1321  
nacgcgtacc gtcgctgac tccccctgg tcgtgaccaa cgcggccggg ttcaccatct  
60  
cggaacgcag caatgatccg gcgtcagtc tctcagtcac cgcaggatga cccggtgcaa  
120  
cgccccgata gctcacggta cgcaacgacg aagcagggat cgctcagacc cgggcacgtc  
180  
atcgtcaaga agatttataa caacaatgtc cttctcggcg tcaacgggtc ggggaccgaa  
240  
atggctcgtca atgctcggg tatcgcctac ggacgacacc gcggggagat cgtcgatgcc  
300  
tcgtcggccc agcgatatgt cgcagagggg gcctatcgca cgaccgccat cgcatactg  
360  
ctaacgaacg ccaactcacac cgaggtgcga gtggcacagg caatcgtcga attggcgcgc  
420  
gaagagctgg gcaactccca tgcccagcgg atgatgctgc ccatcctcga tcacctcgtc  
480  
gcagctgtgc accgagctaa gcagggggcc gtcacgatt tccccctgga atgggaagtc  
540  
cgtcagctct atccccgatga ggcggaactg ggccgacgcg ctgtcgaaat cgtcgacggg  
600  
gctctcgaaa tccatttgca acccgaggaa tgggtggcat tctccctgca cttcatcaat  
660  
cagcgggtggg acagtagaga cgtttcggcg accatgtcga tgactcagac gatctgcgac  
720  
gttttcaccg agctggagga cctgtggcac gttgagatcg accgttcgtc catgagcgca  
780  
tcccgtctcg tcaccacact tcgctatctg ttcgctcggg cctcggacaa caagcagctc  
840  
tctcacgttg acctggacat tgtgggactc atgtcagatc gctaccaga agccacattg  
900  
gcagctagcc aagtggcga gcacatctg aaagcaatcg gcaacgacct gacggaagcc  
960  
gaaatcaact acatcgctt acacaccacc cggctctaca acgaggtgat ggggatggat  
1020  
gactgacgat cgcgcacctg ttaaggctca tcggtagtgg gcaatacaca aaatggcgat  
1080  
gaccttctg ccggaagcc agcaccaaag tcaccagat caaaattcag atgcgtgcct  
1140  
aattccacc ccgacatcca agaggtcagg ggggggtgtg tgggggtgtg ggggtggggg  
1200  
gggggggttt gcatgctcag ggggtggggc tttgttgaag ccatcatgaa gttgcaaacc  
1260  
caggactgtt ccaactagtaa agccccctgc tt  
1292

<210> 1322  
<211> 317  
<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1322

```

Met Ile Arg Arg Gln Cys Ser Gln Ser Pro Gln Asp Asp Pro Val Gln
 1           5           10           15
Arg Pro Asp Arg Ser Arg Tyr Ala Thr Thr Lys Gln Gly Ser Leu Arg
      20           25           30
Pro Gly His Val Ile Val Lys Lys Ile Tyr Asn Asn Asn Val Leu Leu
      35           40           45
Gly Val Asn Gly Ser Gly Thr Glu Met Val Val Asn Ala Arg Gly Ile
      50           55           60
Ala Tyr Gly Arg His Arg Gly Glu Ile Val Asp Ala Ser Ser Ala Gln
65           70           75           80
Arg Tyr Val Ala Glu Gly Ala Tyr Arg Thr Thr Ala Ile Ala Ser Leu
      85           90           95
Leu Thr Asn Ala Thr His Thr Glu Val Arg Val Ala Gln Ala Ile Val
      100          105          110
Glu Leu Ala Arg Glu Glu Leu Gly Thr Pro His Ala Arg Arg Met Met
      115          120          125
Leu Pro Ile Leu Asp His Leu Val Ala Ala Val His Arg Ala Lys Gln
      130          135          140
Gly Ala Val Ile Asp Phe Pro Leu Glu Trp Glu Val Arg Gln Leu Tyr
145          150          155          160
Pro Asp Glu Ala Glu Leu Gly Arg Arg Ala Val Glu Ile Val Asp Gly
      165          170          175
Ala Leu Glu Ile His Leu Gln Pro Glu Glu Trp Val Ala Phe Ser Leu
      180          185          190
His Phe Ile Asn Gln Arg Trp Asp Ser Arg Asp Val Ser Arg Thr Met
      195          200          205
Ser Met Thr Gln Thr Ile Cys Asp Val Phe Thr Glu Leu Glu Asp Leu
      210          215          220
Trp His Val Glu Ile Asp Arg Ser Ser Met Ser Ala Ser Arg Phe Val
225          230          235          240
Thr His Leu Arg Tyr Leu Phe Ala Arg Ala Ser Asp Asn Lys Gln Leu
      245          250          255
Ser His Val Asp Leu Asp Ile Val Gly Leu Met Ser Asp Arg Tyr Pro
      260          265          270
Glu Ala Thr Leu Ala Ala Ser Gln Val Ala Glu His Ile Ser Lys Ala
      275          280          285
Ile Gly Asn Asp Leu Thr Glu Ala Glu Ile Asn Tyr Ile Ala Leu His
      290          295          300
Thr Thr Arg Leu Tyr Asn Glu Val Met Gly Met Asp Asp
305          310          315

```

&lt;210&gt; 1323

&lt;211&gt; 306

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1323

```

cgcgtgatgg gaatgcgtca ctatgatgtt cagttgattg gtggtatcac tctgcacgaa
60
ggcaaaattg ctgagatgcy tacaggtgaa ggtaaaaccc tgatgggtac ttttagcgtgt
120

```

tacctcaatg cattgagtg ttaggggtgtg catgtcatca ccgtcaatga ctatcttgca  
 180.  
 caacgtgatg ctgaactcaa ccgcccatta tttgagtttt tgggtttaag catcggtgtg  
 240  
 atttattcga tgcaaatgcc tgctgagaaa gcacaagctt atttagcaga cattaacttac  
 300  
 ggtacc  
 306

<210> 1324  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 1324  
 Arg Val Met Gly Met Arg His Tyr Asp Val Gln Leu Ile Gly Gly Ile  
 1 5 10 15  
 Thr Leu His Glu Gly Lys Ile Ala Glu Met Arg Thr Gly Glu Gly Lys  
 20 25 30  
 Thr Leu Met Gly Thr Leu Ala Cys Tyr Leu Asn Ala Leu Ser Gly Gln  
 35 40 45  
 Gly Val His Val Ile Thr Val Asn Asp Tyr Leu Ala Gln Arg Asp Ala  
 50 55 60  
 Glu Leu Asn Arg Pro Leu Phe Glu Phe Leu Gly Leu Ser Ile Gly Val  
 65 70 75 80  
 Ile Tyr Ser Met Gln Met Pro Ala Glu Lys Ala Gln Ala Tyr Leu Ala  
 85 90 95  
 Asp Ile Thr Tyr Gly Thr  
 100

<210> 1325  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 1325  
 gtgcacatgg gccactggc gaatccgacg cgcggcctac ggcgcgcaat actggcgggc  
 60  
 attgtcgccg catgttccgt ctccgctcat gccggaagct ggccagagaa accgatcacg  
 120  
 atgggtcgtgc cgtttcccg cggaggcggc accgatctcg tggcgcgctc gatccagccg  
 180  
 cttttgcagc gcgaactcgg acaaccggtg gtgatcgaca accgcagcgg cgcaggcggc  
 240  
 acgctcggtt ccagcttcgt ggcgcgggcc gttgccgacg gctacacggc tggcgtggtc  
 300  
 accacgagca cccacgcggt aagcgtcgcg ctctatcccc ggctggccta caaccgaca  
 360  
 gcggactttg catacgccgg cttcatcggc n  
 391

<210> 1326  
 <211> 130  
 <212> PRT

<213> Homo sapiens

<400> 1326

```

Val His Met Gly Pro Leu Ala Asn Pro Thr Arg Gly Leu Arg Arg Ala
 1             5             10             15
Ile Leu Ala Ala Ile Val Ala Ala Cys Ser Val Ser Ala His Ala Gly
      20             25             30
Ser Trp Pro Glu Lys Pro Ile Thr Met Val Val Pro Phe Pro Ala Gly
      35             40             45
Gly Gly Thr Asp Leu Val Ala Arg Ser Ile Gln Pro Leu Leu Gln Arg
      50             55             60
Glu Leu Gly Gln Pro Val Val Ile Asp Asn Arg Ser Gly Ala Gly Gly
65             70             75             80
Thr Leu Gly Ser Ser Phe Val Ala Arg Ala Val Ala Asp Gly Tyr Thr
      85             90             95
Ala Gly Val Val Thr Thr Ser Thr His Ala Val Ser Val Ala Leu Tyr
      100            105            110
Pro Arg Leu Ala Tyr Asn Pro Thr Ala Asp Phe Ala Tyr Ala Gly Phe
      115            120            125
Ile Gly
      130

```

<210> 1327

<211> 324

<212> DNA

<213> Homo sapiens

<400> 1327

```

nnacgcgtga ttccggaact gcagcagttc gagcagtcgc atggacagag cgacgggagc
60
tactggctat ggttcgagct gctgtggcga gactatttcc gctttctgca tcttcggcat
120
ggcgctcggc tgtaccgcgc acgcggcctc gcaaattgagg tacggcacgc ggagcgccca
180
gatgtgcagg gcttcgagcg ctggcgctcg gcatcgaccg gcgagccgct cgtcgatgcc
240
gcgatgcgcg agctggagac caccggctac ctcagcaaca ggctcagaca ggtggtcgcg
300
agctacctcg tgcacgagct ggga
324

```

<210> 1328

<211> 108

<212> PRT

<213> Homo sapiens

<400> 1328

```

Xaa Arg Val Ile Ser Glu Leu Gln Gln Phe Glu Gln Ser His Gly Gln
 1             5             10             15
Ser Asp Gly Ser Tyr Trp Leu Trp Phe Glu Leu Leu Trp Arg Asp Tyr
      20             25             30
Phe Arg Phe Leu His Leu Arg His Gly Ala Arg Leu Tyr Arg Ala Arg
      35             40             45
Gly Leu Ala Asn Glu Val Arg His Ala Glu Arg Pro Asp Val Gln Gly

```

```

      50              55              60
Phe Glu Arg Trp Arg Arg Ala Ser Thr Gly Glu Pro Leu Val Asp Ala
65              70              75              80
Ala Met Arg Glu Leu Glu Thr Thr Gly Tyr Leu Ser Asn Arg Leu Arg
      85              90              95
Gln Val Val Ala Ser Tyr Leu Val His Glu Leu Gly
      100              105

```

<210> 1329  
 <211> 438  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1329
ngtgcacgct tagcattaga tttagcttcc agtggcaaaa ctacgtcggt gatttcaagc
60
ggcgatatcg gcatttacgc gatggcgacc ctggtgtttg aactgctgga tagacaactc
120
cagggccttg aagaccatcc tgaatgggta gatgttgaaa tcgatgtggt acctggcatc
180
tctgcaatgc aagctggtgc aagtcgtatt ggtgcgatgt taggtcatga cttttgtacg
240
gtgagtttgt ctgatttatt aacccttgg gaaactatta ataaacgtat tcatagtgca
300
ggtgaggggg attttgttat ctctttttat aacctgttt ctaagaaacg tgattggcag
360
cttaaccacg cgcgtgatgt attattgaaa taccgtccag catcaacgcc agttttatta
420
ggtcgtcagt tgacgcgt
438

```

<210> 1330  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1330
Xaa Ala Arg Leu Ala Leu Asp Leu Ala Ser Ser Gly Lys Thr Thr Ser
1      5      10      15
Leu Ile Ser Ser Gly Asp Ile Gly Ile Tyr Ala Met Ala Thr Leu Val
      20      25      30
Phe Glu Leu Leu Asp Arg Gln Leu Gln Gly Leu Glu Asp His Pro Glu
      35      40      45
Trp Leu Asp Val Glu Ile Asp Val Val Pro Gly Ile Ser Ala Met Gln
      50      55      60
Ala Gly Ala Ser Arg Ile Gly Ala Met Leu Gly His Asp Phe Cys Thr
65      70      75      80
Val Ser Leu Ser Asp Leu Leu Thr Pro Trp Glu Thr Ile Asn Lys Arg
      85      90      95
Ile His Ser Ala Gly Glu Gly Asp Phe Val Ile Ser Phe Tyr Asn Pro
      100     105     110
Val Ser Lys Lys Arg Asp Trp Gln Leu Asn His Ala Arg Asp Val Leu
      115     120     125
Leu Lys Tyr Arg Pro Ala Ser Thr Pro Val Leu Leu Gly Arg Gln Leu

```

130  
 Thr Arg  
 145

135  
 140

<210> 1331  
 <211> 453  
 <212> DNA  
 <213> Homo sapiens

<400> 1331  
 gcgtaccgct ccgcggaact ggtgatgatg accgaggcac cgggatgcgg aatccccctgg  
 60  
 catcttcttg ccggcatcgg acgcatcgaa tccgggtcacg ccaacggcgg caagacgacc  
 120  
 tcggtgggta cgaacgtcac cccgatcctc ggccccatcc tcgacggacg gctggcaggc  
 180  
 aacgaagtca ttcgggacac cgacaagggc aatcgacggc gacccactca cgaccgcgcc  
 240  
 gtcggggcga tgcagttcat tccggccacc tgggcccggat atgccagcga cggcaacggg  
 300  
 gacggaatca aggaccccaa caacgtcttc gatgcggcac tctcggcagc gaagtacctc  
 360  
 tgcagcggcg gactcaacct gcgcgatgtc gcccaggaga ccaaagctgt tctgcgatac  
 420  
 aacaactcgg ccgcttacgc agcaaacgtg atc  
 453

<210> 1332  
 <211> 151  
 <212> PRT  
 <213> Homo sapiens

<400> 1332  
 Ala Tyr Arg Ser Ala Glu Leu Val Met Met Thr Glu Ala Pro Gly Cys  
 1 5 10 15  
 Gly Ile Pro Trp His Leu Leu Ala Gly Ile Gly Arg Ile Glu Ser Gly  
 20 25 30  
 His Ala Asn Gly Gly Lys Thr Thr Ser Val Gly Thr Asn Val Thr Pro  
 35 40 45  
 Ile Leu Gly Pro Ile Leu Asp Gly Arg Leu Ala Gly Asn Glu Val Ile  
 50 55 60  
 Arg Asp Thr Asp Lys Gly Asn Arg Arg Arg Pro Thr His Asp Arg Ala  
 65 70 75 80  
 Val Gly Pro Met Gln Phe Ile Pro Ala Thr Trp Ala Gly Tyr Ala Ser  
 85 90 95  
 Asp Gly Asn Gly Asp Gly Ile Lys Asp Pro Asn Asn Val Phe Asp Ala  
 100 105 110  
 Ala Leu Ser Ala Ala Lys Tyr Leu Cys Ser Gly Gly Leu Asn Leu Arg  
 115 120 125  
 Asp Val Ala Gln Glu Thr Lys Ala Val Leu Arg Tyr Asn Asn Ser Ala  
 130 135 140  
 Ala Tyr Ala Ala Asn Val Ile  
 145 150

<210> 1333  
 <211> 540  
 <212> DNA  
 <213> Homo sapiens

<400> 1333  
 acgcgtcgcc cacactgttg ccgccgaggc ggctcgagcc ggggtgtgagg aaggatccgc  
 60  
 ggcacagctc gtcgggtcaag atgggtctag tgctgctcgt atggcgggcg aggcacccgc  
 120  
 gcgaagggct aaagcggatg gactaagcca gcttgtcatc gatgtcaatg gagacgccgt  
 180  
 cagcgtcgcg acggaaatca cccggcctac tcgtctatta gcccttattg gactaaccga  
 240  
 agtacacggg cgggcgagcg aaatgtgtat ttgtctggct cgctgaggcc gttgcagcga  
 300  
 tacaatgatg aggtgtctaa gtattttccg gtccaccgag agaaccgcga gcagcgttct  
 360  
 ctcaatcaga tcgtcgacat cctgcaccat ggcggtctta tcgcctaccc gacagacacg  
 420  
 ggttatgcct tcggtgcccg gntagggaat aaggatgccg tggaccggat tcgcaaactt  
 480  
 cgccagttat ttgacaagca tcacttcacc ctggtcatga gccagtttgc gcaggttggc  
 540

<210> 1334  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

<400> 1334  
 Val His Pro Glu Asn Pro Gln Gln Arg Ser Leu Asn Gln Ile Val Asp  
 1 5 10 15  
 Ile Leu His His Gly Gly Leu Ile Ala Tyr Pro Thr Asp Thr Gly Tyr  
 20 25 30  
 Ala Phe Gly Ala Arg Xaa Gly Asn Lys Asp Ala Val Asp Arg Ile Arg  
 35 40 45  
 Lys Leu Arg Gln Leu Phe Asp Lys His His Phe Thr Leu Val Met Ser  
 50 55 60  
 Gln Phe Ala Gln Val Gly  
 65 70

<210> 1335  
 <211> 748  
 <212> DNA  
 <213> Homo sapiens

<400> 1335  
 nctctcatatc tttttttccc tattcctatc ccccctctct ccgaccgcgt gaagcgttct  
 60  
 gtgaatgccca agaagaagcg tcgtgaggtc ctcgatcagg cctccggtta ccgtgggtcag  
 120  
 cgctcgcgcc tgtaccgcaa ggccaaggag cagaccctcc attcggccac ttattcgttc  
 180

cgtgaccgtc gtgctaagaa gggtagcttc cgctcgctgt ggatccagcg catcaatgct  
 240  
 gcttcccgtg cccagggcat gacctacaac cgtttcatca acgggtctgaa gaacgctggc  
 300  
 gtcgaggtcg accgcaagat gctcgctgag cttgccgtct ccgacattaa cgccttcaac  
 360  
 agcctggctg aggtcgctaa ggctagccag ccgcagaacg ctgctgcctg agatggccat  
 420  
 gactggcggg ccgaacgacg actatttggg atgggatcgc atctcgaagg ggtcattgcg  
 480  
 ttcggcccgt cgttttcat ctcggcgcgg acgcgatgag tccgggctgt tcttggtaga  
 540  
 aggtgcgcag gcagttcgtg aagccctagc atggccgggt aaagtcaatt tgttggaac  
 600  
 ctcggaacca gctcgcatg ctgagcatgt cgagggtggct acatgctgtg gcgttcgggt  
 660  
 cgtggtgctc actgacgagg atgtcaatgc gctttctgat accgtcacca gtcaggggat  
 720  
 cttcgcggta tgcggcagg ttacgcgt  
 748

<210> 1336

<211> 136

<212> PRT

<213> Homo sapiens

<400> 1336

Xaa	Leu	Ile	Leu	Phe	Phe	Pro	Ile	Pro	Ile	Pro	Pro	Leu	Ser	Asp	Arg
1				5					10					15	
Val	Lys	Arg	Ser	Val	Asn	Ala	Lys	Lys	Lys	Arg	Arg	Glu	Val	Leu	Asp
			20					25					30		
Gln	Ala	Ser	Gly	Tyr	Arg	Gly	Gln	Arg	Ser	Arg	Leu	Tyr	Arg	Lys	Ala
	35					40					45				
Lys	Glu	Gln	Thr	Leu	His	Ser	Ala	Thr	Tyr	Ser	Phe	Arg	Asp	Arg	Arg
	50					55					60				
Ala	Lys	Lys	Gly	Asp	Phe	Arg	Ser	Leu	Trp	Ile	Gln	Arg	Ile	Asn	Ala
65				70					75				80		
Ala	Ser	Arg	Ala	Gln	Gly	Met	Thr	Tyr	Asn	Arg	Phe	Ile	Asn	Gly	Leu
			85					90					95		
Lys	Asn	Ala	Gly	Val	Glu	Val	Asp	Arg	Lys	Met	Leu	Ala	Glu	Leu	Ala
	100							105				110			
Val	Ser	Asp	Ile	Asn	Ala	Phe	Asn	Ser	Leu	Val	Glu	Val	Ala	Lys	Ala
	115						120					125			
Ser	Gln	Pro	Gln	Asn	Ala	Ala	Ala								
	130					135									

<210> 1337

<211> 364

<212> DNA

<213> Homo sapiens

<400> 1337

acgcgtgagg ccaggccact gggcaccgcc gttagccagg gcagcctcct tcagtgggtca  
 60



aggcagactc agctcatggg cgagcatgtc agtgaagggc acagcaaggc tcacgagtgg  
 120  
 gcctcttgcc tcatggtcag tgtgggtcag tgctttcgct gtatgagact acaggggttc  
 180  
 tctgcctcac catgggggac gattgggtct gggtcacttc ctgctgtggg acctgtcctg  
 240  
 ggcaactgcag gatgtggggc agggctccta cgtgccagct accagatgcc agcagcaccc  
 300  
 ccagaagtga caaccacaac catctccagg tgttgccagt gtcccctggg ggtcagagtg  
 360  
 gccc  
 364

<210> 1338

<211> 96

<212> PRT

<213> Homo sapiens

<400> 1338

Met	Gly	Glu	His	Val	Ser	Glu	Gly	His	Ser	Lys	Ala	His	Glu	Trp	Ala
1				5					10				15		
Ser	Cys	Leu	Met	Val	Ser	Val	Gly	Gln	Cys	Phe	Arg	Cys	Met	Arg	Leu
		20						25				30			
Gln	Gly	Phe	Ser	Ala	Ser	Pro	Trp	Gly	Thr	Ile	Gly	Ser	Gly	Ser	Leu
	35						40				45				
Pro	Ala	Val	Gly	Pro	Val	Leu	Gly	Thr	Ala	Gly	Cys	Gly	Ala	Gly	Leu
	50					55				60					
Leu	Arg	Ala	Ser	Tyr	Gln	Met	Pro	Ala	Ala	Pro	Pro	Glu	Val	Thr	Thr
65					70					75				80	
Thr	Thr	Ile	Ser	Arg	Cys	Cys	Gln	Cys	Pro	Leu	Gly	Val	Arg	Val	Ala
			85						90					95	

<210> 1339

<211> 653

<212> DNA

<213> Homo sapiens

<400> 1339

cgcggtgtct tcaacatcga cgaaaagcag tgcattgacc tggcgacccg tgggtactgag  
 60  
 tgggtcgtca ggtacgccga caagtacctc ggcgacgttg agttcggcta cgagtactct  
 120  
 ccggagatgt ttagccagac ccgcacggac ttcgctatcg acgtctgtca ctccgtgat  
 180  
 gacgtgtggc agccggggcc aggcctgag attatcctta atctgccggc taccgtcgag  
 240  
 atgagtactc cgaacaccta cgccgaccaa atcgagtact tctgccgcaa tatccgtgat  
 300  
 cgtgagcacg tgtgcgtctc tttgcacccg cacaatgac gtggcacggc gatcgcgggc  
 360  
 gccgagttcg cgcatatggc gggcgccgat cgcgtcgagg gctgtttctt tggccccggc  
 420  
 gagcgcccgg gcaccgtcga cctgggtcacc ctgggcatga acctcgtcag ccagggagtt  
 480

gacgcggta tcgacttctc cgacatgccc aagatccgcc gcaccgtcga gtactgcacc  
 540  
 tgtctgccag taccggcccg ccagccctac tccggcgatc tggctctcac cgccttctcc  
 600  
 ggttcccacc aggacgcat caagaagggt ctggaagacc tggcccggcg cgc  
 653

<210> 1340  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 1340  
 Arg Val Val Phe Asn Ile Asp Glu Lys Gln Cys Ile Asp Leu Ala His  
 1 5 10 15  
 Arg Gly Thr Glu Trp Val Val Arg Tyr Ala Asp Lys Tyr Leu Gly Asp  
 20 25 30  
 Val Glu Phe Gly Tyr Glu Tyr Ser Pro Glu Met Phe Ser Gln Thr Arg  
 35 40 45  
 Thr Asp Phe Ala Ile Asp Val Cys His Ser Val Met Asp Val Trp Gln  
 50 55 60  
 Pro Gly Pro Gly Arg Glu Ile Ile Leu Asn Leu Pro Ala Thr Val Glu  
 65 70 75 80  
 Met Ser Thr Pro Asn Thr Tyr Ala Asp Gln Ile Glu Tyr Phe Cys Arg  
 85 90 95  
 Asn Ile Arg Asp Arg Glu His Val Cys Val Ser Leu His Pro His Asn  
 100 105 110  
 Asp Arg Gly Thr Ala Ile Ala Ala Glu Phe Ala Gln Met Ala Gly  
 115 120 125  
 Ala Asp Arg Val Glu Gly Cys Phe Phe Gly Pro Gly Glu Arg Pro Gly  
 130 135 140  
 Thr Val Asp Leu Val Thr Leu Gly Met Asn Leu Val Ser Gln Gly Val  
 145 150 155 160  
 Asp Ala Gly Ile Asp Phe Ser Asp Met Pro Lys Ile Arg Arg Thr Val  
 165 170 175  
 Glu Tyr Cys Thr Cys Leu Pro Val Pro Ala Arg Gln Pro Tyr Ser Gly  
 180 185 190  
 Asp Leu Val Phe Thr Ala Phe Ser Gly Ser His Gln Asp Ala Ile Lys  
 195 200 205  
 Lys Gly Leu Glu Asp Leu Ala Arg Arg  
 210 215

<210> 1341  
 <211> 666  
 <212> DNA  
 <213> Homo sapiens

<400> 1341  
 accggttgct gatttccttg ttggagtctt caccactatg agcagtgact ccattgtttt  
 60  
 gcaaagtttc ttgccttgct ttgatcatat tttcacaact ggattcccaa cagaagtgtg  
 120  
 gcaatctgta atagaaaagt tggcaaagaa aggattatgg cattcatttc tgcttctgtc  
 180

agcaaaaaaa gaccgattac caagaaatat tcatgtccca gagttatcac tgaaaagtct  
 240  
 ctttgagaaa tacgttttca ttggacttta tgagaagatg gaacaagtgc ccaagttagt  
 300  
 ccagtggctc atctccattg gtgcaagtgt tgagactata ggaccgtatc cccttcattg  
 360  
 cctcatgcga ctctgtatcc aagccagaga aaaccatctt ttccggtggt taatggatca  
 420  
 caagcccagag tggaaaggcc gcattaacca gaaggatggg gatggctgca ctgtcctgca  
 480  
 cgctcgtcgt gccactccc caggatacct cgtaaagcga caaacagagg atgtgcagat  
 540  
 gctcctgcgc tttggggcag atcccacttt gctggatcga cagtctcggt ctgttgtaga  
 600  
 tgtcctgaag aggaataaga acttcaaagc catcgagaaa atcaacagtc acttagaaaa  
 660  
 gctagc  
 666

<210> 1342

<211> 209

<212> PRT

<213> Homo sapiens

<400> 1342

Met	Ser	Ser	Asp	Ser	Ile	Val	Leu	Gln	Ser	Phe	Leu	Pro	Cys	Phe	Asp
1				5					10					15	
His	Ile	Phe	Thr	Thr	Gly	Phe	Pro	Thr	Glu	Val	Trp	Gln	Ser	Val	Ile
			20					25				30			
Glu	Lys	Leu	Ala	Lys	Lys	Gly	Leu	Trp	His	Ser	Phe	Leu	Leu	Leu	Ser
		35					40					45			
Ala	Lys	Lys	Asp	Arg	Leu	Pro	Arg	Asn	Ile	His	Val	Pro	Glu	Leu	Ser
		50				55					60				
Leu	Lys	Ser	Leu	Phe	Glu	Lys	Tyr	Val	Phe	Ile	Gly	Leu	Tyr	Glu	Lys
65					70					75				80	
Met	Glu	Gln	Val	Pro	Lys	Leu	Val	Gln	Trp	Leu	Ile	Ser	Ile	Gly	Ala
				85					90					95	
Ser	Val	Glu	Thr	Ile	Gly	Pro	Tyr	Pro	Leu	His	Ala	Leu	Met	Arg	Leu
			100					105					110		
Cys	Ile	Gln	Ala	Arg	Glu	Asn	His	Leu	Phe	Arg	Trp	Leu	Met	Asp	His
			115				120					125			
Lys	Pro	Glu	Trp	Lys	Gly	Arg	Ile	Asn	Gln	Lys	Asp	Gly	Asp	Gly	Cys
		130				135					140				
Thr	Val	Leu	His	Val	Val	Ala	Ala	His	Ser	Pro	Gly	Tyr	Leu	Val	Lys
145					150					155				160	
Arg	Gln	Thr	Glu	Asp	Val	Gln	Met	Leu	Leu	Arg	Phe	Gly	Ala	Asp	Pro
				165					170					175	
Thr	Leu	Leu	Asp	Arg	Gln	Ser	Arg	Ser	Val	Val	Asp	Val	Leu	Lys	Arg
			180				185						190		
Asn	Lys	Asn	Phe	Lys	Ala	Ile	Glu	Lys	Ile	Asn	Ser	His	Leu	Glu	Lys
		195					200						205		
Leu															

&lt;210&gt; 1343

&lt;211&gt; 270

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1343

ccggaaatgt gccgagttct cctgacgcac gaagtgatgt gtagtcgatg ctgcgaaaag  
60  
aaaagctgtg gaaaccgaaa tgagactcca tcggacccag tcataattga cagattcttt  
120  
ttaaaatttt tcctcaagtg caatcagaat tgtttgaaaa cagcaggaaa cccaagggac  
180  
atgagacggt ttcaggttgt gttgtcaaca acggtgaatg tggatggaca cgctcctggct  
240  
gtttctgaca acatgtttgt tcataacaac  
270

&lt;210&gt; 1344

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1344

Pro	Glu	Met	Cys	Arg	Val	Leu	Leu	Thr	His	Glu	Val	Met	Cys	Ser	Arg
1				5					10					15	
Cys	Cys	Glu	Lys	Lys	Ser	Cys	Gly	Asn	Arg	Asn	Glu	Thr	Pro	Ser	Asp
			20					25					30		
Pro	Val	Ile	Ile	Asp	Arg	Phe	Phe	Leu	Lys	Phe	Phe	Leu	Lys	Cys	Asn
		35				40					45				
Gln	Asn	Cys	Leu	Lys	Thr	Ala	Gly	Asn	Pro	Arg	Asp	Met	Arg	Arg	Phe
	50				55					60					
Gln	Val	Val	Leu	Ser	Thr	Val	Val	Asn	Val	Asp	Gly	His	Val	Leu	Ala
65				70				75						80	
Val	Ser	Asp	Asn	Met	Phe	Val	His	Asn	Asn						
			85					90							

&lt;210&gt; 1345

&lt;211&gt; 402

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1345

acgcgtttga aaccacccga tgacttgctg gtgatacctgg gtacccgcgt cagcaacttc  
60  
agcggcaccg acaacaccga cttctacgac ccgaccaagg ccgacaaccg tctcacctac  
120  
cgccagacgg gcgtcgtcac gccctatgcc ggcatacgtct acgacctgaa tgacatctgg  
180  
tcggtgtaca ccagctacac caagatctac aagccgcaga acagcaagga cgccgaccgc  
240  
aagttgctcg atccgattga aggtgacacc tacgaagccg ggctcaaggc agcgtttttc  
300  
gacggccgcc tgaacgccag ttttgccgca ttccgcatcg aacaggacaa cgtcgcacag  
360

tacggtttccg ggtttgagac cgactcgtgt atcgccatt gc  
402

<210> 1346

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1346

Thr Arg Leu Lys Pro Thr Asp Asp Leu Ser Val Ile Leu Gly Thr Arg  
1 5 10 15  
Val Ser Asn Phe Ser Gly Thr Asp Asn Thr Asp Phe Tyr Asp Pro Thr  
20 25 30  
Lys Ala Asp Asn Arg Leu Thr Tyr Arg Gln Thr Gly Val Val Thr Pro  
35 40 45  
Tyr Ala Gly Ile Val Tyr Asp Leu Asn Asp Ile Trp Ser Val Tyr Thr  
50 55 60  
Ser Tyr Thr Lys Ile Tyr Lys Pro Gln Asn Ser Lys Asp Ala Asp Arg  
65 70 75 80  
Lys Leu Leu Asp Pro Ile Glu Gly Asp Thr Tyr Glu Ala Gly Leu Lys  
85 90 95  
Ala Ala Phe Phe Asp Gly Arg Leu Asn Ala Ser Phe Ala Ala Phe Arg  
100 105 110  
Ile Glu Gln Asp Asn Val Ala Gln Tyr Val Ser Gly Phe Glu Thr Asp  
115 120 125  
Ser Cys Ile Ala His Cys  
130

<210> 1347

<211> 415

<212> DNA

<213> Homo sapiens

<400> 1347

naccaccttc tgggcaggct ctcattcttt cattccaaga agcattttatt aaagactggc  
60  
tagggcgagg gaaccagct aggggctggg gataaaaaat aagaaataac tgaaggacct  
120  
tgctcttaag gaactccatc ttactgggtg gagccaaacg agaaaagaga gctcgggagg  
180  
gcaccaaagc ggtcttgccg aaattgcctg aggcagggga aggggcacgc tttctgaaaa  
240  
acccccccaa accgattcca ggaagcccaa agggcggccc ctctgcccgc agcactgcct  
300  
tcacgtttac ttccatcccg gctcctcct tcccctaagg cttggcatgc aacatccctg  
360  
cttctcacc acccttttatt taagactcct attatctgca cacaatggaa gtttag  
415

<210> 1348

<211> 105

<212> PRT

<213> Homo sapiens

&lt;400&gt; 1348

Met Glu Val Asn Val Lys Ala Val Leu Arg Ala Glu Gly Pro Pro Phe  
 1 5 10 15  
 Gly Leu Pro Gly Ile Gly Leu Gly Gly Phe Phe Arg Lys Arg Ala Pro  
 20 25 30  
 Ser Pro Ala Ser Gly Asn Phe Gly Lys Thr Ala Leu Val Pro Ser Arg  
 35 40 45  
 Ala Leu Phe Ser Arg Leu Ala Pro Pro Ser Lys Met Glu Phe Leu Lys  
 50 55 60  
 Ser Lys Val Leu Gln Leu Phe Leu Ile Phe Tyr Pro Gln Pro Leu Ala  
 65 70 75 80  
 Gly Phe Pro Arg Pro Ser Gln Ser Leu Ile Asn Ala Ser Trp Asn Glu  
 85 90 95  
 Arg Met Arg Ala Cys Pro Glu Gly Gly  
 100 105

&lt;210&gt; 1349

&lt;211&gt; 924

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1349

gccgggacgc tcacaccaca gcaggctcgcg ttaccccatg acgtcttccg tgagcttggc  
 60  
 gctcagacgcg tcatgcgttc gatcgccgaa aagcttggcc ttccggtcat cgtaagccg  
 120  
 gcacgtgggg gctcaagcct cggcgtcaca aaagtcgatg gcgtcgacga tcttctcag  
 180  
 gccgtcgcca acgcctatgc ctatgacgac atggtttag tagaggaatt cattgtgggc  
 240  
 aacgaactcg caataggcat gatcacgacg tctgaaggca cgcgtgtgct gccagccgc  
 300  
 gagattcgcc ctgtcgggtg tgtttatgat tattcagca tgtacaccg tggtagaca  
 360  
 cgactaacag ctctgcaga cattagcgat acggcgccc aaaccgcgac ggcgatggc  
 420  
 cgagtcgtgc aaaaggagct cgatttctcc gggatatctc gtgtcgatgc gatcgtggc  
 480  
 gagtccggtc gcccagtttt cttggaggcc ggtgctgctc ccgggatgac agctacttcg  
 540  
 ctcgtagccg tggctatgaa agctgccggt ctagacctg gcgaggtgtg ctctcgacta  
 600  
 gtcgatgacg tcgtcgcaa ccatggctga cagtgtgcac acgaggggct cgcgccacgc  
 660  
 cgtgcgcgtc aagcaggcat ctgtcgtctt gtcggcgctc gtccttgcca gtgtgatgg  
 720  
 ctctctcgga ctgtggcaga tgaacgtttt tgagtccaa cgtgacgact cgacgcaggc  
 780  
 gcgtatcaac gagccagtga tcacctgga tgaggcgctt aagaaggcca gtgtcatggc  
 840  
 tcagtacgga cgcggggtga cggtagcggg cacgttccaa ccgtcgacca caaccttgat  
 900  
 aggcacatcg tggccagtac gcgt  
 924

<210> 1350  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 1350  
 Ala Gly Ile Val Thr Pro Gln Gln Val Ala Leu Pro His Asp Val Phe  
 1 5 10 15  
 Arg Glu Leu Gly Ala Gln Thr Val Met Arg Ser Ile Ala Glu Lys Leu  
 20 25 30  
 Gly Leu Pro Val Ile Val Lys Pro Ala Arg Gly Gly Ser Ser Leu Gly  
 35 40 45  
 Val Thr Lys Val Asp Gly Val Asp Asp Leu Pro Gln Ala Val Ala Asn  
 50 55 60  
 Ala Tyr Ala Tyr Asp Asp Met Val Val Val Glu Glu Phe Ile Val Gly  
 65 70 75 80  
 Asn Glu Leu Ala Ile Gly Met Ile Thr Thr Ser Glu Gly Thr Arg Val  
 85 90 95  
 Leu Pro Ala Val Glu Ile Arg Pro Val Gly Gly Val Tyr Asp Tyr Ser  
 100 105 110  
 Ala Met Tyr Thr Gly Gly Glu Thr Arg Leu Thr Ala Pro Ala Asp Ile  
 115 120 125  
 Ser Asp Thr Ala Ala Gln Thr Ala Thr Ala Met Ala Arg Val Val Gln  
 130 135 140  
 Lys Glu Leu Asp Phe Ser Gly Ile Ser Arg Val Asp Ala Ile Val Asp  
 145 150 155 160  
 Glu Ser Gly Arg Pro Val Phe Leu Glu Ala Gly Ala Ala Pro Gly Met  
 165 170 175  
 Thr Ala Thr Ser Leu Val Pro Val Ala Met Lys Ala Ala Gly Leu Asp  
 180 185 190  
 Leu Gly Glu Val Cys Ser Arg Leu Val Asp Asp Val Ala Arg Asn His  
 195 200 205  
 Gly

<210> 1351  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens

<400> 1351  
 nngtgcacgg agggcgtgct ggtctacgcc ctgtatctgc tgtctcgatg cacgatgggc  
 60  
 gacgagacgc aaaacgcatt gcttctcagt attctgctgc accccgggtct gctcatcgtc  
 120  
 gaccacattc acttccagta caacgggttc ctaattcgcg ggccccttta tcgtttgggg  
 180  
 gcccgacacg acgcatcggc cctctttctc tgaaccgcc tgtttgcttc gctgctccag  
 240  
 ttcaagcaca ttacgtata cgtcgcgccg gcgtactttg tgtacctgct gcgtgcgtac  
 300  
 atgctccccg gcatgccgac gtccgcatcg acggggagcg cggcgatcga tcgcaccatc  
 360

aagcttggcg cagcgacgct ggtgccttcc tgctgagc  
398

<210> 1352  
<211> 70  
<212> PRT  
<213> Homo sapiens

<400> 1352  
Xaa Cys Thr Glu Gly Val Leu Val Tyr Ala Leu Tyr Leu Leu Ser Arg  
1 5 10 15  
Cys Thr Met Gly Asp Glu Thr Gln Asn Ala Leu Leu Leu Ser Ile Leu  
20 25 30  
Leu His Pro Gly Leu Leu Ile Val Asp His Ile His Phe Gln Tyr Asn  
35 40 45  
Gly Phe Leu Ile Arg Gly Pro Leu Tyr Arg Leu Gly Ala Arg Thr Asp  
50 55 60  
Ala Ser Ala Leu Phe Leu  
65 70

<210> 1353  
<211> 480  
<212> DNA  
<213> Homo sapiens

<400> 1353  
ngggcccca tccctagcct agggcctgga ggtcccctga gtttgctcag ccaactcatt  
60  
accctcacac ccaccccacc ccagtcaca cggatcgtgc ggggcattgg acagcctcgg  
120  
ggcaacatgc tcctggtggg tatcgggggc agcggacgcc agagtctggc ccgcctggct  
180  
tcattccatct gcgactacac caccttccag atcgagggtca ccaaactta tcggaagcag  
240  
gagttccgag atgatataaa gcgtctgtat cgccaggctg ggggtggagct caagaccacg  
300  
tccttcattt ttgtggacac ccaaatagct gatgagtcct tcctagagga catcaacaac  
360  
atcctcagct caggcgaggt gcccacatt ttcaggcctg atgaattga agagatccag  
420  
tcgcatatca tagaccaggc ccgggtggag caggtgcctg agtcacgga cagcctcttc  
480

<210> 1354  
<211> 160  
<212> PRT  
<213> Homo sapiens

<400> 1354  
Xaa Ala Pro Ile Pro Ser Leu Gly Pro Gly Gly Pro Leu Ser Leu Leu  
1 5 10 15  
Ser Gln Leu Ile Thr Leu Thr Pro Thr Pro Pro Val Thr Arg Ile  
20 25 30  
Val Arg Gly Ile Gly Gln Pro Arg Gly Asn Met Leu Leu Val Gly Ile



1154

agggtgggcc gctgttttgc caacccaac ttccaaggca cccattgtga gctctgcgcg  
 1020  
 ccagggttct acggccccgg ctgccctggg tcccttcacg cgt  
 1063

<210> 1356  
 <211> 244  
 <212> PRT  
 <213> Homo sapiens

<400> 1356  
 Ala Pro Ala Thr Cys Leu Gln Asp Gly Pro Asp Pro Pro Ser Cys Val  
 1 5 10 15  
 Pro His Arg Leu Gln Cys Thr Cys Gln His Asn Thr Cys Gly Gly Thr  
 20 25 30  
 Cys Asp Arg Cys Cys Pro Gly Phe Asn Gln Gln Pro Trp Lys Pro Ala  
 35 40 45  
 Thr Ala Asn Ser Ala Asn Glu Cys Gln Ser Cys Asn Cys Tyr Gly His  
 50 55 60  
 Ala Thr Asp Cys Tyr Tyr Asp Pro Glu Val Asp Arg Arg Arg Ala Ser  
 65 70 75 80  
 Gln Ser Leu Asp Gly Thr Tyr Gln Gly Gly Val Cys Ile Asp Cys  
 85 90 95  
 Gln His His Thr Ala Gly Val Asn Cys Glu Arg Cys Leu Pro Gly Phe  
 100 105 110  
 Tyr Arg Ser Pro Asn His Pro Leu Asp Ser Pro His Val Cys Arg Arg  
 115 120 125  
 Cys Asn Cys Glu Ser Asp Phe Thr Asp Gly Thr Cys Glu Asp Leu Thr  
 130 135 140  
 Gly Arg Cys Tyr Cys Arg Pro Asn Phe Ser Gly Glu Arg Cys Asp Val  
 145 150 155 160  
 Cys Ala Glu Gly Phe Thr Gly Phe Pro Ser Cys Tyr Pro Thr Pro Ser  
 165 170 175  
 Ser Ser Asn Asp Thr Arg Glu Gln Val Leu Pro Ala Gly Gln Ile Val  
 180 185 190  
 Asn Cys Asp Cys Ser Ala Ala Gly Thr Gln Gly Asn Ala Cys Arg Lys  
 195 200 205  
 Asp Pro Arg Val Gly Arg Cys Phe Ala Asn Pro Asn Phe Gln Gly Thr  
 210 215 220  
 His Cys Glu Leu Cys Ala Pro Gly Phe Tyr Gly Pro Gly Cys Pro Gly  
 225 230 235 240  
 Ser Leu His Ala

<210> 1357  
 <211> 663  
 <212> DNA  
 <213> Homo sapiens

<400> 1357  
 ntcccccccc ccccgggggg gggggggggg ggaaacaaca ccagaaaagt agacagatac  
 60  
 ccaagttagt ccagctggtc catatacggc cccaggtgcg gattcggtac cgaagttgaa  
 120

ttcaacacccc ccgttttgcc tgtggggggg gtacgccctg taatcctgca aaggcccggg  
 180  
 tgggtgtccgg gggttttcgt cggctcctccc aaccatcatc tagacggcgt ggcgatgtgg  
 240  
 tgcgagctgc ttgcggcggg gttctgtgcc cgagcttgcc tcgcctggct gcaagaatcc  
 300  
 ctggctcatc gagcttcagc gtcagtcaag tcgcaattgc ggcgcgacat cctgcaagcc  
 360  
 aggttgctgc gtcccaactga cgcaacaatg ccgtcgagaa cctcatcag cctgatgaca  
 420  
 acaggtctgg acgccctcga cggctactac tcgaagtacc ttcccagct tgtgctggcc  
 480  
 gtcacgtgct cagcagtgtc agccaccgct atcggcctaa acgacctcac cagcctcgtc  
 540  
 atcgtcgtcg tgacgatccc gtcacatccc gttttcatgg cctcattgg ctggcggacc  
 600  
 gaggcggccg tagcaaaacg gttcaaggta gccacccgac tggccaacca cttcgtgat  
 660  
 ctg  
 663

&lt;210&gt; 1358

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1358

Xaa Pro Pro Pro Gly Gly Gly Gly Gly Asn Asn Thr Arg Lys  
 1 5 10 15  
 Val Asp Arg Tyr Pro Ser Trp Ser Ser Trp Ser Ile Tyr Gly Pro Arg  
 20 25 30  
 Cys Gly Phe Gly Thr Glu Val Glu Phe Asn Thr Pro Val Leu Pro Val  
 35 40 45  
 Gly Gly Val Arg Pro Val Ile Leu Gln Arg Pro Gly Trp Cys Pro Gly  
 50 55 60  
 Val Phe Val Gly Leu Pro Asn His His Leu Asp Gly Val Ala Met Trp  
 65 70 75 80  
 Cys Glu Leu Leu Ala Ala Val Phe Cys Ala Arg Ala Cys Leu Ala Trp  
 85 90 95  
 Leu Gln Glu Ser Leu Ala His Arg Ala Ser Ala Ser Val Lys Ser Gln  
 100 105 110  
 Leu Arg Arg Asp Ile Leu Gln Ala Arg Leu Ser Arg Pro Thr Asp Ala  
 115 120 125  
 Thr Met Pro Ser Arg Thr Leu Ile Ser Leu Met Thr Thr Gly Leu Asp  
 130 135 140  
 Ala Leu Asp Gly Tyr Tyr Ser Lys Tyr Leu Pro Gln Leu Val Leu Ala  
 145 150 155 160  
 Val Ile Val Pro Ala Val Leu Ala Thr Ala Ile Gly Leu Asn Asp Leu  
 165 170 175  
 Thr Ser Leu Val Ile Val Val Val Thr Ile Pro Leu Ile Pro Val Phe  
 180 185 190  
 Met Ala Leu Ile Gly Trp Arg Thr Glu Ala Ala Val Ala Lys Arg Phe  
 195 200 205  
 Lys Val Ala Thr Arg Leu Ala Asn His Phe Ala Asp Leu

210 215 220

<210> 1359  
 <211> 423  
 <212> DNA  
 <213> Homo sapiens

<400> 1359  
 acgcgtattc ctctgttttg acctgcgctc ttacatctgt actaagacct tgtttttgca  
 60  
 tgataaagtt ccaagactcc aaaatgtcac atgggtgtacg agaaacaaaa ggttgtttgt  
 120  
 ctatttgctt aatagataga gaggtgtagt cagctagcca atagccgact ggcacgcga  
 180  
 cgacgtaatc gtcttcccat aaagggtaaa atacatcatc ttctttggtg taactgtcgc  
 240  
 aagtaaagcg taaatcagcg ctttctgagg catcgactaa actgagtgtg agtcttgga  
 300  
 tategtcgag catggttttg atcacttgac taatcagggt gccagataga aaagggtgcta  
 360  
 atgaaataga cagcgccagg ttgcgcggtt ttacgaaac atatccttaa tategttaag  
 420  
 ctt  
 423

<210> 1360  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 1360  
 Met Leu Asp Asp Ile Pro Gly Leu Thr Leu Ser Leu Val Asp Ala Ser  
 1 5 10 15  
 Glu Ser Ala Asp Leu Arg Phe Thr Cys Asp Ser Tyr Thr Lys Glu Asp  
 20 25 30  
 Asp Val Phe Tyr Pro Leu Trp Glu Asp Asp Tyr Val Val Ala Met Pro  
 35 40 45  
 Val Gly Tyr Trp Leu Ala Asp Tyr Thr Ser Leu Ser Ile Lys Gln Ile  
 50 55 60  
 Asp Lys Gln Pro Phe Val Ser Arg Thr Pro Cys Asp Ile Leu Glu Ser  
 65 70 75 80  
 Trp Asn Phe Ile Met Gln Lys Gln Gly Leu Ser Thr Asp Val Arg Ala  
 85 90 95  
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<211> 1587

<212> PRT

<213> Homo sapiens

<400> 1362

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 Phe Met Val Ala Pro Pro Met Arg His Leu His Leu Pro Ser His Pro  
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<400> 1365

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&lt;211&gt; 150

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&lt;213&gt; Homo sapiens

&lt;400&gt; 1366

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			20					25					30		
Pro	Trp	Asn	Glu	Val	Asp	Glu	Val	Trp	Pro	Asn	Val	Phe	Ile	Ala	Glu
		35					40					45			
Lys	Ser	Val	Ala	Val	Asn	Lys	Gly	Arg	Leu	Lys	Arg	Leu	Gly	Ile	Thr
		50				55				60					
His	Ile	Leu	Asn	Ala	Ala	His	Gly	Thr	Gly	Val	Tyr	Thr	Gly	Pro	Glu
65				70					75					80	
Phe	Tyr	Thr	Gly	Leu	Glu	Ile	Gln	Tyr	Leu	Gly	Val	Glu	Val	Asp	Asp
			85					90					95		
Phe	Pro	Glu	Val	Asp	Ile	Ser	Gln	His	Phe	Arg	Lys	Ala	Ser	Glu	Phe
		100					105					110			
Leu	Asp	Glu	Ala	Leu	Leu	Thr	Tyr	Arg	Gly	Lys	Val	Leu	Val	Ser	Ser
		115				120					125				
Glu	Met	Gly	Ile	Ser	Arg	Ser	Ala	Val	Leu	Val	Val	Ala	Tyr	Leu	Met
	130					135					140				
Ile	Phe	His	Asn	Met	Ala										
145					150										

&lt;210&gt; 1367

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1367

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 120

tcgtcgtcgc attgctgctg gtcacgtcgc cactgcccgt cagcgcactc gtcggccaga  
 180  
 gcttcttcga ccgcgaaggc gccttcgtcg gcctcgccaa cttegtcgc tacctcgaca  
 240  
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 300  
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 330

<210> 1368

<211> 82

<212> PRT

<213> Homo sapiens

<400> 1368

Thr	Ala	Asn	Ala	Gly	Ser	Pro	Ala	Pro	Leu	Tyr	Cys	Ser	Ser	Ser	His
1				5				10						15	
Cys	Cys	Trp	Ser	Ser	Ser	His	Cys	Pro	Ser	Ala	His	Ser	Ser	Ala	Arg
			20					25					30		
Ala	Ser	Ser	Thr	Ala	Lys	Ala	Pro	Ser	Ser	Ala	Ser	Pro	Thr	Ser	Leu
		35					40					45			
Ala	Thr	Ser	Thr	Thr	Pro	Pro	Trp	Ser	Ser	Pro	Pro	Ser	Thr	Ala	Ser
	50					55					60				
Gly	Trp	Pro	Arg	Ser	Ala	Pro	Ser	Ser	Ala	Pro	Pro	Ser	Pro	Thr	Ser
65					70					75				80	
Thr	Arg														

<210> 1369

<211> 356

<212> DNA

<213> Homo sapiens

<400> 1369

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 120  
 cccctggacc cctacagcca ggagcagcgg gaggagctgc aggtcctacg ccaggctgcc  
 180  
 ttcgaggtgg agggggagtc ctcgggtgcc gggctaagtg ctgaccgtcg ccgttccttc  
 240  
 tgtgcccag agttccgcaa actgggcttt tctaacagca acccagcaca ggacctggag  
 300  
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 356

<210> 1370

<211> 104

<212> PRT

<213> Homo sapiens

<400> 1370

Met Gly Asp Glu Met Ala His His Leu Tyr Val Leu Gln Ala Leu Met

```

      1             5             10             15
Leu Gly Leu Leu Glu Pro Arg Met Arg Thr Pro Leu Asp Pro Tyr Ser
      20             25             30
Gln Glu Gln Arg Glu Gln Leu Gln Val Leu Arg Gln Ala Ala Phe Glu
      35             40             45
Val Glu Gly Glu Ser Ser Gly Ala Gly Leu Ser Ala Asp Arg Arg Arg
      50             55             60
Ser Leu Cys Ala Arg Glu Phe Arg Lys Leu Gly Phe Ser Asn Ser Asn
65             70             75             80
Pro Ala Gln Asp Leu Glu Arg Val Pro Pro Gly Leu Leu Ala Leu Asp
      85             90             95
Asn Met Leu Tyr Phe Ser Arg Asn
      100

```

&lt;210&gt; 1371

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1371

```

tcgcgagcac actccagcct ctgggctgcc tttttcaggt tttgcaaact ggctatgaat
60
tggtcagcgg ttggattagc cagttctgca gactggctca caccagacc atctggaccg
120
cttatagaga agacatgttc caagtaccct ctttcctttg tctgcttttc tcatgggtac
180
tttgccctct aagaagccta ctttcctctt ttctctcct cctctcccta tttctctttg
240
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300
ggaaagtcca tgccctcacc agagtaatga ctaccatttc tccaaaactc tcctcatgcc
360
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420
ttaagttata cctacaataa aagaccagc cttagcccat ggctgaatgt tgaatactgt
480
tgcattgaaa tttgggattt ctagttagag gctttataaa ggtagaatca tgcagacaca
540
tatacctgga aatattcgga acattctatt agcagaaatg caatgtagga agcttattgg
600
ttctagaaga atgtgtcatt gtcagtaatt ggaattactg acagatct
648

```

&lt;210&gt; 1372

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1372

```

Met Phe Gln Val Pro Ser Phe Leu Cys Leu Leu Phe Ser Trp Val Leu
      1             5             10             15
Cys Pro Leu Arg Ser Leu Leu Ser Ser Phe Pro Leu Leu Leu Ser Leu
      20             25             30
Phe Leu Phe Val Glu Arg Ala Val Arg Leu Thr Gln Gln Leu Leu Glu

```

```

      35              40              45
Cys Leu Gly His Leu Arg Ala Trp Lys Val His Ala Leu Thr Arg Val
      50              55              60
Met Thr Thr Ile Ser Pro Lys Leu Ser Ser Cys His Pro Ile Gly Ser
65              70              75              80
Ile Asp Gln Lys Gly Lys Ser Ser Val Leu Lys Leu Ile Asn Gln Leu
      85              90              95
Lys Leu Tyr Leu Gln
      100

```

&lt;210&gt; 1373

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1373

```

caattggttt tcccgaactt tctacttgca aagcaacttc ttagacctgg ggtcctctct
60
tgcaggcgcc ctgcatggca gagaactttt tccaccacaa ccttcgtgta acaggcagtt
120
acatgggttt catgggtcga catgggttcc gtgtcctgct tgccgggcct gagctgtttg
180
tcagggtgtac aaccgagaac cttgcagacc agaattccaag actccgcagc atgtgtgtgc
240
cggggcgggg cagcagctgt tggaggagaa agccatcagt gtatttagag gcaaagggct
300
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360
ctctccgca
369

```

&lt;210&gt; 1374

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1374

```

Met Ala Glu Asn Phe Phe His His Asn Leu Arg Val Thr Gly Ser Tyr
  1              5              10              15
Met Gly Phe Met Gly Arg His Gly Phe Arg Val Leu Leu Ala Gly Pro
      20              25              30
Glu Leu Phe Val Arg Cys Thr Thr Glu Asn Leu Ala Asp Gln Asn Pro
      35              40              45
Arg Leu Arg Ser Met Cys Val Pro Gly Arg Asp Thr Ser Cys Trp Arg
      50              55              60
Arg Lys Pro Ser Val Tyr Leu Glu Ala Lys Gly Phe Leu Asn Arg Gly
65              70              75              80
Cys Ala Gly Leu Leu Lys Val Leu Thr Gln Ala Ser Glu Val Asn Pro
      85              90              95
Leu Arg

```

&lt;210&gt; 1375

&lt;211&gt; 282



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1375

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 60  
 ggctggcact ggcccgcctt caacatcgct gacatggcca tcgtgggcgg ggcgatcgcg  
 120  
 ctggtggccc agtcgttcat gagcgtggag aaccggccg ccacaaagga gtcccagtga  
 180  
 cattgggacg atccggaaat tcgcaatgca cacggtgcag gacaccaatc tgaagagaac  
 240  
 ggccccagc atgagcggcc gcggcttggc ctcattgcta gc  
 282

&lt;210&gt; 1376

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1376

Xaa	Ala	Phe	Asp	Arg	Ala	Thr	Arg	Gly	His	Val	Ile	Asp	Tyr	Ile	Asp
1				5				10					15		
Phe	His	Leu	His	Gly	Trp	His	Trp	Pro	Ala	Phe	Asn	Ile	Ala	Asp	Met
			20					25				30			
Ala	Ile	Val	Gly	Gly	Ala	Ile	Ala	Leu	Val	Ala	Gln	Ser	Phe	Met	Ser
		35					40					45			
Val	Glu	Asn	Pro	Ala	Ala	Thr	Lys	Glu	Ser	Gln					
	50					55									

&lt;210&gt; 1377

&lt;211&gt; 6306

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1377

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 60  
 tgctctgtgt cactgtggat tggagttgaa aaagcttgac tggcgtcatt caggagctgg  
 120  
 atggcgtggg acatgtgcaa ccaggactct gactctgtat ggagtgcacat cgagtgtgct  
 180  
 gctctgggtg gtgaagacca gcctctttgc ccagatcttc ctgaacttga tctttctgaa  
 240  
 ctagatgtga acgacttggg tacagacagc tttctgggtg gactcaagtg gtgcagtgcac  
 300  
 caatcagaaa taatatccaa tcagtacaac aatgagcctt caaacatatt tgagaagata  
 360  
 gatgaagaga atgaggcaaa cttgctagca gtcctcacag agacactaga cagtctccct  
 420  
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 480  
 aatgaggcta gtccttctc catgectgac ggcacccctc caccacagga ggcagaagag  
 540

ccgtctctac ttaagaagct cttactggca ccagccaaca ctcagctaag ttataatgaa  
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tgcagtgggc tcagtaccca gaacatgca aatcacatc acaggatcag aacaaaccct  
660  
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720  
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780  
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2160

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&lt;210&gt; 1378

&lt;211&gt; 798

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1378

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 Ile Glu Cys Ala Ala Leu Val Gly Glu Asp Gln Pro Leu Cys Pro Asp  
 20 25 30  
 Leu Pro Glu Leu Asp Leu Ser Glu Leu Asp Val Asn Asp Leu Asp Thr  
 35 40 45  
 Asp Ser Phe Leu Gly Gly Leu Lys Trp Cys Ser Asp Gln Ser Glu Ile  
 50 55 60  
 Ile Ser Asn Gln Tyr Asn Asn Glu Pro Ser Asn Ile Phe Glu Lys Ile  
 65 70 75 80  
 Asp Glu Glu Asn Glu Ala Asn Leu Leu Ala Val Leu Thr Glu Thr Leu  
 85 90 95  
 Asp Ser Leu Pro Val Asp Glu Asp Gly Leu Pro Ser Phe Asp Ala Leu  
 100 105 110  
 Thr Asp Gly Asp Val Thr Thr Asp Asn Glu Ala Ser Pro Ser Ser Met

```

      115      120      125
Pro Asp Gly Thr Pro Pro Pro Gln Glu Ala Glu Glu Pro Ser Leu Leu
  130      135      140
Lys Lys Leu Leu Leu Ala Pro Ala Asn Thr Gln Leu Ser Tyr Asn Glu
  145      150      155      160
Cys Ser Gly Leu Ser Thr Gln Asn His Ala Asn His Asn His Arg Ile
      165      170      175
Arg Thr Asn Pro Ala Ile Val Lys Thr Glu Asn Ser Trp Ser Asn Lys
      180      185      190
Ala Lys Ser Ile Cys Gln Gln Gln Lys Pro Gln Arg Arg Pro Cys Ser
      195      200      205
Glu Leu Leu Lys Tyr Leu Thr Thr Asn Asp Asp Pro Pro His Thr Lys
  210      215      220
Pro Thr Glu Asn Arg Asn Ser Ser Arg Asp Lys Cys Thr Ser Lys Lys
  225      230      235      240
Lys Ser His Thr Gln Ser Gln Ser Gln His Leu Gln Ala Lys Pro Thr
      245      250      255
Thr Leu Ser Leu Pro Leu Thr Pro Glu Ser Pro Asn Asp Pro Lys Gly
      260      265      270
Ser Pro Phe Glu Asn Lys Thr Ile Glu Arg Thr Leu Ser Val Glu Leu
      275      280      285
Ser Gly Thr Ala Gly Leu Thr Pro Pro Thr Thr Pro Pro His Lys Ala
  290      295      300
Asn Gln Asp Asn Pro Phe Arg Ala Ser Pro Lys Leu Lys Ser Ser Cys
  305      310      315      320
Lys Thr Val Val Pro Pro Pro Ser Lys Lys Pro Arg Tyr Ser Glu Ser
      325      330      335
Ser Gly Thr Gln Gly Asn Asn Ser Thr Lys Lys Gly Pro Glu Gln Ser
      340      345      350
Glu Leu Tyr Ala Gln Leu Ser Lys Ser Ser Val Leu Thr Gly Gly His
      355      360      365
Glu Glu Arg Lys Thr Lys Arg Pro Ser Leu Arg Leu Phe Gly Asp His
  370      375      380
Asp Tyr Cys Gln Ser Ile Asn Ser Lys Thr Glu Ile Leu Ile Asn Ile
  385      390      395      400
Ser Gln Glu Leu Gln Asp Ser Arg Gln Leu Glu Asn Lys Asp Val Ser
      405      410      415
Ser Asp Trp Gln Gly Gln Ile Cys Ser Ser Thr Asp Ser Asp Gln Cys
      420      425      430
Tyr Leu Arg Glu Thr Leu Glu Ala Ser Lys Gln Val Ser Pro Cys Ser
      435      440      445
Thr Arg Lys Gln Leu Gln Asp Gln Glu Ile Arg Ala Glu Leu Asn Lys
      450      455      460
His Phe Gly His Pro Ser Gln Ala Val Phe Asp Asp Glu Ala Asp Lys
  465      470      475      480
Thr Gly Glu Leu Arg Asp Ser Asp Phe Ser Asn Glu Gln Phe Ser Lys
      485      490      495
Leu Pro Met Phe Ile Asn Ser Gly Leu Ala Met Asp Gly Leu Phe Asp
      500      505      510
Asp Ser Glu Asp Glu Ser Asp Lys Leu Ser Tyr Pro Trp Asp Gly Thr
      515      520      525
Gln Ser Tyr Ser Leu Phe Asn Val Ser Pro Ser Cys Ser Ser Phe Asn
      530      535      540
Ser Pro Cys Arg Asp Ser Val Ser Pro Pro Lys Ser Leu Phe Ser Gln

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545                      550                      555                      560  
 Arg Pro Gln Arg Met Arg Ser Arg Ser Arg Ser Phe Ser Arg His Arg  
                                  565                      570                      575  
 Ser Cys Ser Arg Ser Pro Tyr Ser Arg Ser Arg Ser Arg Ser Pro Gly  
                                  580                      585                      590  
 Ser Arg Ser Ser Ser Arg Ser Cys Tyr Tyr Tyr Glu Ser Ser His Tyr  
                                  595                      600                      605  
 Arg His Arg Thr His Arg Asn Ser Pro Leu Tyr Val Arg Ser Arg Ser  
                                  610                      615                      620  
 Arg Ser Pro Tyr Ser Arg Arg Pro Arg Tyr Asp Ser Tyr Glu Glu Tyr  
 625                                   630                      635                      640  
 Gln His Glu Arg Leu Lys Arg Glu Glu Tyr Arg Arg Glu Tyr Glu Lys  
                                  645                      650                      655  
 Arg Glu Ser Glu Arg Ala Lys Gln Arg Glu Arg Gln Arg Gln Lys Ala  
                                  660                      665                      670  
 Ile Glu Glu Arg Arg Val Ile Tyr Val Gly Lys Ile Arg Pro Asp Thr  
                                  675                      680                      685  
 Thr Arg Thr Glu Leu Arg Asp Arg Phe Glu Val Phe Gly Glu Ile Glu  
                                  690                      695                      700  
 Glu Cys Thr Val Asn Leu Arg Asp Asp Gly Asp Ser Tyr Gly Phe Ile  
 705                                   710                      715                      720  
 Thr Tyr Arg Tyr Thr Cys Asp Ala Phe Ala Ala Leu Glu Asn Gly Tyr  
                                  725                      730                      735  
 Thr Leu Arg Arg Ser Asn Glu Thr Asp Phe Glu Leu Tyr Phe Cys Gly  
                                  740                      745                      750  
 Arg Lys Gln Phe Phe Lys Ser Asn Tyr Ala Asp Leu Asp Ser Asn Ser  
                                  755                      760                      765  
 Asp Asp Phe Asp Pro Ala Ser Thr Lys Ser Lys Tyr Asp Ser Leu Asp  
                                  770                      775                      780  
 Phe Asp Ser Leu Leu Lys Glu Ala Gln Arg Ser Leu Arg Arg  
 785                                   790                      795

&lt;210&gt; 1379

&lt;211&gt; 590

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1379

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 cgcgtnacc catctctgcc ctccgagtc ctgccgtgtg gccgtgtcna cccacctctg  
 420  
 ccctcggtgt ccctgccgtg tggccgagtc naccacctc tgccctcggg gtccctgccg  
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tgtggccgcg tcnaccacc tctgccctcg gtgtccccgc cgtgtggccg cgtcnaccca  
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<210> 1380  
 <211> 141  
 <212> PRT  
 <213> Homo sapiens

<400> 1380  
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 Lys Gly Leu Trp Gly Leu Val Pro Trp Glu Asp Val Arg Ala Ile Trp  
 20 25 30  
 Cys Pro Cys Arg Val Ala Ala Ser Pro Ile Ser Ala Leu Gly Val Pro  
 35 40 45  
 Ala Leu Trp Pro Arg His Pro Ser Leu Pro Ser Glu Ser Leu Pro Cys  
 50 55 60  
 Gly Arg Val Xaa Pro Ser Leu Pro Ser Glu Ser Leu Pro Cys Gly Arg  
 65 70 75 80  
 Val Xaa Pro Pro Leu Pro Ser Val Ser Leu Pro Cys Gly Arg Val Xaa  
 85 90 95  
 Pro Pro Leu Pro Ser Val Ser Leu Pro Cys Gly Arg Val Xaa Pro Pro  
 100 105 110  
 Leu Pro Ser Val Ser Pro Pro Cys Gly Arg Val Xaa Pro Ser Leu Pro  
 115 120 125  
 Ser Val Ser Pro Pro Cys Gly Arg Val Thr His Leu Cys  
 130 135 140

<210> 1381  
 <211> 433  
 <212> DNA  
 <213> Homo sapiens

<400> 1381  
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 120  
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 180  
 cgtgtcctgg ctgccatcag agaggaggca ggtcccacag atctgctctt gtttctgctg  
 240  
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 300  
 ccaggcattg gccctgtacc tgttcctcac ggaagccgaa ctctgctta tgggccccag  
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 420  
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 433

<210> 1382



<211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 1382  
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 Thr Phe Trp Pro Arg Pro Asp Thr Met Cys Glu Ala Thr Glu Ser Pro  
 20 25 30  
 Gly Arg Ser Thr Leu Thr Ala Leu Ala Lys His Ser Phe Pro Cys Pro  
 35 40 45  
 Gly Cys His Gln Arg Gly Gly Arg Ser His Arg Ser Ala Leu Val Ser  
 50 55 60  
 Ala Gly Leu Lys Trp Gly Phe Ser Phe Cys Val Glu Gln Phe Ile Arg  
 65 70 75 80  
 Gly Leu Ile Ser Lys Pro Arg His Trp Pro Cys Thr Cys Ser Ser Arg  
 85 90 95  
 Lys Pro Asn Ser Cys Leu Trp Ala Pro Ala Tyr Arg Gln Pro Asn Gly  
 100 105 110  
 Leu Ala Pro Ala Lys Gly Leu Phe Gly Asp Leu  
 115 120

<210> 1383  
 <211> 906  
 <212> DNA  
 <213> Homo sapiens

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 180  
 caaacgcctc acatgagctc acccacaccc ccaagagcca tgggtgtcac aaagcaaaga  
 240  
 ccaagccaga ctcaatcctg tggccccagg gtcagccgca gagcagacaa ctagaacctc  
 300  
 acaagaagct gaacacaggc tgggtcacct ataaacaggg aggccatcct gaagggagga  
 360  
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 420  
 aatgggcaca gttctnccgg cgtccccacg gcctgggtctc tgaatgcgtt gagacagatt  
 480  
 gggcagctct ctgcatcatc atcagaattg aaagagccag cggtttccag tttcccctga  
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 720  
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<210> 1384  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 1384  
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 20 25 30  
 Met Ala Pro Met Ser Thr Arg Val Ser Ala Ala Gly Pro Gly Arg Pro  
 35 40 45  
 Thr Ala Ser Ser Leu Leu Pro Leu Thr Asn Thr Pro Gln Thr Pro His  
 50 55 60  
 Met Ser Ser Pro Thr Pro Pro Arg Ala Met Val Leu Thr Lys Gln Arg  
 65 70 75 80  
 Pro Ser Gln Thr Gln Ser Cys Gly Pro Arg Val Ser Arg Arg Ala Asp  
 85 90 95  
 Asn

<210> 1385  
 <211> 210  
 <212> DNA  
 <213> Homo sapiens

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 120  
 gtggcgtgta tgcattggtgt gtgcacgtgt gcactgtgtg tggggtgtat gncatggtg  
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 gtgcacatat gcactggggg gtgtgtatgc  
 210

<210> 1386  
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 <212> PRT  
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<400> 1386  
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 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met  
 20 25 30  
 Val Met Cys Thr Cys Ala Leu Cys Val Ala Cys Met His Gly Val Cys

35 40 45  
 r Cys Ala Leu Cys Val Gly Cys Met Xaa Trp Trp Val His Ile Cys  
 50 55 60  
 Thr Gly Gly Cys Val Cys  
 65 70

<210> 1387

<211> 521

<212> DNA

<213> Homo sapiens

<400> 1387

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 420  
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 521

<210> 1388

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1388

Gly Arg Asn Ser Thr Ser Glu Gly Asp Val Arg Ala His Glu Gly Thr  
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 Lys Gly Gln Val Val Gln Ala Glu Gly Val Ser Gly Cys Gly Lys His  
 20 25 30  
 Ser Pro Gly Gly Gln His Thr Glu Ala Gly Glu Asp Glu Gly Val Val  
 35 40 45  
 Ala Ala Asp Gly Ser Ser Asp Ser Thr Ala Gly Asp Gly Gly Lys Glu  
 50 55 60  
 Ser Glu Asp Glu Asp Ser Asp Arg Gly Gly Glu His Arg Cys Ser Phe  
 65 70 75 80  
 Val Arg Ala Gly Tyr Pro Ala Ile Cys His Pro His Ala Ala Thr Gly  
 85 90 95  
 Ala Ala Phe Ser Gly His Pro  
 100

<210> 1389

<211> 4013

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1389

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180  
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240  
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300  
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360  
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&lt;210&gt; 1390

&lt;211&gt; 1156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1390

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			20					25					30		
Thr	Ile	Ile	Ser	Thr	Ile	Pro	Ser	Thr	Ala	Met	His	Thr	Arg	Ser	Thr
			35				40					45			
Ala	Ala	Pro	Ile	Pro	Ile	Leu	Pro	Glu	Arg	Gly	Val	Ser	Leu	Phe	Pro
			50			55					60				
Tyr	Gly	Ala	Asp	Ala	Gly	Asp	Leu	Glu	Phe	Val	Arg	Arg	Thr	Val	Asp
65					70					75				80	
Phe	Thr	Ser	Pro	Leu	Phe	Lys	Pro	Ala	Thr	Gly	Phe	Pro	Leu	Gly	Ser
			85					90						95	
Ser	Leu	Arg	Asp	Ser	Leu	Tyr	Phe	Thr	Asp	Asn	Gly	Gln	Ile	Ile	Phe
			100					105					110		
Pro	Glu	Ser	Asp	Tyr	Gln	Ile	Phe	Ser	Tyr	Pro	Asn	Pro	Leu	Pro	Thr
			115				120					125			
Gly	Phe	Thr	Gly	Arg	Asp	Pro	Val	Ala	Leu	Val	Ala	Pro	Phe	Trp	Asp

130 135 140  
 Asp Ala Asp Phe Ser Thr Gly Arg Gly Thr Thr Phe Tyr Gln Glu Tyr  
 145 150 155 160  
 Glu Thr Phe Tyr Gly Glu His Ser Leu Leu Val Gln Gln Ala Glu Ser  
 165 170 175  
 Trp Ile Arg Lys Ile Thr Asn Asn Gly Gly Tyr Lys Ala Arg Trp Ala  
 180 185 190  
 Leu Lys Val Thr Trp Val Asn Ala His Ala Tyr Pro Ala Gln Trp Thr  
 195 200 205  
 Leu Gly Ser Asn Thr Tyr Gln Ala Ile Leu Ser Thr Asp Gly Ser Arg  
 210 215 220  
 Ser Tyr Ala Leu Phe Leu Tyr Gln Ser Gly Gly Met Gln Trp Asp Val  
 225 230 235 240  
 Ala Gln Arg Ser Gly Asn Pro Val Leu Met Gly Phe Ser Ser Gly Asp  
 245 250 255  
 Gly Tyr Phe Glu Asn Ser Pro Leu Met Ser Gln Pro Val Trp Glu Arg  
 260 265 270  
 Tyr Arg Pro Asp Arg Phe Leu Asn Ser Asn Ser Gly Leu Gln Gly Leu  
 275 280 285  
 Gln Phe Tyr Arg Leu His Arg Glu Glu Arg Pro Asn Tyr Arg Leu Glu  
 290 295 300  
 Cys Leu Gln Trp Leu Lys Ser Gln Pro Arg Trp Pro Ser Trp Gly Trp  
 305 310 315 320  
 Asn Gln Val Ser Cys Pro Cys Ser Trp Gln Gln Gly Arg Arg Asp Leu  
 325 330 335  
 Arg Phe Gln Pro Val Ser Ile Gly Arg Trp Gly Leu Gly Ser Arg Gln  
 340 345 350  
 Leu Cys Ser Phe Thr Ser Trp Arg Gly Gly Val Cys Cys Ser Tyr Gly  
 355 360 365  
 Pro Trp Gly Glu Phe Arg Glu Gly Trp His Val Gln Arg Pro Trp Gln  
 370 375 380  
 Leu Ala Gln Glu Leu Glu Pro Gln Ser Trp Cys Cys Arg Trp Asn Asp  
 385 390 395 400  
 Lys Pro Tyr Leu Cys Ala Leu Tyr Gln Gln Arg Arg Pro His Val Gly  
 405 410 415  
 Cys Ala Thr Tyr Arg Pro Pro Gln Pro Ala Trp Met Phe Gly Asp Pro  
 420 425 430  
 His Ile Thr Thr Leu Asp Gly Val Ser Tyr Thr Phe Asn Gly Leu Gly  
 435 440 445  
 Asp Phe Leu Leu Val Gly Ala Gln Asp Gly Asn Ser Ser Phe Leu Leu  
 450 455 460  
 Gln Gly Arg Thr Ala Gln Thr Gly Ser Ala Gln Ala Thr Asn Phe Ile  
 465 470 475 480  
 Ala Phe Ala Ala Gln Tyr Arg Ser Ser Ser Leu Gly Pro Val Thr Val  
 485 490 495  
 Gln Trp Leu Leu Glu Pro His Asp Ala Ile Arg Val Leu Leu Asp Asn  
 500 505 510  
 Gln Thr Val Thr Phe Gln Pro Asp His Glu Asp Gly Gly Gln Glu  
 515 520 525  
 Thr Phe Asn Ala Thr Gly Val Leu Leu Ser Arg Asn Gly Ser Glu Val  
 530 535 540  
 Ser Ala Ser Phe Asp Gly Trp Ala Thr Val Ser Val Ile Ala Leu Ser  
 545 550 555 560  
 Asn Ile Leu His Ala Ser Ala Ser Leu Pro Pro Glu Tyr Gln Asn Arg

Thr	Glu	Gly	Leu	Leu	Gly	Val	Trp	Asn	Asn	Asn	Pro	Glu	Asp	Asp	Phe
			580					585					590		
Arg	Met	Pro	Asn	Gly	Ser	Thr	Ile	Pro	Pro	Gly	Ser	Pro	Glu	Glu	Met
			595				600					605			
Leu	Phe	His	Phe	Gly	Met	Thr	Trp	Gln	Ile	Asn	Gly	Thr	Gly	Leu	Leu
	610					615					620				
Gly	Lys	Arg	Asn	Asp	Gln	Leu	Pro	Ser	Asn	Phe	Thr	Pro	Val	Phe	Tyr
625					630					635					640
Ser	Gln	Leu	Gln	Lys	Asn	Ser	Ser	Trp	Ala	Glu	His	Leu	Ile	Ser	Asn
				645					650					655	
Cys	Asp	Gly	Asp	Ser	Ser	Cys	Ile	Tyr	Asp	Thr	Leu	Ala	Leu	Arg	Asn
			660					665					670		
Ala	Ser	Ile	Gly	Leu	His	Thr	Arg	Glu	Val	Ser	Lys	Asn	Tyr	Glu	Gln
			675				680					685			
Ala	Asn	Ala	Thr	Leu	Asn	Gln	Tyr	Pro	Pro	Ser	Ile	Asn	Gly	Gly	Arg
			690				695				700				
Val	Ile	Glu	Ala	Tyr	Lys	Gly	Gln	Thr	Thr	Leu	Ile	Gln	Tyr	Thr	Ser
705					710					715					720
Asn	Ala	Glu	Asp	Ala	Asn	Phe	Thr	Leu	Arg	Asp	Ser	Cys	Thr	Asp	Leu
				725					730					735	
Glu	Leu	Phe	Glu	Asn	Gly	Thr	Leu	Leu	Trp	Thr	Pro	Lys	Ser	Leu	Glu
			740					745					750		
Pro	Phe	Thr	Leu	Glu	Ile	Leu	Ala	Arg	Ser	Ala	Lys	Ile	Gly	Leu	Ala
			755				760					765			
Ser	Ala	Leu	Gln	Pro	Arg	Thr	Val	Val	Cys	His	Cys	Asn	Ala	Glu	Ser
			770				775				780				
Gln	Cys	Leu	Tyr	Asn	Gln	Thr	Ser	Arg	Val	Gly	Asn	Ser	Ser	Leu	Glu
785					790					795					800
Val	Ala	Gly	Cys	Lys	Cys	Asp	Gly	Gly	Thr	Phe	Gly	Arg	Tyr	Cys	Glu
				805					810					815	
Gly	Ser	Glu	Asp	Ala	Cys	Glu	Glu	Pro	Cys	Phe	Pro	Ser	Val	His	Cys
			820					825					830		
Val	Pro	Gly	Lys	Gly	Cys	Glu	Ala	Cys	Pro	Pro	Asn	Leu	Thr	Gly	Asp
			835				840					845			
Gly	Arg	His	Cys	Ala	Ala	Leu	Gly	Ser	Ser	Phe	Leu	Cys	Gln	Asn	Gln
						855					860				
Ser	Cys	Pro	Val	Asn	Tyr	Cys	Tyr	Asn	Gln	Gly	His	Cys	Tyr	Ile	Ser
865					870					875					880
Gln	Thr	Leu	Gly	Cys	Gln	Pro	Met	Cys	Thr	Cys	Pro	Pro	Ala	Phe	Thr
				885					890					895	
Asp	Ser	Arg	Cys	Phe	Leu	Ala	Gly	Asn	Asn	Phe	Ser	Pro	Thr	Val	Asn
				900				905					910		
Leu	Glu	Leu	Pro	Leu											



```

      995              1000              1005
Pro Arg Arg Ser Glu Glu Pro Arg Asn Asp Val Val Phe Gln Pro Ile
 1010              1015              1020
Ser Gly Glu Asp Val Arg Asp Val Thr Ala Leu Asn Val Ser Thr Leu
 1025              1030              1035              1040
Lys Ala Tyr Phe Arg Cys Asp Gly Tyr Lys Gly Tyr Asp Leu Val Tyr
      1045              1050              1055
Ser Pro Gln Ser Gly Phe Thr Cys Val Ser Pro Cys Ser Arg Gly Tyr
      1060              1065              1070
Cys Asp His Gly Gly Gln Cys Gln His Leu Pro Ser Gly Pro Arg Cys
      1075              1080              1085
Ser Cys Val Ser Phe Ser Ile Tyr Thr Ala Trp Gly Glu His Cys Glu
      1090              1095              1100
His Leu Ser Met Lys Leu Asp Ala Phe Phe Gly Ile Phe Phe Gly Ala
 1105              1110              1115              1120
Leu Gly Gly Leu Leu Leu Leu Gly Val Gly Thr Phe Val Val Leu Arg
      1125              1130              1135
Phe Trp Gly Cys Ser Gly Ala Arg Phe Ser Tyr Phe Leu Asn Ser Ala
      1140              1145              1150
Glu Ala Leu Pro
      1155

```

&lt;210&gt; 1391

&lt;211&gt; 481

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1391

```

gtcgacggca tcgaggtcca tgacaaggca accgacctca accgcctgcg ccagaagatc
60
ggcattgtgt tccagcagtg gaacgccttc ccgcacctca ccgtgctgga aaacgtgatg
120
ctggcgccgc gcaaggtgct cggtaaaagc aagcagaagg ccgaggagct ggcggtccgg
180
caactgaccc acgtgggcct gagcgacaag ctcaagacct ttcccgcana gctttccggc
240
ggccagcaac agcgcagtcg gattgcccgg gccctggcca tgtcgccgga ctacatgctg
300
ttcgacgaag ccacctcggc ccttgatccg cagttggtgg gcgaggtgct ggacaccatg
360
cgcatgctcg ccgaagacgg catgacctatg gtcttggtga cccatgaaat ccgctttggc
420
cgcgatgtgt ccgatcgctt ggcgttcttt cgcaacggcc tgggtgcacga gatcggcgcg
480
c
481

```

&lt;210&gt; 1392

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1392

```

Val Asp Gly Ile Glu Val His Asp Lys Ala Thr Asp Leu Asn Arg Leu

```

```

      1           5           10           15
Arg Gln Lys Ile Gly Ile Val Phe Gln Gln Trp Asn Ala Phe Pro His
      20           25           30
Leu Thr Val Leu Glu Asn Val Met Leu Ala Pro Arg Lys Val Leu Gly
      35           40           45
Lys Ser Lys Gln Lys Ala Glu Glu Leu Ala Val Arg Gln Leu Thr His
      50           55           60
Val Gly Leu Ser Asp Lys Leu Lys Thr Phe Pro Ala Xaa Leu Ser Gly
      65           70           75           80
Gly Gln Gln Gln Arg Met Ala Ile Ala Arg Ala Leu Ala Met Ser Pro
      85           90           95
Asp Tyr Met Leu Phe Asp Glu Ala Thr Ser Ala Leu Asp Pro Gln Leu
      100          105          110
Val Gly Glu Val Leu Asp Thr Met Arg Met Leu Ala Glu Asp Gly Met
      115          120          125
Thr Met Val Leu Val Thr His Glu Ile Arg Phe Ala Arg Asp Val Ser
      130          135          140
Asp Arg Val Ala Phe Phe Arg Asn Gly Leu Val His Glu Ile Gly Ala
      145          150          155          160

```

&lt;210&gt; 1393

&lt;211&gt; 309

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1393

```

cggcgcgcat cggcgcgggc cttgtgggat atggccatta ctgaggtgct ggccggctac
60
tacgaaccgc acgaacacgc acaccgcaag cccgagtcgt tgtacggcgc ggtcaagatg
120
tgggcccttc tgcgccgtca gggcatcagg tggcccgtg cancgggtgga gcgcctcatg
180
cgggacaacc ggtggcgtgg ggtgacccgc cgtaagaagg ttncgcacca ccacgctga
240
cccggctgcc gggcgagccc cggatctggt ggaccgccag ttccgcgtcg aggcgcccac
300
caagttgct
309

```

&lt;210&gt; 1394

&lt;211&gt; 79

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1394

```

Arg Pro Pro Ser Ala Arg Ala Leu Trp Asp Met Ala Ile Thr Glu Val
      1           5           10           15
Leu Ala Gly Tyr Tyr Glu Pro Asp Glu His Gly His Arg Lys Pro Glu
      20           25           30
Ser Leu Tyr Gly Ala Val Lys Met Trp Ala Leu Leu Arg Arg Gln Gly
      35           40           45
Ile Arg Trp Pro Ala Ala Xaa Val Glu Arg Leu Met Arg Asp Asn Arg
      50           55           60
Trp Arg Gly Val Thr Arg Arg Lys Lys Val Xaa His His His Arg

```

65

70

75

&lt;210&gt; 1395

&lt;211&gt; 347

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1395

accggtggg ttcgtggtgg cctggttact ttttggcgcg agcgggtgtgg tgtgggcccgt  
60  
tatgacggtg gtcgtgggcg aaacgggtgct gtcgtttgtg cgccgtcaac gtcgaagagc  
120  
ccagattctt aaaggcggtc gcgatgttgc ccgggcgaca agggccttgg ctggacgggt  
180  
gtcgggtgggg gagatccccct cagttgcact agagcacgtg gccgatgacg tggaggtatt  
240  
ggctcaggct aggcggggtc atgcagtggg cggaagcgtt tccgacgccc tcattgccac  
300  
ctcccgcaa ccagggatgg ctggtctggt gccactagcc caccgct  
347

&lt;210&gt; 1396

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1396

Met	Thr	Val	Val	Gly	Glu	Thr	Val	Leu	Val	Val	Val	Arg	Arg	Gln
1			5				10				15			
Arg	Arg	Arg	Ala	Gln	Ile	Leu	Lys	Gly	Gly	Arg	Asp	Val	Ala	Ala
			20				25				30			
Thr	Arg	Ala	Leu	Ala	Gly	Arg	Val	Ser	Val	Gly	Glu	Ile	Pro	Ser
		35				40					45			
Ala	Leu	Glu	His	Val	Ala	Asp	Asp	Val	Glu	Val	Leu	Ala	Gln	Ala
	50					55				60				
Arg	Ala	His	Ala	Val	Gly	Ser	Val	Ser	Asp	Ala	Leu	Ile	Ala	Thr
65				70				75				80		
Ser	Arg	Gln	Pro	Gly	Met	Ala	Gly	Leu	Val	Pro	Leu	Ala	His	Ala
			85				90					95		

&lt;210&gt; 1397

&lt;211&gt; 308

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1397

caattgcgcg gggtactgca ggcgaagatg cagatgatgt cggacaccaa tttcctcgac  
60  
ctggccccgcg tcgcgattgc cgccactatc cattctccgg aacgcgcgca agacatggtc  
120  
aaccgcttga gcaaacgcca agaaggcttc acgcaatggg tacgtgccgc acaggacgat  
180  
ggtcgactgt cctgcagcga cccggcggtc gctgcccacc agatacaaag cctgctcaag  
240

gcgttcgcct tttggccgca aatcacccctg ggccagccgg tgctggatgc cgccagccag  
 300  
 gccaacgt  
 308

<210> 1398  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 1398  
 Met Gln Met Met Ser Asp Thr Asn Phe Leu Asp Leu Ala Arg Val Ala  
 1 5 10 15  
 Ile Ala Ala Thr Ile His Ser Pro Glu Arg Ala Gln Asp Met Val Asn  
 20 25 30  
 Arg Leu Ser Lys Arg Glu Glu Gly Phe Thr Gln Trp Val Arg Ala Ala  
 35 40 45  
 Gln Asp Asp Gly Arg Leu Ser Cys Ser Asp Pro Ala Phe Ala Ala His  
 50 55 60  
 Gln Ile Gln Ser Leu Leu Lys Ala Phe Ala Phe Trp Pro Gln Ile Thr  
 65 70 75 80  
 Leu Gly Gln Pro Val Leu Asp Ala Ala Ser Gln Ala Asn  
 85 90

<210> 1399  
 <211> 539  
 <212> DNA  
 <213> Homo sapiens

<400> 1399  
 gctagctaac atttattttt gtttttatta ttgttatcta gtggtaaaaa tttcttaagc  
 60  
 aatgaactga agtctagatt tttagatgt agtcctttac tgattataaa gcaaatgcct  
 120  
 ttagatattt taacttcac agtactatct gtagtaggag gctgatttta ctaaaattag  
 180  
 ataattatat acatctgttc ctattccttt ggtaggacct ttaagaaagt catgctgaat  
 240  
 ctgagaatgc caggacattt cacgtggtat gaatgtagga tattcattta cacatcgctg  
 300  
 cacagacagc ctctatataa cccaccctgt tgggggtattg aattttttct tttcccgccc  
 360  
 tacttttaaa tcttgatcag taatttcaac acataatttg tggcacttta gtttttttac  
 420  
 cctttatagt ttaataactt atacatgtac atgcttaaaa tgtcaaacia tacaatggg  
 480  
 aacaaagaaa attgcttcac catctgtgaa cccctccttt ttagtcccc ttcacgcgt  
 539

<210> 1400  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 1400

Met Asn Val Gly Tyr Ser Phe Thr His Arg Cys Thr Asp Ser Leu Tyr  
 1 5 10 15  
 Ile Thr His Pro Val Gly Val Leu Asn Phe Phe Phe Ser Arg Pro Thr  
 20 25 30  
 Phe Lys Ser Cys His Val Ile Ser Thr His Asn Leu Trp His Phe Ser  
 35 40 45  
 Phe Phe Thr Leu Tyr Ser Leu Ile Thr Tyr Thr Cys Thr Cys Leu Lys  
 50 55 60  
 Cys Gln Thr Ile Gln Met Gly Thr Lys Lys Ile Ala Ser Pro Ser Val  
 65 70 75 80  
 Asn Pro Ser Phe Cys Ser Pro Leu His Ala  
 85 90

&lt;210&gt; 1401

&lt;211&gt; 653

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1401

ttcgaggggt cacttggact caagcttcgc gaagtcggg acctcggacg accgattttt  
 60  
 cggtctgtgca ccgtcaccgc aaggctggcg tgggttnnct catcaccggc gggcgatgg  
 120  
 ncattgggggt ttgatggcgc cgtttccctg ctgctgggcg cgatcctcat cgtcaccggc  
 180  
 ccaacggtga ttaaccgat cctgcgtcag ttgcgtccta cccggcgagt gagtgtctg  
 240  
 ttgaggtggg aaggaatcgt cgtcgatccg ctggcgcca tcctggcatt actggtgtat  
 300  
 caggccataa ccagcatcga ccgatcttcc atcggaacaag gcgtcttgaa tctggggctc  
 360  
 accctattgg tcgggctgct ctgcgtggc cccatcggtt ggatcgtcac cgcatgatg  
 420  
 aaacggcacc tcattcccga ctctctacaa ggcgtgattt tcgttgggggt cgcggttga  
 480  
 acgtgtgttg gcgctaactg cattcgggag gaatcgggccc tggcgcgct tacgatgctc  
 540  
 ggcattctacc tggcgaacca gcgcaacctc gagcttgagc ccgtcatcga gttcaaggaa  
 600  
 cacctgcagg tgctcctcgt tggcgtccta ttcatcatgc ttgcaggacg cgt  
 653

&lt;210&gt; 1402

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1402

Phe Glu Gly Ser Leu Gly Leu Lys Leu Arg Glu Val Arg Asp Leu Gly  
 1 5 10 15  
 Arg Pro Ile Phe Arg Leu Cys Thr Val Thr Ala Arg Leu Ala Trp Val  
 20 25 30  
 Xaa Ser Ser Pro Ala Arg Arg Trp Xaa Leu Gly Phe Asp Gly Arg Val

```

      35          40          45
Ser Leu Leu Leu Gly Ala Ile Leu Ile Val Thr Gly Pro Thr Val Ile
  50          55          60
Asn Pro Ile Leu Arg Gln Leu Arg Pro Thr Arg Arg Val Ser Ala Leu
  65          70          75          80
Leu Arg Trp Glu Gly Ile Val Val Asp Pro Leu Gly Ala Ile Leu Ala
      85          90          95
Leu Leu Val Tyr Gln Ala Ile Thr Ser Ile Asp Arg Ser Ser Ile Gly
      100          105          110
Gln Gly Val Leu Asn Leu Gly Leu Thr Leu Leu Val Gly Leu Leu Phe
      115          120          125
Ala Gly Pro Ile Gly Trp Ile Val Thr Ala Met Met Lys Arg His Leu
      130          135          140
Ile Pro Asp Phe Leu Gln Gly Val Ile Phe Val Gly Val Ala Val Gly
      145          150          155          160
Thr Cys Val Gly Ala Asn Val Ile Arg Glu Glu Ser Gly Leu Val Ala
      165          170          175
Val Thr Met Leu Gly Ile Tyr Leu Ala Asn Gln Arg Asn Leu Glu Leu
      180          185          190
Glu Pro Val Ile Glu Phe Lys Glu His Leu Gln Val Leu Leu Val Gly
      195          200          205
Val Leu Phe Ile Met Leu Ala Gly Arg
      210          215

```

&lt;210&gt; 1403

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1403

```

aagctttgca gtttcttggt atccaaatcc aggcgttctt ggtctttttc cacaacagt
60
tgtgccacat gaaatggaac acgggcaaac atatctgac caggaaacat tagccaagta
120
tggtccttgg ggcatgac tccacaagtt ggcatatct cctttatcag ctgcttgcca
180
gagcttcctt ccattctctt cattatgacc tcaaaggag atggcacgct agtcttggac
240
gtcctagctt gtttccgaag ggctgtcaga gcctccctgt taccatttct tatcttatca
300
ttttccacca actgatgtct agccagaaga actttttctg catcagcttc aatatcaacc
360
agagcctctt gaagctgctt catgttggga. tcc
393

```

&lt;210&gt; 1404

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1404

```

Met Lys Gln Leu Gln Glu Ala Leu Val Asp Ile Glu Thr Asp Ala Glu
  1          5          10          15
Lys Val Leu Leu Ala Arg His Gln Leu Val Glu Asn Asp Lys Ile Arg

```

```

      20      25      30
Asn Gly Asn Arg Glu Ala Leu Thr Ala Leu Arg Lys Gln Ala Arg Thr
      35      40      45
Ser Lys Thr Ser Val Pro Ser Pro Phe Glu Val Ile Met Lys Glu Met
      50      55      60
Glu Gly Ser Ser Gly Lys Gln Leu Ile Lys Glu Ile Cys Pro Thr Cys
      65      70      75      80
Gly Asp His Asp Pro Lys Glu His Thr Trp Leu Met Phe Pro Gly Ser
      85      90      95
Asp Met Phe Ala Arg Val Pro Phe His Val Ala His Thr Val Val Glu
      100      105      110
Lys Asp Gln Glu Arg Leu Asp Leu Asp Thr Lys Lys Leu Gln Ser
      115      120      125

```

&lt;210&gt; 1405

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1405

```

nnccgactgc acaaggccct gggcatcgaa ctgcccggcg cactgcaggt catcgtcaaa
60
ggcgaaacca gcctgcaatg gctcgccccg gacgaatggc tgctgatcgt gccagcggg
120
gaagagttcg ccgccgagca aaacctgcgt gccgccctgg gcgagttgca tatccaggtc
180
gtcaacgtca gcggtggcca gcagatcctc gaactcagcg gcccgaaagt gcgcgacgtg
240
ctgatgaaat ccaccagcta cgacgtacac cccaacaact tcccgggtggg caaggcgggtg
300
ggcacggtgt tcgccaagtc gcaactgggtg atccgccata ccgccgaaga cacctgggaa
360
ctgctgatcc gtcgcagctt ctcggattac tggtggctgt gggtgcagga cgcggctgca
420
t
421

```

&lt;210&gt; 1406

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1406

```

Xaa Arg Leu His Lys Ala Leu Gly Ile Glu Leu Pro Gly Ala Leu Gln
1      5      10      15
Val Ile Val Lys Gly Glu Thr Ser Leu Gln Trp Leu Gly Pro Asp Glu
      20      25      30
Trp Leu Leu Ile Val Pro Ser Gly Glu Glu Phe Ala Ala Glu Gln Asn
      35      40      45
Leu Arg Ala Ala Leu Gly Glu Leu His Ile Gln Val Val Asn Val Ser
      50      55      60
Gly Gly Gln Gln Ile Leu Glu Leu Ser Gly Pro Asn Val Arg Asp Val
      65      70      75      80
Leu Met Lys Ser Thr Ser Tyr Asp Val His Pro Asn Asn Phe Pro Val

```

```
<210> 1408
<211> 335
<212> PRT
<213> Homo sapiens
```



<400> 1408  
 Xaa Gly Arg Glu Lys Leu Glu Leu Val Leu Ser Asn Leu Gln Ala Asp  
 1 5 10 15  
 Val Leu Glu Leu Leu Leu Glu Phe Val Tyr Thr Gly Ser Leu Val Ile  
 20 25 30  
 Asp Ser Ala Asn Ala Lys Thr Leu Leu Glu Ala Ala Ser Lys Phe Gln  
 35 40 45  
 Phe His Thr Phe Cys Lys Val Cys Val Ser Phe Leu Glu Lys Gln Leu  
 50 55 60  
 Thr Ala Ser Asn Cys Leu Glu Val Ala Ala Met Ala Glu Ala Met Gln  
 65 70 75 80  
 Cys Ser Glu Leu Tyr His Xaa Ala Lys Ala Phe Ala Leu Gln Ile Phe  
 85 90 95  
 Pro Glu Val Ala Ala Gln Glu Glu Ile Leu Ser Ile Ser Lys Asp Asp  
 100 105 110  
 Phe Ile Ala Tyr Val Ser Asn Asp Ser Leu Asn Thr Lys Ala Glu Glu  
 115 120 125  
 Leu Val Tyr Glu Thr Val Ile Lys Trp Ile Lys Lys Asp Pro Ala Thr  
 130 135 140  
 Arg Thr Gln Tyr Ala Ala Glu Leu Leu Ala Val Val Arg Leu Pro Phe  
 145 150 155 160  
 Ile His Pro Ser Tyr Leu Leu Asn Val Val Asp Asn Glu Glu Leu Ile  
 165 170 175  
 Lys Ser Ser Glu Ala Cys Arg Asp Leu Val Asn Glu Ala Lys Arg Tyr  
 180 185 190  
 His Met Leu Pro His Ala Arg Gln Glu Met Gln Thr Pro Arg Thr Arg  
 195 200 205  
 Pro Arg Leu Ser Ala Gly Val Ala Glu Val Ile Val Leu Val Gly Gly  
 210 215 220  
 Arg Gln Met Val Gly Met Thr Gln Arg Ser Leu Val Ala Val Thr Cys  
 225 230 235 240  
 Trp Asn Pro Gln Asn Asn Lys Trp Tyr Pro Leu Ala Ser Val Pro Phe  
 245 250 255  
 Leu Gly Pro Gly Phe Phe Ser Val Val Ser Ala Gly Ala Asn Ile Tyr  
 260 265 270  
 Leu Ser Gly Gly Met Glu Ser Gly Val Pro Leu Ala Asp Val Trp Cys  
 275 280 285  
 Tyr Met Ser Leu Leu Asp Asn Trp Asn Leu Val Ser Arg Met Pro Val  
 290 295 300  
 Pro Arg Cys Arg Pro His Ser Leu Val Tyr Asp Gly Lys Ile Tyr Thr  
 305 310 315 320  
 Leu Gly Gly Leu Gly Val Ala Gly Asn Val Asp His Val Glu Arg  
 325 330 335

<210> 1409

<211> 279

<212> DNA

<213> Homo sapiens

<400> 1409

nnnatgaagt tcttggtttt ttcagaaaaa cgcgcttttt gctatgctgg ccgccccgcg  
 60  
 gcacgagata gcaccatgca actgatcgat atcggcgctca acctgaccaa cagcagtttc  
 120

cacgaccaac aggccgcaat cgtcgagcgc gcgctggagg ccggcggttac gcaaattgctg  
 180  
 ctgacaggca ccagcctggc ggtcagcgaa caagccctgg aactgtgcca tcaactggat  
 240  
 gcaagcggcg cccacctgtt cgccacggcc ggcgtgcac  
 279

<210> 1410  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 1410  
 Xaa Met Lys Phe Leu Val Phe Ser Glu Lys Arg Ala Phe Cys Tyr Ala  
 1 5 10 15  
 Gly Arg Pro Ala Ala Arg Asp Ser Thr Met Gln Leu Ile Asp Ile Gly  
 20 25 30  
 Val Asn Leu Thr Asn Ser Ser Phe His Asp Gln Gln Ala Ala Ile Val  
 35 40 45  
 Glu Arg Ala Leu Glu Ala Gly Val Thr Gln Met Leu Leu Thr Gly Thr  
 50 55 60  
 Ser Leu Ala Val Ser Glu Gln Ala Leu Glu Leu Cys His Gln Leu Asp  
 65 70 75 80  
 Ala Ser Gly Ala His Leu Phe Ala Thr Ala Gly Val His  
 85 90

<210> 1411  
 <211> 321  
 <212> DNA  
 <213> Homo sapiens

<400> 1411  
 nnnctattt caggaatgaa gaacgaacct gaatggatgc ttgaatggcg cttgagtgc  
 60  
 tttcgtgaat ggtagaaat ggaagagcct agctgggctc atgtcgatta ccctaaaatt  
 120  
 gattttcaat ctatttctta ctattccgcg ccaaaaagca tgaaggataa gcctaagtcg  
 180  
 ttagacgaag tcgatcctga attgttacgt acttatgaaa aactgggcat tctctcata  
 240  
 gaacagcaaa tgcttgctgg tatcgccgta gatgctgtct ttgactcagt gtctgtcgtt  
 300  
 actacttttc gtcaaaagct t  
 321

<210> 1412  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 1412  
 Xaa Arg Ile Ser Gly Met Lys Asn Glu Pro Glu Trp Met Leu Glu Trp  
 1 5 10 15  
 Arg Leu Ser Ala Phe Arg Glu Trp Leu Glu Met Glu Glu Pro Ser Trp

20 25 30  
 Ala His Val Asp Tyr Pro Lys Ile Asp Phe Gln Ser Ile Ser Tyr Tyr  
 35 40 45  
 Ser Ala Pro Lys Ser Met Lys Asp Lys Pro Lys Ser Leu Asp Glu Val  
 50 55 60  
 Asp Pro Glu Leu Leu Arg Thr Tyr Glu Lys Leu Gly Ile Pro Leu Ile  
 65 70 75 80  
 Glu Gln Gln Met Leu Ala Gly Ile Ala Val Asp Ala Val Phe Asp Ser  
 85 90 95  
 Val Ser Val Val Thr Thr Phe Arg Gln Lys Leu  
 100 105

&lt;210&gt; 1413

&lt;211&gt; 385

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1413

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 60  
 ggcgaaatcg gcctcgacct gatcatcgac ctgccacgtc cgcgtgcccg tgggtcacac  
 120  
 cgcctggccg cggttgaagc cgaagtata aaccgtgtgc tgtcataacc cngcacgaag  
 180  
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 240  
 gaggaacacc atcatgacta taaaagccat caacgtgcgt aaccagttaa aaggcaccat  
 300  
 caaggaaatc gtagtcggca acgtgctctc ggaaatcgac gtgcagaccg cctccgggat  
 360  
 cgtcacttct gtgatcacta cgcgt  
 385

&lt;210&gt; 1414

&lt;211&gt; 55

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1414

Met Thr His Asp Val Ser Glu Ala Val Ala Ile Ala Asp Arg Val Ile  
 1 5 10 15  
 Leu Ile Glu Asp Gly Glu Ile Gly Leu Asp Leu Ile Ile Asp Leu Pro  
 20 25 30  
 Arg Pro Arg Ala Arg Gly Ser His Arg Leu Ala Ala Leu Glu Ala Glu  
 35 40 45  
 Val Ile Asn Arg Val Leu Ser  
 50 55

&lt;210&gt; 1415

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1415

acgcgtgcag gcaaacatta atatgagtta acaccacaca ggatgagact gtttgtacct  
 60  
 gtaactgtcc ttgtcatctg tcttgcatgat ttagaagagg aatcagaaag ctgggacaac  
 120  
 tctgaggctg aagaggagga gaaagcccct gtgttgccag agagtacaga agggcgggag  
 180  
 ctgacccagg gcccggcaga gtctctctct ctctcaggct gtgggagctg gcagccccgg  
 240  
 aagctgccag tcttcaagtc cctccggcac atgaggcagg tcctgggtgc cccttctttc  
 300  
 cgcattgctg cctggcacgt tctcatgggg aaccagggtga tctggaaaag cagagacgtg  
 360  
 gacctcgtcc agtcagcttt tgaagtactt cgggtgagaa catcttttcc ttaggtgtgc  
 420

<210> 1416

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1416

Met	Arg	Leu	Phe	Val	Pro	Val	Thr	Val	Leu	Val	Ile	Cys	Leu	Ala	Asp
1				5					10					15	
Leu	Glu	Glu	Glu	Ser	Glu	Ser	Trp	Asp	Asn	Ser	Glu	Ala	Glu	Glu	Glu
			20					25					30		
Glu	Lys	Ala	Pro	Val	Leu	Pro	Glu	Ser	Thr	Glu	Gly	Arg	Glu	Leu	Thr
		35					40					45			
Gln	Gly	Pro	Ala	Glu	Ser	Ser	Ser	Leu	Ser	Gly	Cys	Gly	Ser	Trp	Gln
	50					55					60				
Pro	Arg	Lys	Leu	Pro	Val	Phe	Lys	Ser	Leu	Arg	His	Met	Arg	Gln	Val
65					70					75				80	
Leu	Gly	Ala	Pro	Ser	Phe	Arg	Met	Leu	Ala	Trp	His	Val	Leu	Met	Gly
			85						90					95	
Asn	Gln	Val	Ile	Trp	Lys	Ser	Arg	Asp	Val	Asp	Leu	Val	Gln	Ser	Ala
		100						105					110		
Phe	Glu	Val	Leu	Arg	Val	Arg	Thr	Ser	Phe	Pro					
		115					120								

<210> 1417

<211> 5058

<212> DNA

<213> Homo sapiens

<400> 1417

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 120  
 taggagggtg gccacccat ttccagtgtg acctgttccc attcccccat gtctcctccc  
 180  
 atccctcccg ccactcagct caggctgatg agaagcagag caacgggtgt atcgggtgtt  
 240  
 tctttcctgg tgggtagtg ggggtgggct gaggagagaa aagggtgatt agcgtggggc  
 300

cccgccctct tttgtcctct tcccagggtc cctggccctc tcggagaaac gcacttggtt  
360  
cgggccagcc gcctgagggg acggggctcac gtctgtcctc cactactgcag ctgctgggccc  
420  
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480  
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540  
ccaggaacca cagaggacac attaataact ggaagtaaaa ctctgcccc agtcacctca  
600  
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aatcaggaca tatcagcttc atctcagaac caccagacta agagcacgga gaccaccagc  
720  
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780  
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900  
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960  
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1020  
acttcctgga ggacctctat ccaagacaca tcagcttctt ctccagaacca ctggactcgg  
1080  
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tcagggtgaaa cagctacctc atccctctgt agtgtcacia acacatccat gatgacatca  
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gagaagataa cagtgacaac ctccacaggc tccactcttg gaaacccagg ggagacatca  
1320  
tcagtacctg ttactggaag tcttatgcc a gtcacctcag cagccttagt aacagttgat  
1380  
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1440  
tctaagaacc accagactca gagcgtggag accaccagag tatctcaa at caacaccctc  
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1980  
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5058

&lt;210&gt; 1418

&lt;211&gt; 1532

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1418

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Met Lys Gly Ala Arg Trp Arg Arg Val Pro Trp Val Ser Leu Ser Cys
 1           5           10           15
Leu Cys Leu Cys Leu Leu Pro His Val Val Pro Gly Thr Thr Glu Asp
      20           25           30
Thr Leu Ile Thr Gly Ser Lys Thr Pro Ala Pro Val Thr Ser Thr Gly
      35           40           45
Ser Thr Thr Ala Thr Leu Glu Gly Gln Ser Thr Ala Ala Ser Ser Arg
      50           55           60
Thr Ser Asn Gln Asp Ile Ser Ala Ser Ser Gln Asn His Gln Thr Lys
65           70           75           80
Ser Thr Glu Thr Thr Ser Lys Ala Gln Thr Asp Thr Leu Thr Gln Met
      85           90           95
Met Thr Ser Thr Leu Phe Ser Ser Pro Ser Val His Asn Val Met Glu
      100          105          110
Thr Val Thr Gln Glu Thr Ala Pro Pro Asp Glu Met Thr Thr Ser Phe
      115          120          125
Pro Ser Ser Val Thr Asn Thr Leu Met Met Thr Ser Lys Thr Ile Thr
      130          135          140
Met Thr Thr Ser Thr Asp Ser Thr Leu Gly Asn Thr Glu Glu Thr Ser
145          150          155          160
Thr Ala Gly Thr Glu Ser Ser Thr Pro Val Thr Ser Ala Val Ser Ile
      165          170          175
Thr Ala Gly Gln Glu Gly Gln Ser Arg Lys Thr Ser Trp Arg Thr Ser
      180          185          190
Ile Gln Asp Thr Ser Ala Ser Ser Gln Asn His Trp Thr Arg Ser Thr
      195          200          205
Gln Thr Thr Arg Glu Ser Gln Thr Ser Thr Leu Thr His Arg Thr Thr
      210          215          220
Ser Thr Pro Ser Phe Ser Pro Ser Val His Asn Val Thr Gly Thr Val
225          230          235          240
Ser Gln Lys Thr Ser Pro Ser Gly Glu Thr Ala Thr Ser Ser Leu Cys
      245          250          255
Ser Val Thr Asn Thr Ser Met Met Thr Ser Glu Lys Ile Thr Val Thr
      260          265          270
Thr Ser Thr Gly Ser Thr Leu Gly Asn Pro Gly Glu Thr Ser Ser Val
      275          280          285
Pro Val Thr Gly Ser Leu Met Pro Val Thr Ser Ala Ala Leu Val Thr
      290          295          300
Val Asp Pro Glu Gly Gln Ser Pro Ala Thr Phe Ser Arg Thr Ser Thr
305          310          315          320
Gln Asp Thr Thr Ala Phe Ser Lys Asn His Gln Thr Gln Ser Val Glu
      325          330          335
Thr Thr Arg Val Ser Gln Ile Asn Thr Leu Asn Thr Leu Thr Pro Val
      340          345          350
Thr Thr Ser Thr Val Leu Ser Ser Pro Ser Gly Phe Asn Pro Ser Gly
      355          360          365
Thr Val Ser Gln Glu Thr Phe Pro Ser Gly Glu Thr Thr Ile Ser Ser
      370          375          380
Pro Ser Ser Val Ser Asn Thr Phe Leu Val Thr Ser Lys Val Phe Arg

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385          390          395          400
Met Pro Ile Ser Arg Asp Ser Thr Leu Gly Asn Thr Glu Glu Thr Ser
          405          410          415
Leu Ser Val Ser Gly Thr Ile Ser Ala Ile Thr Ser Lys Val Ser Thr
          420          425          430
Ile Trp Trp Ser Asp Thr Leu Ser Thr Ala Leu Ser Pro Ser Ser Leu
          435          440          445
Pro Pro Lys Ile Ser Thr Ala Phe His Thr Gln Gln Ser Glu Gly Ala
          450          455          460
Glu Thr Thr Gly Arg Pro His Glu Arg Ser Ser Phe Ser Pro Gly Val
465          470          475          480
Ser Gln Glu Ile Phe Thr Leu His Glu Thr Thr Thr Trp Pro Ser Ser
          485          490          495
Phe Ser Ser Lys Gly His Thr Thr Trp Ser Gln Thr Glu Leu Pro Ser
          500          505          510
Thr Ser Thr Gly Ala Ala Thr Arg Leu Val Thr Gly Asn Pro Ser Thr
          515          520          525
Gly Ala Ala Gly Thr Ile Pro Arg Val Pro Ser Lys Val Ser Ala Ile
          530          535          540
Gly Glu Pro Gly Glu Pro Thr Thr Tyr Ser Ser His Ser Thr Thr Leu
545          550          555          560
Pro Lys Thr Thr Gly Ala Gly Ala Gln Thr Gln Trp Thr Gln Glu Thr
          565          570          575
Gly Thr Thr Gly Glu Ala Leu Leu Ser Ser Pro Ser Tyr Ser Val Thr
          580          585          590
Gln Met Ile Lys Thr Ala Thr Ser Pro Ser Ser Ser Pro Met Leu Asp
          595          600          605
Arg His Thr Ser Gln Gln Ile Thr Thr Ala Pro Ser Thr Asn His Ser
          610          615          620
Thr Ile His Ser Thr Ser Thr Ser Pro Gln Glu Ser Pro Ala Val Ser
625          630          635          640
Gln Arg Gly His Thr Gln Ala Pro Gln Thr Thr Gln Glu Ser Gln Thr
          645          650          655
Thr Arg Ser Val Ser Pro Met Thr Asp Thr Lys Thr Val Thr Thr Pro
          660          665          670
Gly Ser Ser Phe Thr Ala Ser Gly His Ser Pro Ser Glu Ile Val Pro
          675          680          685
Gln Asp Ala Pro Thr Ile Ser Ala Ala Thr Thr Phe Ala Pro Ala Pro
          690          695          700
Thr Gly Asp Gly His Thr Thr Gln Ala Pro Thr Thr Ala Leu Gln Ala
705          710          715          720
Thr Pro Ser Ser His Asp Ala Thr Leu Gly Pro Ser Gly Gly Thr Ser
          725          730          735
Leu Ser Lys Thr Gly Ala Leu Thr Leu Ala Asn Ser Val Val Ser Thr
          740          745          750
Pro Gly Gly Pro Glu Gly Gln Trp Thr Ser Ala Ser Ala Ser Thr Ser
          755          760          765
Pro Asp Thr Ala Ala Ala Met Thr His Thr His Gln Ala Glu Ser Thr
          770          775          780
Glu Ala Ser Gly Gln Thr Gln Thr Ser Glu Pro Ala Ser Ser Gly Ser
785          790          795          800
Arg Thr Thr Ser Ala Gly Thr Ala Thr Pro Ser Ser Ser Gly Ala Ser
          805          810          815
Gly Thr Thr Pro Ser Gly Ser Glu Gly Ile Ser Thr Ser Gly Glu Thr

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820										825					830				
Thr	Arg	Phe	Ser	Ser	Asn	Pro	Ser	Arg	Asp	Ser	His	Thr	Thr	Gln	Ser				
835						840					845								
Thr	Thr	Glu	Leu	Leu	Ser	Ala	Ser	Ala	Ser	His	Gly	Ala	Ile	Pro	Val				
850						855					860								
Ser	Thr	Gly	Met	Ala	Ser	Ser	Ile	Val	Pro	Gly	Thr	Phe	His	Pro	Thr				
865						870					875								
Leu	Ser	Glu	Ala	Ser	Thr	Ala	Gly	Arg	Pro	Thr	Gly	Gln	Ser	Ser	Pro				
885						890					895								
Thr	Ser	Pro	Ser	Ala	Ser	Pro	Gln	Glu	Thr	Ala	Ala	Ile	Ser	Arg	Met				
900						905					910								
Ala	Gln	Thr	Gln	Arg	Thr	Arg	Thr	Ser	Arg	Gly	Ser	Asp	Thr	Ile	Ser				
915						920					925								
Leu	Ala	Ser	Gln	Ala	Thr	Asp	Thr	Phe	Ser	Thr	Val	Pro	Pro	Thr	Pro				
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Pro	Ser	Ile	Thr	Ser	Ser	Gly	Leu	Thr	Ser	Pro	Gln	Thr	Gln	Thr	His				
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Thr	Leu	Ser	Pro	Ser	Gly	Ser	Gly	Lys	Thr	Phe	Thr	Thr	Ala	Leu	Ile				
965						970					975								
Ser	Asn	Ala	Thr	Pro	Leu	Pro	Val	Thr	Tyr	Ala	Ser	Ser	Ala	Ser	Thr				
980						985					990								
Gly	His	Thr	Thr	Pro	Leu	His	Val	Thr	Asp	Ala	Ser	Ser	Val	Ser	Thr				
995						1000					1005								
Gly	His	Ala	Thr	Pro	Leu	Pro	Val	Thr	Ser	Pro	Ser	Ser	Val	Ser	Thr				
1010						1015					1020								
Gly	Asp	Thr	Thr	Pro	Leu	Pro	Val	Thr	Ser	Pro	Ser	Ser	Ala	Ser	Ser				
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Gly	His	Ala	Thr	Ser	Leu	Pro	Val	Thr	Asp	Ala	Ser	Ser	Leu	Ser	Thr				
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Gly	His	Ala	Thr	Ser	Leu	His	Val	Thr	Asp	Ala	Ser	Ser	Val	Ser	Thr				
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Gly	His	Ala	Thr	Leu	Leu	His	Val	Thr	Asp	Ala	Ser	Ser	Ala	Ser	Thr				
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Gly	His	Thr	Thr	Ser	Leu	Pro	Val	Thr	Asp	Ala	Ser	Ser	Val	Ser	Thr				
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Gly	Asp	Thr	Thr	Pro	Leu	Pro	Val	Thr	Asp	Thr	Ser	Ser	Ala	Ser	Thr				
1105						1110					1115								
Gly	Asp	Thr	Thr	Pro	Leu	His	Val	Thr	Asp	Ala	Ser	Ser	Val	Ser	Thr				
1125						1130					1135								
Gly	His	Ala	Thr	Pro	Leu	His	Val	Thr	Ser	Leu	Ser	Ser	Val	Ser	Thr				
1140						1145					1150								
Gly	Asp	Thr	Thr	Pro	Leu	Pro	Val	Thr	Ser	Pro	Ser	Ser	Ala	Ser	Ser				
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Gly	His	Ala	Thr	Ser	Leu	Pro	Val	Thr	Asp	Ala	Ser	Ser	Val	Ser	Thr				
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1220						1225					1230								
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1235						1240					1245								
Gly	His	Ala	Thr	Ser	Leu	Leu	Val	Thr	Asp	Ala	Ser								

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Gly His Ala Thr Pro Leu His Val Thr Asp Ala Ser Ser Val Ser Thr		
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Gly Asp Thr Thr Pro Leu Pro Val Thr Ser Pro Ser Ser Ala Ser Thr		1280
	1285	1290
Gly Asp Thr Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr		1295
	1300	1305
Gly Asp Thr Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Val Ser Thr		1310
	1315	1320
Ser His Ala Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr		1325
	1330	1335
Ser His Ala Thr Ser Leu Pro Val Thr Asp Pro Ser Ser Ala Ser Thr		1340
1345	1350	1355
Gly Asp Thr Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Val Ser Thr		1360
	1365	1370
Gly His Ala Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr		1375
	1380	1385
Gly Asp Thr Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr		1390
	1395	1400
Gly His Ala Thr Pro Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr		1405
	1410	1415
Gly His Ala Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Ala Ser Thr		1420
1425	1430	1435
Gly His Thr Thr Pro Leu His Val Thr Ser Pro Ser Ser Ala Ser Thr		1440
	1445	1450
Gly His Ala Thr Pro Leu Pro Val Thr Ser Pro Ser Ser Ala Ser Thr		1455
	1460	1465
Ser His Ala Thr Ser Leu Pro Val Thr Asp Thr Ser Ser Ala Ser Thr		1470
	1475	1480
Gly His Ala Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Ala Ser Thr		1485
	1490	1495
Gly His Ala Thr Pro Leu Leu Val Thr Asp Thr Ser Ser Ala Ser Thr		1500
1505	1510	1515
Gly His Ala Thr Pro Leu Pro Val Thr Asp Thr Ser		1520
	1525	1530

&lt;210&gt; 1419

&lt;211&gt; 309

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1419

aaggctatgg gaattcaaaa gtatgtgttc tattccatcc acaactgtga caagcagcct  
60

gaggttccct tgatggaaat caagtattgt actggtaaatt ttattcagga cagtgggtctg  
120

gattatatca tcatccgttt gtgtgggttc atgcagggtc ttattgggca atatgctgtt  
180

cctatactag aagagaagtc cgtctgggga actgatgctc caactcggat tgcttacatg  
240

gatacccagg acgtagctcg actaacgttt atagctatgc ggaatgagaa ggccaacaag  
300

aaactcatg

309

&lt;210&gt; 1420

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1420

Lys Ala Met Gly Ile Gln Lys Tyr Val Phe Tyr Ser Ile His Asn Cys  
 1 5 10 15  
 Asp Lys Gln Pro Glu Val Pro Leu Met Glu Ile Lys Tyr Cys Thr Gly  
 20 25 30  
 Lys Phe Ile Gln Asp Ser Gly Leu Asp Tyr Ile Ile Ile Arg Leu Cys  
 35 40 45  
 Gly Phe Met Gln Gly Leu Ile Gly Gln Tyr Ala Val Pro Ile Leu Glu  
 50 55 60  
 Glu Lys Ser Val Trp Gly Thr Asp Ala Pro Thr Arg Ile Ala Tyr Met  
 65 70 75 80  
 Asp Thr Gln Asp Val Ala Arg Leu Thr Phe Ile Ala Met Arg Asn Glu  
 85 90 95  
 Lys Ala Asn Lys Lys Leu Met  
 100

&lt;210&gt; 1421

&lt;211&gt; 385

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1421

ccatggcggc atgggtggag agagaagctg gggagaagaa atgatgcaga gatctcgcca  
 60  
 ggccagggag ctgggctggg cagccaggag tagagaaaca acgctcccag aggaggggag  
 120  
 gatgttagag caaagccgag cccagctgct ggccaatgca tctgtgatgc ccatgagcag  
 180  
 ccaggatttc agctccgctc tactttctga ctgctgcaga actcagcacc agctccagt  
 240  
 ccctcagagc cctgattttt cacaaccga ctctccaag cctcccctgt gggcgggata  
 300  
 cacaagccag agtcgccttg tcacatctct tctctctcca ccaggtcag ggcaaacctt  
 360  
 cctgacatac tttacgacat tacag  
 385

&lt;210&gt; 1422

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1422

Met Gly Gly Glu Arg Ser Trp Gly Glu Glu Met Met Gln Arg Ser Arg  
 1 5 10 15  
 Gln Ala Arg Glu Leu Gly Trp Ala Ala Arg Ser Arg Glu Thr Thr Leu  
 20 25 30  
 Pro Glu Glu Gly Arg Met Leu Glu Gln Ser Arg Ala Gln Leu Leu Ala

```

      35              40              45
Asn Ala Ser Val Met Pro Met Ser Ser Gln Asp Phe Ser Ser Ala Leu
 50              55              60
Leu Leu Asp Cys Cys Arg Thr Gln His Gln Leu Gln Cys Pro Gln Ser
65              70              75              80
Pro Asp Phe Ser Gln Thr Asp Ser Ser Lys Pro Pro Leu Trp Ala Gly
      85              90              95
Tyr Thr Ser Gln Ser Arg Leu Val Thr Ser Leu Leu Ser Pro Pro Gly
      100              105              110
His Gly Gln Thr Phe Leu Thr Tyr Phe Thr Thr Leu Gln
      115              120              125

```

&lt;210&gt; 1423

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1423

```

nntattcttc aatccttcca caatgtgcaa caaatggcga ttgactggct cactcgaaat
60
ctctattttg tggaccatgt cggtgaccgg atctttgttt gtaattccaa cggttctgta
120
tgtgtcacc c tgattgatct ggagcttcac aatcctaaag caatagcagt agatccaata
180
gcaggaaaac ttttctttac tgactacggg aatgtcgcca aagtgagag atgtgacatg
240
gatgggatga accgaacaag gataattgat tcaaagacag agcagccagc tgcactggca
300
ctagacctag tcaacaaatt ggtttactgg gtagat
336

```

&lt;210&gt; 1424

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1424

```

Xaa Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp Trp
 1              5              10              15
Leu Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile Phe
      20              25              30
Val Cys Asn Ser Asn Gly Ser Val Cys Val Thr Leu Ile Asp Leu Glu
      35              40              45
Leu His Asn Pro Lys Ala Ile Ala Val Asp Pro Ile Ala Gly Lys Leu
      50              55              60
Phe Phe Thr Asp Tyr Gly Asn Val Ala Lys Val Glu Arg Cys Asp Met
65              70              75              80
Asp Gly Met Asn Arg Thr Arg Ile Ile Asp Ser Lys Thr Glu Gln Pro
      85              90              95
Ala Ala Leu Ala Leu Asp Leu Val Asn Lys Leu Val Tyr Trp Val Asp
      100              105              110

```

&lt;210&gt; 1425

&lt;211&gt; 672

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1425

```

accggtgttt tcgatcacct gggcggttg agtgactatc gcagtcagat cggcccgatg
60
gccccgcatg tcgaagacct ggccttggtg ctacaggtca ttgccgtga agatggggtc
120
gatgccgggg tgattccgat gccgtgcgc cgtatgcaa ctcaaactg gaaggggttg
180
cgagtcgcct ggtacagcga tgggtggcatt gagccgttg acgcgtcac gcacaccaca
240
ttgcaggcgg tcgccgatct attggacgct gaaggcgct tgatccgcc ggccttcccc
300
tcggcggttg gcaatgcccg tgacattacc gaacgtatt gggcaatgag tcaaagctcc
360
ggcgcgcatg cgatccagct gttttcagat tgggatcagt tccgtacagc catgctgggg
420
ttcatggccg actacgacat taccctgtgc cctgtcgatg ccgcgccggc gacccaactg
480
ggagagacgc ggccagggct gttcagttcc ccccttccta atggcttggc gggttggcct
540
tgtgtggtgg tccgggcccg aacggatagc gcggttttgc cggttggcgt gcagattgtc
600
gcgcgacctt ggcacgagcc tgtcgcgttg gcggcagcag cggccattga gcgcgcgtg
660
ccgttcacgc gt
672

```

&lt;210&gt; 1426

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1426

```

Thr Gly Val Phe Asp His Leu Gly Gly Leu Ser Asp Tyr Arg Ser Gln
1      5      10      15
Ile Gly Pro Met Ala Arg His Val Glu Asp Leu Ala Leu Ala Leu Gln
20     25     30
Val Ile Ala Gly Glu Asp Gly Val Asp Ala Gly Val Ile Pro Met Pro
35     40     45
Leu Arg Arg Met Gln Thr Gln Thr Leu Lys Gly Leu Arg Val Ala Trp
50     55     60
Tyr Ser Asp Gly Gly Ile Glu Pro Val Asp Ala Leu Thr His Thr Thr
65     70     75     80
Leu Gln Ala Val Ala Asp Leu Leu Asp Ala Glu Gly Ala Leu Ile Arg
85     90     95
Pro Ala Phe Pro Ser Ala Leu Ser Asn Ala Arg Asp Ile Thr Glu Arg
100    105    110
Tyr Trp Ala Met Ser Gln Ser Ser Gly Ala Gln Ser Ile Gln Leu Phe
115    120    125
Ser Asp Trp Asp Gln Phe Arg Thr Ala Met Leu Gly Phe Met Ala Asp
130    135    140
Tyr Asp Ile Ile Leu Cys Pro Val Asp Ala Ala Pro Ala Thr Gln Leu

```

```

145          150          155          160
Gly Glu Thr Arg Pro Gly Leu Phe Ser Ser Pro Leu Pro Asn Gly Leu
          165          170          175
Ala Gly Trp Pro Cys Val Val Val Arg Ala Gly Thr Asp Ser Ala Gly
          180          185          190
Leu Pro Val Gly Val Gln Ile Val Ala Arg Pro Trp His Glu Pro Val
          195          200          205
Ala Leu Ala Ala Ala Ala Ala Ile Glu Arg Ala Leu Pro Phe Thr Arg
          210          215          220

```

<210> 1427  
 <211> 270  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1427
atggcttgct atctgaagca ggtggctgcc accgtctgca taaatgggcc cagcgagtc
60
tttgatgttc cactaagata cggggatctg gtggtgacac ccatgcgact ggcttcggaa
120
ttgatgcaag tccatccctc aggggctgta cgcttcgctc actgttcagt tccccagaat
180
aaactcaact cacaaaagat acttccggtg gaaaaggccc aagggaagat cctcttcatt
240
gcaggagaga atgacgaaag cttggctagc
270

```

<210> 1428  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1428
Met Ala Cys Tyr Leu Lys Gln Val Ala Ala Thr Val Cys Ile Asn Gly
1          5          10          15
Pro Ser Ala Val Phe Asp Val Pro Leu Arg Tyr Gly Asp Leu Val Val
          20          25          30
Thr Pro Met Arg Leu Ala Ser Glu Leu Met Gln Val His Pro Ser Gly
          35          40          45
Ala Val Arg Phe Arg His Cys Ser Val Pro Gln Asn Lys Leu Asn Ser
          50          55          60
Gln Lys Ile Leu Pro Val Glu Lys Ala Gln Gly Lys Ile Leu Phe Ile
65          70          75          80
Ala Gly Glu Asn Asp Glu Ser Leu Ala Ser
          85          90

```

<210> 1429  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1429
ncttagggga ttatcgacat aaacgcgact gcgtaagggtt ggtgactcat cccccagcga
60

```

catgaggcaa acgccatgac atccgagaat gcaccgccgc gaggaagat catcatgatg  
 120  
 gcggtgatcg ccggcgcggt ggtcaccaac atttactgca cccagccggt gctgccggtg  
 180  
 atcgccctcg acatgggcgt cgcagtgtcg acggtcaacc tgggtggcagg cgcggccttg  
 240  
 ctgggggttg ccaccgggtt ggcgttttta ttgcccatgg gcgaccgctt tgaccggcgc  
 300  
 aagctggtac tcgggcagat tgcgctggcg ttctgctttg ccttggcggc ggcttttgcg  
 360  
 ccgaggatct gggcgttgat cggc  
 384

<210> 1430

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1430

Met	Thr	Ser	Glu	Asn	Ala	Pro	Pro	Arg	Gly	Lys	Ile	Ile	Met	Met	Ala
1				5					10					15	
Val	Ile	Ala	Gly	Ala	Val	Val	Thr	Asn	Ile	Tyr	Cys	Thr	Gln	Pro	Val
		20						25					30		
Leu	Pro	Leu	Ile	Ala	Ser	Asp	Met	Gly	Val	Ala	Val	Ser	Thr	Val	Asn
		35					40					45			
Leu	Val	Ala	Gly	Ala	Ala	Leu	Leu	Gly	Phe	Ala	Thr	Gly	Leu	Ala	Phe
	50					55					60				
Leu	Leu	Pro	Met	Gly	Asp	Arg	Phe	Asp	Arg	Arg	Lys	Leu	Val	Leu	Gly
65				70					75					80	
Gln	Ile	Ala	Leu	Ala	Phe	Cys	Phe	Ala	Leu	Ala	Ala	Ala	Phe	Ala	Pro
			85						90					95	
Arg	Ile	Trp	Ala	Leu	Ile	Gly									
				100											

<210> 1431

<211> 414

<212> DNA

<213> Homo sapiens

<400> 1431

aagcttcagg gcagggtgcc cctgaagtca agcctgattc tgcattatct tgtatagcac  
 60  
 aaactggcga cacctgtgac ttgaccttc ccagggtccc tgcctccgc tccaggtagg  
 120  
 ctgacctga gggagggtgct ggcaggagcc tcggaggcag gaggggctgg cgtgcttcac  
 180  
 tccttcagct tgtcttgga gagctgtggg ctgcatcccc ctggctcttc gtcccacagg  
 240  
 cagccccgct gtgtgtctgg tcttgaggt tggctgcagc ttctgggcc tgcttcacg  
 300  
 ccctcttccc atgacctcc agccttgga ggtgtaatag tttccatgt tgctgatctt  
 360  
 tagtttgct ccctctctt ggcgtgtctt tctgctgttc catctctgt gcac  
 414



<210> 1432  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 1432  
 Met Gly Asn Tyr Tyr Thr Phe Gln Gly Trp Arg Ile Met Gly Arg Gly  
 1 5 10 15  
 Ala Gly Ser Arg Ala Gln Lys Leu Gln Pro Thr Cys Lys Thr Arg His  
 20 25 30  
 Thr Ala Gly Leu Pro Val Gly Arg Gly Ala Arg Gly Met Gln Pro Thr  
 35 40 45  
 Ala Leu Pro Arg Gln Ala Glu Gly Val Lys His Ala Ser Pro Ser Cys  
 50 55 60  
 Leu Arg Gly Ser Cys Gln His Leu Pro Gln Ala Glu Pro Thr Trp Ser  
 65 70 75 80  
 Gly Glu Gln Gly Pro Trp Glu Arg Gln Ser His Arg Cys Arg Gln Phe  
 85 90 95  
 Val Leu Tyr Lys Met Met Gln Asn Gln Ala  
 100 105

<210> 1433  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<400> 1433  
 aaattttcga tgggaactggg cggcaatgca ccgtttattg tatttgatga tgcggatgtg  
 60  
 gacgcggccg tcagcaatgc tgtggcttgc aagttccgct gtggtggaca aacgtgcatt  
 120  
 tcggccaacc gaatctacgt gcacgaacaa gtgcacgacg agtttgtctc taagtttggc  
 180  
 gagagagtca agaagcttcg cgtgggctac ggtctggacg aaaacatcaa cattggaccg  
 240  
 ctagtgaatg aggctagtca ggacaaagca gagtcacatg tccgtgcat gcaa  
 294

<210> 1434  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 1434  
 Lys Phe Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Asp  
 1 5 10 15  
 Asp Ala Asp Val Asp Ala Ala Val Ser Asn Ala Val Ala Cys Lys Phe  
 20 25 30  
 Arg Cys Gly Gly Gln Thr Cys Ile Ser Ala Asn Arg Ile Tyr Val His  
 35 40 45  
 Glu Gln Val His Asp Glu Phe Val Ser Lys Phe Gly Glu Arg Val Lys  
 50 55 60  
 Lys Leu Arg Val Gly Tyr Gly Leu Asp Glu Asn Ile Asn Ile Gly Pro

65                                      70                                      75                                      80  
 Leu Val Asn Glu Ala Ser Gln Asp Lys Ala Glu Ser His Val Arg Ala  
    85                                      90                                      95  
 Met Gln

<210> 1435

<211> 1772

<212> DNA

<213> Homo sapiens

<400> 1435

nttttctggct tatgtggttt ccccggtgtgt gaggtgggat ccactccccg catagtctct  
 60  
 cgtggcgatg ggacacctgg aaagtgctgt gatgtctttg aatgtgttaa tgatacaaag  
 120  
 ccagcctgcy tattaacaa tgtggaatat tatgatggag acatgtttcg aatggacaac  
 180  
 tgtcggttct gtcgatgcca agggggcggt gccatctgct tcaactgcca gtgtggtgag  
 240  
 ataaactgcy agaggtacta cgtgccccgaa ggagagtgtt gccagtgtg tgaaatccag  
 300  
 tgtatccttt taataatccc gctggctgct gccaatggcc tgatccttgc ccacggagac  
 360  
 cggtaggcggg aagacgactg cacattctgc cagtgcgtca acggtgaacg ccactgcgtt  
 420  
 gcgaccgtct gcggacagac ctgcacaaac cctgtgaaag tgcctgggga gtgttgccct  
 480  
 gtgtgcgaag aaccaaccat catcacagtt gatccacctg catgtgggga gttatcaaac  
 540  
 tgcactctga cagggaagga ctgcattaat ggtttcaaac gcgatcaca tggttgcg  
 600  
 acctgtcagt gcataaacac cgaggaacta tgttcagaac gtaaacaagg ctgcacctg  
 660  
 aactgtccct tcggtttcct tactgatgcc caaaactgtg agatctgtga gtgccgcccc  
 720  
 aggcccaaga agtcagacc cataatctgt gacaagtatt gtccacttgg attgtggaag  
 780  
 aataagcacg gctgtgacat ctgtcgctgt aagaaatgtc cagagctctc atgcagtaag  
 840  
 natctgcccc ttgggtttcc agcaggacag tcacggctgt cttatctgca agtcagaga  
 900  
 ggcctctgct tcagctgggc caccatcctt gtcgggcaact tgtctcaccg tggatggtca  
 960  
 tcatcataaa aatgaggaga gctggcacga tgggtgccg gaatgctact gtctcaatgg  
 1020  
 acgggaaatg tgtgccctga tcacctgccc ggtgcctgcc tgtggcaacc ccaccattca  
 1080  
 ccctggacag tgctgcccac catgtgcaga tgactttgtg gtgcagaagc cagagctcag  
 1140  
 tactccnct ccatttgcca cggccctgga ggagaatact ttgtggaagg agaaacgtgg  
 1200  
 aacattgact cctgtactca gtgcacctgc cacagcggac ggggtgctgtg tgagacagag  
 1260

gtgtgcccac cgctgctctg ccagaacccc tcacgcaccc aggattcctg ctgcccacag  
 1320  
 tgtacagatc aaccttttcg gccttccttg tcccgcaata acagcgtacc taattactgc  
 1380  
 aaaaatgatg aaggggatat attcctggca gctgagtcct ggaagcctga cgtttgtacc  
 1440  
 agctgcatct gcattgatag cgtaattagc tgtttctctg agtcctgccc ttctgtatcc  
 1500  
 tgtgaaaaac ctgtcttgag aaaaggccag tgttgtccct actgcataga agacacaatt  
 1560  
 ccaaagaagg tggtgtgccca cttcagtggg aaggcctatg ccgacgagga gcggtgggac  
 1620  
 cttgacagct gcacccactg ctactgcctg cagggccaga ccttctgctc gaccgtcagc  
 1680  
 tgcccccttc tgccctgtgt tgagcccatc aacgtggaag gaagttgctg cccaatgtgt  
 1740  
 ccagaaatgt atgtcccagt ccccttcacgc gt  
 1772

&lt;210&gt; 1436

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1436

Xaa	Ser	Gly	Leu	Cys	Gly	Phe	Pro	Val	Cys	Glu	Val	Gly	Ser	Thr	Pro
1				5					10					15	
Arg	Ile	Val	Ser	Arg	Gly	Asp	Gly	Thr	Pro	Gly	Lys	Cys	Cys	Asp	Val
		20						25					30		
Phe	Glu	Cys	Val	Asn	Asp	Thr	Lys	Pro	Ala	Cys	Val	Phe	Asn	Asn	Val
		35					40					45			
Glu	Tyr	Tyr	Asp	Gly	Asp	Met	Phe	Arg	Met	Asp	Asn	Cys	Arg	Phe	Cys
	50					55					60				
Arg	Cys	Gln	Gly	Gly	Val	Ala	Ile	Cys	Phe	Thr	Ala	Gln	Cys	Gly	Glu
65					70					75				80	
Ile	Asn	Cys	Glu	Arg	Tyr	Tyr	Val	Pro	Glu	Gly	Glu	Cys	Cys	Pro	Val
			85					90						95	
Cys	Glu	Ile	Gln	Cys	Ile	Leu	Leu	Ile	Pro	Leu	Ala	Ala	Ala	Asn	
		100						105					110		
Gly	Leu	Ile	Leu	Ala	His	Gly	Asp	Arg	Trp	Arg	Glu	Asp	Asp	Cys	Thr
	115						120				125				
Phe	Cys	Gln	Cys	Val	Asn	Gly	Glu	Arg	His	Cys	Val	Ala	Thr	Val	Cys
	130					135					140				
Gly	Gln	Thr	Cys	Thr	Asn	Pro	Val	Lys	Val	Pro	Gly	Glu	Cys	Cys	Pro
145					150					155				160	
Val	Cys	Glu	Glu	Pro	Thr	Ile	Ile	Thr	Val	Asp	Pro	Pro	Ala	Cys	Gly
			165					170						175	
Glu	Leu	Ser	Asn	Cys	Thr	Leu	Thr	Gly	Lys	Asp	Cys	Ile	Asn	Gly	Phe
		180						185					190		
Lys	Arg	Asp	His	Asn	Gly	Cys	Arg	Thr	Cys	Gln	Cys	Ile	Asn	Thr	Glu
	195						200					205			
Glu	Leu	Cys	Ser	Glu	Arg	Lys	Gln	Gly	Cys	Thr	Leu	Asn	Cys	Pro	Phe
	210					215					220				
Gly	Phe	Leu	Thr	Asp	Ala	Gln	Asn	Cys	Glu	Ile	Cys	Glu	Cys	Arg	Pro

```

225          230          235          240
Arg Pro Lys Lys Cys Arg Pro Ile Ile Cys Asp Lys Tyr Cys Pro Leu
          245          250          255
Gly Leu Leu Lys Asn Lys His Gly Cys Asp Ile Cys Arg Cys Lys Lys
          260          265          270
Cys Pro Glu Leu Ser Cys Ser Lys Xaa Leu Pro Leu Gly Phe Pro Ala
          275          280          285
Gly Gln Ser Arg Leu Ser Tyr Leu Gln Val Gln Arg Gly Leu Cys Phe
          290          295          300
Ser Trp Ala Thr His Pro Val Gly His Leu Ser His Arg Gly Trp Ser
305          310          315          320
Ser Ser

```

<210> 1437  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1437
cgggaactgt gctcgccac catccggtga ccggtgtcgg gcagtggcaa ctcaacaccc
60
aggccatgac cggagccatc ccgagcagca ggtgcacggc ccgggccggt gactcgtgga
120
cccgtaacct catgacctcg atgcaacttc cacgggtggc caccgatcac atcgaccgct
180
cgggtccatgt cgatgctgag cagttcgacc ggttgcgcag cgagttcctg tcccgtgggc
240
acagttcttg ccctgccgca catgggggtcc tgggacttgg ccggggcctg ggtggccaga
300
cgcggtttct ccccgagttc cgtcgcgagg aatcttccga gggcacagtt cgagttgttc
360
tgccgcacgc gt
372

```

<210> 1438  
 <211> 62  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1438
Met Ser Met Leu Ser Ser Ser Thr Gly Cys Ala Ala Ser Ser Cys Pro
1          5          10          15
Val Gly Thr Val Leu Ala Leu Pro His Met Gly Ser Trp Asp Leu Ala
20          25          30
Gly Ala Trp Val Ala Arg Arg Gly Phe Ser Pro Ser Ser Val Ala Glu
35          40          45
Asn Leu Pro Arg Ala Gln Phe Glu Leu Phe Cys Arg Thr Arg
50          55          60

```

<210> 1439  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 1439

accggtttgc tttccacaag gagagctaaa atgccggttg ctaagcagca tacatgccgc  
60  
tgcttctttc cacaatgtag acttaaaaaa atcgccgtaa acattttacc atatgattga  
120  
gtcaggtgtg gggagtcgca gtaaacattt taccatgtga ttgagtcatg ggtggggagt  
180  
cgcggaataa cacagggcag gcagttcgct atcacgatgt tctctctcat ttctgtcttt  
240  
ggtctgtctt cctgggtaat gtcacatgga gaccagggg atctgccatc agctgtgtgc  
300  
agtgggttaa caagacgacg gggaacttca gagtgcaggc agtcctcatc tttggcagat  
360  
tctgtatttg cacattcacc cactcactga aatgcatttg taaccccaaa atcaatacag  
420  
cggtttcaca gtcattttcc gacacgggca gaggggtgaa gatactgagt c  
471

&lt;210&gt; 1440

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1440

Met	Gly	Gly	Glu	Ser	Arg	Lys	Tyr	Thr	Gly	Gln	Ala	Val	Arg	Tyr	His
1				5				10						15	
Asp	Val	Leu	Ser	His	Phe	Cys	Leu	Trp	Ser	Val	Phe	Leu	Gly	Asn	Val
		20						25					30		
Thr	Trp	Arg	Pro	Arg	Gly	Ser	Ala	Ile	Ser	Cys	Val	Gln	Trp	Val	Asn
		35					40					45			
Lys	Thr	Thr	Gly	Asn	Phe	Arg	Val	Gln	Ala	Val	Leu	Ile	Phe	Gly	Arg
	50					55					60				
Phe	Cys	Ile	Cys	Thr	Phe	Thr	His	Ser	Leu	Lys	Cys	Ile	Cys	Asn	Pro
65				70					75					80	
Lys	Ile	Asn	Thr	Ala	Val	Ser	Gln	Ser	Phe	Ser	Asp	Thr	Gly	Arg	Gly
			85					90						95	
Val	Lys	Ile	Leu	Ser											
			100												

&lt;210&gt; 1441

&lt;211&gt; 376

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1441

nnngagtcgc ggggaccttc atggactctc tcgtgctccg tagctcacac tcaccgcacg  
60  
gcagctcaca ttcaccacac gggaactcac tctcaccaca cggcagctca ctctctctgc  
120  
accgcagctc acactcaccg cacggcagct cactctcacc gcacggcagc tcacactcac  
180  
cacacagcag ctactctta ccggacgggg aacctaaact taccggacgg gaagcctcac  
240

tctcaccgca cggaaagctc acactcaccg caccgcagcc actctcaccg cacggcagct  
 300  
 cactctcacc gcaccgcagc tcaactctcac cggacgggag ctcaactctca ccacacggca  
 360  
 cctcactctc acgcgt  
 376

<210> 1442  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 1442  
 Xaa Glu Ser Arg Gly Pro Ser Trp Thr Leu Ser Cys Ser Val Ala His  
 1 5 10 15  
 Thr His Arg Thr Ala Ala His Ile His His Thr Gly Thr His Ser His  
 20 25 30  
 His Thr Ala Ala His Ser Leu Cys Thr Ala Ala His Thr His Arg Thr  
 35 40 45  
 Ala Ala His Ser His Arg Thr Ala Ala His Thr His His Thr Ala Ala  
 50 55 60  
 His Ser Tyr Arg Thr Gly Asn Leu Asn Leu Pro Asp Gly Lys Pro His  
 65 70 75 80  
 Ser His Arg Thr Glu Ser Ser His Ser Pro His Arg Ser His Ser His  
 85 90 95  
 Arg Thr Ala Ala His Ser His Arg Thr Ala Ala His Ser His Arg Thr  
 100 105 110  
 Gly Ala His Ser His His Thr Ala Pro His Ser His Ala  
 115 120 125

<210> 1443  
 <211> 286  
 <212> DNA  
 <213> Homo sapiens

<400> 1443  
 atggcagccc tgcgtcccaa ggagctgccca caactaatgg tcgccatcgg caatgcgagc  
 60  
 ataaaacgga caacacgctg cctgatcgaa tggcaactcc acaccatgac cgtcctcgcg  
 120  
 gaagccgcta cgacttctctg ggctgacatc gactgcgaca agaaaacctg gacgatccca  
 180  
 gcggagcgta tgaaaaagcg acgtgccccat gtcataccgc taaccgagca cgcacttgcc  
 240  
 ttgcttgaga caatcaaacc ctacagcggn cacagagagt acgcgt  
 286

<210> 1444  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 1444  
 Met Ala Ala Leu Arg Pro Lys Glu Leu Pro Gln Leu Met Val Ala Ile

```

1           5           10           15
Gly Asn Ala Ser Ile Lys Arg Thr Thr Arg Cys Leu Ile Glu Trp Gln
      20           25           30
Leu His Thr Met Thr Arg Pro Ala Glu Ala Ala Thr Thr Ser Trp Ala
      35           40           45
Asp Ile Asp Cys Asp Lys Lys Thr Trp Thr Ile Pro Ala Glu Arg Met
      50           55           60
Lys Lys Arg Arg Ala His Val Ile Pro Leu Thr Glu His Ala Leu Ala
      65           70           75           80
Leu Leu Glu Thr Ile Lys Pro Tyr Ser Gly His Arg Glu Tyr Ala
      85           90           95

```

&lt;210&gt; 1445

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1445

```

naccggttca ccggggaggg cttcgatggg ggcaaggtca gcatggttgg cccgattccc
60
atgtacctgt atggcacctt cgtcgttccg gacttcgacg cattcatctc cggcaagcag
120
actccctacc gggagacggt ctccaagcgg accactactt ggttctttcg agccggctca
180
gaggtttatg agctggccnt cccccgagga gtcgtgttcg ccatgcaaag cgctcgttg
240
agggtggacc ccgacaacac cgtcgacaag ctgccaacac tcggcgagcg cctg
294

```

&lt;210&gt; 1446

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1446

```

Xaa Arg Phe Thr Gly Glu Ala Phe Asp Gly Gly Lys Val Ser Met Val
1           5           10           15
Gly Pro Ile Pro Met Tyr Leu Tyr Gly Thr Phe Val Val Pro Asp Phe
      20           25           30
Asp Ala Phe Ile Ser Gly Lys Gln Thr Pro Tyr Arg Glu Thr Val Ser
      35           40           45
Lys Arg Thr Thr Thr Trp Phe Phe Arg Ala Gly Ser Glu Val Tyr Glu
      50           55           60
Leu Ala Xaa Pro Arg Gly Val Val Phe Ala Met Gln Ser Ala Ser Leu
      65           70           75           80
Arg Val Asp Pro Asp Asn Thr Val Asp Lys Leu Pro Thr Leu Gly Glu
      85           90           95
Arg Leu

```

&lt;210&gt; 1447

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1447

```

nnncagaacc agaagatcaa cctgcatgac ggctcgttct ccgacgttgg cggcatgggtg
60
ggtaatatct ccattgcccc ggggtgtcacg atcgagaacg ccgtcggcgg ttcgggcaac
120
gacctgctga tcggcaacga tgcggccaac gaactgcgcg gcggtgccgg caacgatatc
180
ctctacgggg ctggcgggtgc cgaccagggtt tgggttggtt cgggcaacaa taccttcgtg
240
ttcgccgccc tttccgactc ggcgccgaaa gcggccgacc ggatcatgga cttcaccagt
300
ggccaggaca agatcgatct gtcggggatc acccatgggt cgggcctgac cttcgtcaac
360
gcg
363

```

&lt;210&gt; 1448

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1448

```

Xaa Gln Asn Gln Lys Ile Asn Leu His Asp Gly Ser Phe Ser Asp Val
1      5      10      15
Gly Gly Met Val Gly Asn Ile Ser Ile Ala Gln Gly Val Thr Ile Glu
20     25     30
Asn Ala Val Gly Gly Ser Gly Asn Asp Leu Leu Ile Gly Asn Asp Ala
35     40     45
Ala Asn Glu Leu Arg Gly Gly Ala Gly Asn Asp Ile Leu Tyr Gly Ala
50     55     60
Gly Gly Ala Asp Gln Val Trp Val Gly Ser Gly Asn Asn Thr Phe Val
65     70     75     80
Phe Ala Ala Val Ser Asp Ser Ala Pro Lys Ala Ala Asp Arg Ile Met
85     90     95
Asp Phe Thr Ser Gly Gln Asp Lys Ile Asp Leu Ser Gly Ile Thr His
100    105    110
Gly Ser Gly Leu Thr Phe Val Asn Ala
115    120

```

&lt;210&gt; 1449

&lt;211&gt; 541

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1449

```

aggcgctacc agattatggg ctgcccgacc tcaatgacat gcgcttgagc ctgcatgaat
60
cactcagcca atcgcgcttg gcgattgaac gctttatcca ggcgtacgag cctcggttgg
120
ggaatgtacg tgtcaggagg agggagggtg cctacaaccc tttggtactg gcgtttgtga
180
ttgaggcaac cgtcgtcatc gatggtgtca tccaacctgt ggtgtttaac gcacacctgg
240

```



tggggggggg gacgggtcga gtgtgttacc tgatgttctt tgagctcttt taccagagtg  
 300  
 aactcagtgc attgcgcacg cttggggcgc gtttttctga acgcaatccc gccctggcac  
 360  
 cttttcttgc cgattccagg ccaggaccgc gacgtcgagg gtctattgaa agtctttgcc  
 420  
 tttctccccg ggcgcctgcg ccagaagctt gctgacgagc ttctgaggtt gacccattca  
 480  
 ttgatgcact tgggtgtggc caattacatg cggccattgc cggccttcag tattttgcag  
 540  
 t  
 541

<210> 1450

<211> 138

<212> PRT

<213> Homo sapiens

<400> 1450

Met	Arg	Leu	Ser	Leu	His	Glu	Ser	Leu	Ser	Gln	Ser	Arg	Leu	Ala	Ile
1				5				10					15		
Glu	Arg	Phe	Ile	Gln	Ala	Tyr	Glu	Pro	Arg	Leu	Gly	Asn	Val	Arg	Val
			20				25					30			
Arg	Arg	Arg	Glu	Gly	Ala	Tyr	Asn	Pro	Leu	Val	Leu	Ala	Phe	Val	Ile
			35				40					45			
Glu	Ala	Thr	Val	Val	Ile	Asp	Gly	Val	Ile	Gln	Pro	Val	Val	Phe	Asn
			50				55				60				
Ala	His	Leu	Val	Gly	Gly	Gly	Thr	Gly	Arg	Val	Cys	Tyr	Leu	Met	Phe
65						70				75				80	
Phe	Glu	Leu	Phe	Tyr	Gln	Ser	Glu	Leu	Ser	Ala	Leu	Arg	Thr	Leu	Gly
			85						90					95	
Arg	Arg	Phe	Ser	Glu	Arg	Asn	Pro	Ala	Leu	Ala	Pro	Phe	Leu	Ala	Asp
			100					105					110		
Ser	Arg	Pro	Gly	Pro	Gly	Arg	Arg	Gly	Ser	Ile	Glu	Ser	Leu	Cys	Leu
			115					120					125		
Ser	Pro	Arg	Ala	Pro	Ala	Pro	Glu	Ala	Cys						
			130					135							

<210> 1451

<211> 326

<212> DNA

<213> Homo sapiens

<400> 1451

aggcctctgg cgagttgatc tacagcttcg gaccgggtgc tatggctact ggcgtcaagt  
 60  
 acacgaacac agtttgact cctgtgggcg actacgaggt ggtgctgacg gattcttggg  
 120  
 gtgatggctg gaacccgggt tcttacctga acatgtacga cagctcggac aacttgatcc  
 180  
 aggagttcac gatggattac gacgcctctt ctcgtaacat taaggagaag cacggcttct  
 240  
 tcacggtggc ttccaccacg agcagcggca ctgtctggaa gattatggcg aacaagaagg  
 300

tggacaagga gtggaactct gtggac  
326

<210> 1452

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1452

Met Ala Thr Gly Val Lys Tyr Thr Asn Thr Val Cys Thr Pro Val Gly  
1 5 10 15  
Asp Tyr Glu Val Val Leu Thr Asp Ser Trp Gly Asp Gly Trp Asn Pro  
20 25 30  
Gly Ser Tyr Leu Asn Met Tyr Asp Ser Ser Asp Asn Leu Ile Gln Glu  
35 40 45  
Phe Thr Met Asp Tyr Asp Ala Ser Ser Arg Asn Ile Lys Glu Lys His  
50 55 60  
Gly Phe Phe Thr Val Ala Ser Thr Thr Ser Ser Gly Thr Val Trp Lys  
65 70 75 80  
Ile Met Ala Asn Lys Lys Val Asp Lys Glu Trp Asn Ser Val Asp  
85 90 95

<210> 1453

<211> 326

<212> DNA

<213> Homo sapiens

<400> 1453

cggccgcgcg gccccacgtg caccgcgtgc atggtccttc gaggacgcgc atctgcagcc  
60  
cccgtcctcc gcaaacctcc aggccggaga gctccggcca aggccgctgc atcacatgat  
120  
acaggagggg catgcacacg ctacagtgca cacagcctca aacacgctca tccgtacata  
180  
caggagtgtg tgaacgcact gaggtgcaca ggacaaagac acagacacct gtttgcacac  
240  
cgactgcct atagaaatgt gcaaaccacc cgtgcgcaca ggcccctcca cccatgcagg  
300  
cgtgtgcaca tcaccacac ggacac  
326

<210> 1454

<211> 98

<212> PRT

<213> Homo sapiens

<400> 1454

Met Val Pro Arg Gly Arg Ala Ser Ala Ala Pro Ala Pro Arg Lys Pro  
1 5 10 15  
Pro Gly Arg Arg Ala Pro Ala Lys Ala Ala Ala Ser His Asp Thr Gly  
20 25 30  
Gly Ala Cys Thr Arg Ser Arg Ala His Ser Leu Lys His Ala His Pro  
35 40 45  
Tyr Ile Gln Glu Cys Val Asn Ala Leu Arg Cys Thr Gly Gln Arg His

```

      50              55              60
Arg His Leu Phe Ala His Arg Leu Ala Tyr Arg Asn Val Gln Thr Thr
65              70              75              80
Arg Ala His Arg Pro Leu His Pro Cys Arg Arg Val His Ile Thr His
      85              90              95
Thr Asp

```

<210> 1455  
 <211> 314  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1455
gatccagtca aaaaagcatg tgggggttgct cacgctgggt ggaaaggtac ttgtttgggt
60
gttgctatgg ctacagtga tgcctatgata gcagaatag gctgccgttt ggaaaaactt
120
tggtggacct tggacccttc agtgggacct ggctgtttta ctcttcagg ggaatcagca
180
gaggcatttc ataattctta tcctgcatgt gtacaactat ttgattcacc aaatccctgt
240
atcgacatcc gtaaagccac aagataactg actggatttt tgtataactg ctctctgect
300
ccttccaaac tgac
314

```

<210> 1456  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1456
Asp Pro Val Lys Lys Ala Cys Gly Val Ala His Ala Gly Trp Lys Gly
1      5      10      15
Thr Leu Leu Gly Val Ala Met Ala Thr Val Asn Ala Met Ile Ala Glu
      20      25      30
Tyr Gly Cys Arg Leu Glu Lys Leu Trp Trp Thr Leu Asp Pro Ser Val
      35      40      45
Gly Pro Gly Cys Phe Thr Leu Pro Gly Glu Ser Ala Glu Ala Phe His
      50      55      60
Asn Leu His Pro Ala Cys Val Gln Leu Phe Asp Ser Pro Asn Pro Cys
65      70      75      80
Ile Asp Ile Arg Lys Ala Thr Arg Tyr Leu Thr Gly Phe Leu Tyr Asn
      85      90      95
Cys Phe Leu Pro Pro Ser Lys Leu
      100

```

<210> 1457  
 <211> 437  
 <212> DNA  
 <213> Homo sapiens

<400> 1457

nattcaccag aatccccaga atcccccaaa tactacattg cacttttaggg ttcctttcta  
 60  
 gcacatgcat tgctaaaatc ggcgccaga accttctctg cccctctccc atgggatgca  
 120  
 atgtcagcgg agaaacagac caagtctgca cttagcctgtc cctacaccct cccagggaaa  
 180  
 aggtccccct ggcgaagtc aacagctccc agaggaagcc cactgactgc tctcttcagg  
 240  
 gtgggggaca caggaagtcc acgcttgac ggaggggacg ggcacaccta ccgtgactgc  
 300  
 cagagcccat tttgggagtc tgattggaat ttatacagca ggagcactgg gcactcggac  
 360  
 aactccagcc cacaaccaag tcaactgggt gcctaccac tgccaagtg cctcaagtca  
 420  
 acacattcct gcaactgn  
 437

<210> 1458

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1458

Met	Ser	Ala	Glu	Lys	Gln	Thr	Lys	Ser	Ala	Leu	Ala	Cys	Pro	Tyr	Thr
1				5					10					15	
Leu	Pro	Arg	Lys	Arg	Ser	Pro	Cys	Ala	Lys	Ser	Thr	Ala	Pro	Arg	Gly
			20					25					30		
Ser	Pro	Leu	Thr	Ala	Leu	Phe	Arg	Val	Gly	Asp	Thr	Gly	Ser	Pro	Arg
			35				40					45			
Leu	His	Gly	Gly	Asp	Gly	His	Thr	Tyr	Arg	Asp	Cys	Gln	Ser	Pro	Phe
		50				55					60				
Trp	Glu	Ser	Asp	Trp	Asn	Leu	Tyr	Ser	Arg	Ser	Thr	Gly	His	Ser	Asp
65					70					75				80	
Asn	Ser	Ser	Pro	Gln	Pro	Ser	His	Trp	Ala	Ala	Tyr	Pro	Leu	Pro	Lys
				85					90					95	
Cys	Leu	Lys	Ser	Thr	His	Ser	Cys	Thr							
			100					105							

<210> 1459

<211> 295

<212> DNA

<213> Homo sapiens

<400> 1459

ngagaggtca ccggccacga gattcccgcg gaggtcgcgc cccgccgcgc gggcgaccgc  
 60  
 gccgtactca tcgcttcttc ggagaagatc aagcgggagc tgggctggaa cccgacgcgc  
 120  
 acggatctgc gccgcatcgt cgaggacgcc tgggccttta cggctggggg ggccgaacgg  
 180  
 taaacccttg gtaaggcgac gcagttatcc tcgatctcct cccagagcag gcggcagccc  
 240  
 gccactgcgg tgtcgagcat gccctccac tccccgatcg ccatgagctg gcgan  
 295

<210> 1460  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 1460  
 Xaa Glu Val Thr Gly His Glu Ile Pro Ala Glu Val Ala Pro Arg Arg  
 1 5 10 15  
 Ala Gly Asp Pro Ala Val Leu Ile Ala Ser Ser Glu Lys Ile Lys Arg  
 20 25 30  
 Glu Leu Gly Trp Asn Pro Thr Arg Thr Asp Leu Arg Arg Ile Val Glu  
 35 40 45  
 Asp Ala Trp Ala Phe Thr Ala Gly Gly Ala Glu Arg  
 50 55 60

<210> 1461  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

<400> 1461  
 nnaagcttac gtgaaatgaa acgtcaatgg caacaggcga caatcgtgcc agagaaattg  
 60  
 gttgaagcac agtcaattgc gggttctaaa tgcgaacacg cctggcgctt acaacgttca  
 120  
 gaaaatgact gggtaggctt tgaaaaaaat tggaaagagg ttgttgcatc atccccgtgaa  
 180  
 gaagcacaaa ttcgcggtga agcgcttaat ctaacgcctt atgatgcgat gcttgataag  
 240  
 tttgaaccag gcacgacaac ggtttcgctc aatactttgt tttcaaaggt aaagacgtgg  
 300  
 ttacctacgt taattgaaaa agcgtagtaa aagcagcaat cagaatctat cattatgcc  
 360  
 tcaggcacct tttccacggc gaatcaaaaa gcccttggat tagaaataat gaaattgtta  
 420  
 aaattcgact tt  
 432

<210> 1462  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 1462  
 Xaa Ser Leu Arg Glu Met Lys Arg Gln Trp Gln Gln Ala Thr Ile Val  
 1 5 10 15  
 Pro Glu Lys Leu Val Glu Ala Gln Ser Ile Ala Gly Ser Lys Cys Glu  
 20 25 30  
 His Ala Trp Arg Leu Gln Arg Ser Glu Asn Asp Trp Val Gly Phe Glu  
 35 40 45  
 Lys Asn Trp Lys Glu Val Val Ala Leu Ser Arg Glu Glu Ala Gln Ile  
 50 55 60  
 Arg Gly Glu Ala Leu Asn Leu Thr Pro Tyr Asp Ala Met Leu Asp Lys

```

65          70          75          80
Phe Glu Pro Gly Thr Thr Thr Val Ser Leu Asn Thr Leu Phe Ser Lys
          85          90          95
Val Lys Thr Trp Leu Pro Thr Leu Ile Glu Lys Ala Leu Glu Lys Gln
          100          105          110
Gln Ser Glu Ser Ile Ile Met Pro Ser Gly Thr Phe Ser Thr Ala Asn
          115          120          125
Gln Lys Ala Leu Gly Leu Glu Ile Met Lys Leu Leu Lys Phe Asp Phe
          130          135          140

```

&lt;210&gt; 1463

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1463

```

naccgcgttcc agagcaagct ggacctgacc gccttcgaat tcttctccga caaggccctg
60
gccaaagtca tgggcccgtgg cgacgtaccg gcaccgttcg aaaccgaatg cccgttctac
120
gcgctgctgg aattcgaagc caccaccgaa gaagtcgcca accacgccct ggaaaccttc
180
gagcactgcg ttgagcaggg ctgggtgctg gacggcgtga tgagccagag cgaaacccaa
240
ctgcacaacc tgtggaaact gcgcgagtac atctcggaga ctatttccca ctggacgccc
300
tacaagaacg acatctccgt gaccgtttcc aaagtccccg cgttcttgaa ggaaattgac
360
gcgatcgctg tgagcattac ccggacttcg aaattgttgg tcggccacat cggcgacgca
420
a
421

```

&lt;210&gt; 1464

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1464

```

Xaa Ala Phe Gln Ser Lys Leu Asp Leu Thr Ala Phe Glu Phe Phe Ser
1          5          10          15
Asp Lys Ala Leu Ala Lys Val Met Gly Arg Gly Asp Val Pro Ala Pro
          20          25          30
Phe Glu Thr Glu Cys Pro Phe Tyr Ala Leu Leu Glu Phe Glu Ala Thr
          35          40          45
Thr Glu Glu Val Ala Asn His Ala Leu Glu Thr Phe Glu His Cys Val
          50          55          60
Glu Gln Gly Trp Val Leu Asp Gly Val Met Ser Gln Ser Glu Thr Gln
65          70          75          80
Leu His Asn Leu Trp Lys Leu Arg Glu Tyr Ile Ser Glu Thr Ile Ser
          85          90          95
His Trp Thr Pro Tyr Lys Asn Asp Ile Ser Val Thr Val Ser Lys Val
          100          105          110
Pro Ala Phe Leu Lys Glu Ile Asp Ala Ile Val Val Ser Ile Thr Arg

```

115                      120                      125  
 Thr Ser Lys Leu Leu Val Gly His Ile Gly Asp Ala  
 130                      135                      140

<210> 1465  
 <211> 424  
 <212> DNA  
 <213> Homo sapiens

<400> 1465  
 gtgcacggtc tttgagctgc aattcccagg aatcaggggc cataggcggg agatggcatg  
 60  
 cagcctctcg ggcgggaaaag tggctctacag tgcctgcttg cccgggcagg cagctcgtag  
 120  
 gcttatatgc ttagtggtta tggccctac cactgttttt gaccgcgcta ccattcgcca  
 180  
 caacctcacc gaattcaaac tccggtggat ttcccacgcc gagcagtgga aggcggaaaa  
 240  
 ccgtctcgca acagagtcta aagccgctga gacggactgc tcagtacatg gggatctctg  
 300  
 gaccttggcc acggaagttt tcggtcaagc acccgaattc gacttcccat atatgaaact  
 360  
 cactcggcag gaatgtaggt tcctttttct gccgagaaac gacatcagct tgagctgctt  
 420  
 cacg  
 424

<210> 1466  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 1466  
 Met Ala Cys Ser Leu Ser Gly Gly Lys Val Val Tyr Ser Ala Cys Leu  
 1                      5                      10                      15  
 Pro Gly Gln Ala Ala Arg Arg Leu Ile Cys Leu Val Val Met Ala Pro  
 20                      25                      30  
 Thr Thr Val Phe Asp Arg Ala Thr Ile Arg His Asn Leu Thr Glu Phe  
 35                      40                      45  
 Lys Leu Arg Trp Ile Ser His Ala Glu Gln Trp Lys Ala Glu Asn Arg  
 50                      55                      60  
 Pro Ala Thr Glu Ser Lys Ala Ala Glu Thr Asp Cys Ser Val His Gly  
 65                      70                      75                      80  
 Asp Leu Trp Thr Leu Ala Thr Glu Val Phe Gly Gln Ala Pro Glu Phe  
 85                      90                      95  
 Asp Phe Pro Tyr Met Lys Leu Thr Arg Gln Glu Cys Arg Phe Leu Phe  
 100                      105                      110  
 Leu Pro Arg Asn Asp Ile Ser Leu Ser Cys Phe Thr  
 115                      120

<210> 1467  
 <211> 441  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 1467

nacgcgtgac ggcgaaatgag cggcggaggc atgacaacga gcgcaccgtt ccgcagcttg  
 60  
 gtgccgtgca tcatggctca agtgccgcgc aactttcggc tgctcgagga gctggagaaa  
 120  
 ggcgaaaagg ggctaggaaa tggctcgtgc tcttacggcc ttgcgaacag tgatgacatt  
 180  
 cgtacgtatg cgctgtgct gatggctcatg acaacgtgga atgccacgat cctaggccccg  
 240  
 gccaaactcgg tgcatagaaa ccgcataatac tgcttcgccc tcgtgtgtgg cgactcgtac  
 300  
 cctcttctgc cgctgagat ttggttccag acgcgcatac acttgccgtg cgtcgatgcc  
 360  
 cacacggggc gcgtcatgcc cgatcagttc tcgcccctct tgcattggcg tgatgagtag  
 420  
 actatggaaa gctgctgcat g  
 441

&lt;210&gt; 1468

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1468

Met	Ala	Gln	Val	Pro	Arg	Asn	Phe	Arg	Leu	Leu	Glu	Glu	Leu	Glu	Lys
1				5					10					15	
Gly	Glu	Lys	Gly	Leu	Gly	Asn	Gly	Ser	Cys	Ser	Tyr	Gly	Leu	Ala	Asn
			20					25					30		
Ser	Asp	Asp	Ile	Arg	Thr	Tyr	Ala	Pro	Val	Leu	Met	Val	Met	Thr	Thr
		35					40					45			
Trp	Asn	Ala	Thr	Ile	Leu	Gly	Pro	Ala	Asn	Ser	Val	His	Glu	Asn	Arg
	50					55					60				
Ile	Tyr	Cys	Leu	Arg	Leu	Val	Cys	Gly	Asp	Ser	Tyr	Pro	Leu	Val	Pro
65				70					75					80	
Pro	Glu	Ile	Trp	Phe	Gln	Thr	Arg	Ile	Asn	Leu	Pro	Cys	Val	Asp	Ala
				85					90					95	
His	Thr	Gly	Arg	Val	Met	Pro	Asp	Gln	Phe	Ser	Pro	Leu	Leu	His	Trp
			100					105					110		
Arg	Asp	Glu	Tyr	Thr	Met	Glu	Ser	Cys	Cys	Met					
		115						120							

&lt;210&gt; 1469

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1469

nngctcgatc tagtctatgg gctaaatgat cgaccgaacc cttttattgc ttttttagcg  
 60  
 gcgcttcaac atcttttagc gatttttagtg ccaattgtca ccnctggatt attgatttgt  
 120  
 ttggcattag gcgtgtctcg cgaagacacc aatatgattc tttctatgtc attaattatt  
 180



tcagggatcg cgactttctt gcaatgtaaa aaagttgggc catttggcgc tggattactt  
 240  
 attgttcaag gaactagctt taatttcatt ggctctatca ttggtatagg tagctcaatg  
 300  
 gtggctgctg gcacacctgt cgaacaagtt atggctgcga tttttgggtg cgtaatcgca  
 360  
 gggtcattta tcgaaatggg cgtatctcaa attttacctt gggtaaaaaa gctgattact  
 420  
 cctctcgta caggaatcgt cgttctgttg attggtctac cattaatg  
 468

<210> 1470

<211> 156

<212> PRT

<213> Homo sapiens

<400> 1470

Xaa	Leu	Asp	Leu	Val	Tyr	Gly	Leu	Asn	Asp	Arg	Pro	Asn	Pro	Phe	Ile
1				5					10					15	
Ala	Phe	Leu	Ala	Ala	Leu	Gln	His	Leu	Leu	Ala	Ile	Leu	Val	Pro	Ile
		20						25					30		
Val	Thr	Xaa	Gly	Leu	Leu	Ile	Cys	Leu	Ala	Leu	Gly	Val	Ser	Arg	Glu
		35					40					45			
Asp	Thr	Asn	Met	Ile	Leu	Ser	Met	Ser	Leu	Ile	Ile	Ser	Gly	Ile	Ala
		50				55					60				
Thr	Phe	Leu	Gln	Cys	Lys	Lys	Val	Gly	Pro	Phe	Gly	Ala	Gly	Leu	Leu
65					70				75					80	
Ile	Val	Gln	Gly	Thr	Ser	Phe	Asn	Phe	Ile	Gly	Pro	Ile	Ile	Gly	Ile
			85						90					95	
Gly	Ser	Ser	Met	Val	Ala	Ala	Gly	Thr	Pro	Val	Glu	Gln	Val	Met	Ala
		100						105					110		
Ala	Ile	Phe	Gly	Val	Val	Ile	Ala	Gly	Ser	Phe	Ile	Glu	Met	Gly	Val
		115					120					125			
Ser	Gln	Ile	Leu	Pro	Trp	Val	Lys	Lys	Leu	Ile	Thr	Pro	Leu	Val	Thr
	130					135					140				
Gly	Ile	Val	Val	Leu	Leu	Ile	Gly	Leu	Pro	Leu	Met				
145					150					155					

<210> 1471

<211> 341

<212> DNA

<213> Homo sapiens

<400> 1471

gcgtggatgg ggatcctgaa aaacaatggc gtgctgaata acttcttgcg gtggctcggc  
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 gttatcgatc agccgctgac gattttgcac accaatctgg cggtgtatat cggcattgtg  
 120  
 tacgcttata tgccgtttat ggtactgccc atttatacgg cgctgacgcg cattgattac  
 180  
 tcgctgggtgg aggcctcact ggatctcggt gccgctccgc tgaaaacggt tttcaatgtg  
 240  
 attgtccccg tcaccaaagg cggcattatc gcgggggtcga tgctgggtgtt tatcccggcg  
 300

gtcgggtgagt ttgttatccc ggaactgctc ggcggcggcc g  
341

<210> 1472

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1472

Ala Trp Met Gly Ile Leu Lys Asn Asn Gly Val Leu Asn Asn Phe Leu  
1 5 10 15  
Leu Trp Leu Gly Val Ile Asp Gln Pro Leu Thr Ile Leu His Thr Asn  
20 25 30  
Leu Ala Val Tyr Ile Gly Ile Val Tyr Ala Tyr Leu Pro Phe Met Val  
35 40 45  
Leu Pro Ile Tyr Thr Ala Leu Thr Arg Ile Asp Tyr Ser Leu Val Glu  
50 55 60  
Ala Ser Leu Asp Leu Gly Ala Arg Pro Leu Lys Thr Phe Phe Asn Val  
65 70 75 80  
Ile Val Pro Leu Thr Lys Gly Gly Ile Ile Ala Gly Ser Met Leu Val  
85 90 95  
Phe Ile Pro Ala Val Gly Glu Phe Val Ile Pro Glu Leu Leu Gly Gly  
100 105 110  
Gly

<210> 1473

<211> 352

<212> DNA

<213> Homo sapiens

<400> 1473

tccggaactg ctcaatgtct gtccagcaca taagatccat gcttgaagaa tgagtctcaa  
60  
gaaactgacg gaaatgttca aactccagtt tgttggttaag cagatcacta aacttaaaat  
120  
gcttgtattc tgcaggaaca ttatcccaat attctgttcg tttagagacg ttagagagtg  
180  
ataaaatgcc agttccaatt tcacaagtgg tgtcctcagc tttcttggaa aatgtctctt  
240  
tatgcaaagc ctgtagcttt ctgaagtatg tggagtctaa ctgtcgagtt tcttccacca  
300  
gctccacctt ttataagca atttggtccg attttaccat ctttgtccat gg  
352

<210> 1474

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1474

Met Val Lys Ser Asp Gln Ile Ala Tyr Lys Lys Val Glu Leu Val Glu  
1 5 10 15  
Glu Thr Arg Gln Leu Asp Ser Thr Tyr Phe Arg Lys Leu Gln Ala Leu

```

      20      25      30
His Lys Glu Thr Phe Ser Lys Lys Ala Glu Asp Thr Thr Cys Glu Ile
      35      40      45
Gly Thr Gly Ile Leu Ser Leu Ser Asn Val Ser Lys Arg Thr Glu Tyr
      50      55      60
Trp Asp Asn Val Pro Ala Glu Tyr Lys His Phe Lys Phe Ser Asp Leu
65      70      75      80
Leu Asn Asn Lys Leu Glu Phe Glu His Phe Arg Gln Phe Leu Glu Thr
      85      90      95
His Ser Ser Ser Met Asp Leu Met Cys Trp Thr Asp Ile Glu Gln Phe
      100      105      110
Arg

```

&lt;210&gt; 1475

&lt;211&gt; 389

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1475

```

accggtgccg gagccgatct ccacgatggc cttggcgccg gtgcggccga accactcatc
60
gacatcgata agctcatcgc ttaagacgcg gccagctcg ggccagcatt gctcaaaaag
120
ctggtgctgg ttgtccgtga gcgtgccgcg ggggaaaggg acctttgccc aggcgcgggt
180
agtccaggtc attatcaaag accgcattga agtccgtttg cggcgggcca cccggcggca
240
tttctccggc aggggggtgtt ttgagaatta tccgtgctat acatcgcgcc ctatttttcc
300
ctgtccaggc atggcaagca atatgccgcg ccgggtatct tccccgccgt atggggaggg
360
ggataaccgg agcttgacgg ggtggtgtc
389

```

&lt;210&gt; 1476

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1476

```

Met Val Leu Ala Pro Val Arg Pro Asn His Ser Ser Thr Ser Ile Ser
1      5      10      15
Ser Ser Leu Lys Thr Arg Pro Ser Ser Gly Gln His Cys Ser Lys Ser
      20      25      30
Trp Cys Trp Leu Ser Val Ser Val Pro Arg Gly Lys Gly Thr Phe Ala
      35      40      45
Gln Ala Arg Val Val Gln Val Ile Ile Lys Asp Arg Ile Glu Val Arg
50      55      60
Leu Arg Arg Ala Thr Arg Arg His Phe Ser Gly Arg Gly Cys Phe Glu
65      70      75      80
Asn Tyr Pro Cys Tyr Thr Ser Arg Pro Ile Phe Pro Cys Pro Gly Met
      85      90      95
Ala Ser Asn Met Pro Arg Arg Val Phe Ser Pro Pro Tyr Gly Glu Gly

```

100 105 110  
 Asp Asn Arg Ser Leu Thr Gly Trp Cys  
 115 120

<210> 1477

<211> 500

<212> DNA

<213> Homo sapiens

<400> 1477

tacagcgaga atctgcacga taccacattc ctcaaacct attgcgttgg cttcgagcaa  
 60  
 ttctccctt atttgctggg ccaaacggac ggccaaccta aagatgccca atgggcatcg  
 120  
 gcgctgtgtg gtattgatgc cgaaatcatc cgggcactgg cccgccaaat ggcgccaac  
 180  
 cgtacgcaaa tcattgcggg ctggtgcgtg caacgtatgc aacacggcga acaatgggcg  
 240  
 tggatgacgg tagtgctggc ggcgatgctt ggccaaatcg gcttaccggg cggcgggttc  
 300  
 ggttttggtt ggccctccaa cggcgcaggt acccccagac cgcaaggggt gatcctgagc  
 360  
 ggtttctccg gttccccgc tacgccggca cgccatgcc aaggggattt caaaggttac  
 420  
 agcagtacca ttccgatgc gcgctttatc gatgccatgc tggagccggg caaggagatc  
 480  
 gattggaatg gcaaacgcgt  
 500

<210> 1478

<211> 166

<212> PRT

<213> Homo sapiens

<400> 1478

Tyr Ser Glu Asn Leu His Asp Thr His Phe Leu Lys Thr Tyr Cys Val  
 1 5 10 15  
 Gly Phe Glu Gln Phe Leu Pro Tyr Leu Leu Gly Gln Thr Asp Gly Gln  
 20 25 30  
 Pro Lys Asp Ala Gln Trp Ala Ser Ala Leu Cys Gly Ile Asp Ala Glu  
 35 40 45  
 Ile Ile Arg Ala Leu Ala Arg Gln Met Ala Ala Asn Arg Thr Gln Ile  
 50 55 60  
 Ile Ala Gly Trp Cys Val Gln Arg Met Gln His Gly Glu Gln Trp Ala  
 65 70 75 80  
 Trp Met Thr Val Val Leu Ala Ala Met Leu Gly Gln Ile Gly Leu Pro  
 85 90 95  
 Gly Gly Gly Phe Gly Phe Gly Trp Pro Ser Asn Gly Ala Gly Thr Pro  
 100 105 110  
 Glu Pro Gln Gly Val Ile Leu Ser Gly Phe Ser Gly Ser Pro Ala Thr  
 115 120 125  
 Pro Ala Arg His Ala Lys Gly Asp Phe Lys Gly Tyr Ser Ser Thr Ile  
 130 135 140  
 Pro Ile Ala Arg Phe Ile Asp Ala Met Leu Glu Pro Gly Lys Glu Ile

145                      150  
 Asp Trp Asn Gly Lys Arg  
                          165

155

160

&lt;210&gt; 1479

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1479

acgcgtgtgg agctggcacc atgaaagcac gatgtgcac actcatagag gcaggcacac  
 60  
 ttaagtatgt tctttacatt gaaacagaaa ggaaagaaga taggaaaaat ggtgccagca  
 120  
 cgctgggctt tttttgtttg ctgttttggg tggggtgtgc tagtgcagtg tccggtgtac  
 180  
 gcttttgtcc tcaaacaggc ttgttccccg gtcagagttt cattattgtt gctggtaaac  
 240  
 aaatgccaaag tttgacaaaa aacagtgaaa taaagcaaaa gattttgaaa aatgcttcat  
 300  
 catgtcagaa ggaaagaacc cttttcacgg gtgcctgccc acatttcctt gcccagcctg  
 360  
 agaaccctatt gactttgaat tatcttttgc tgttttattt ctatgaaaat tatatacgcg  
 420  
 t  
 421

&lt;210&gt; 1480

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1480

Met	Lys	Ala	Arg	Cys	Ala	Ser	Leu	Ile	Glu	Ala	Gly	Thr	Leu	Lys	Tyr
1				5					10					15	
Val	Leu	Tyr	Ile	Glu	Thr	Glu	Arg	Lys	Glu	Asp	Arg	Lys	Asn	Gly	Ala
		20					25						30		
Ser	Thr	Leu	Gly	Phe	Phe	Cys	Leu	Phe	Trp	Val	Gly	Cys	Ala	Ser	
		35					40				45				
Ala	Val	Ser	Gly	Val	Arg	Phe	Cys	Pro	Gln	Thr	Gly	Leu	Phe	Pro	Gly
		50				55				60					
Gln	Ser	Phe	Ile	Ile	Val	Ala	Gly	Lys	Gln	Met	Pro	Ser	Leu	Thr	Lys
		65			70				75					80	
Asn	Ser	Glu	Ile	Lys	Gln	Lys	Ile	Leu	Lys	Asn	Ala	Ser	Ser	Cys	Gln
			85					90					95		
Lys	Glu	Arg	Thr	Leu	Phe	Thr	Gly	Ala	Cys	Pro	His	Phe	Leu	Ala	Gln
			100				105						110		
Pro	Glu	Thr	Leu	Leu	Thr	Leu	Asn	Tyr	Leu	Leu	Leu	Phe	Tyr	Phe	Tyr
		115				120						125			
Glu	Asn	Tyr	Ile	Arg											
		130													

&lt;210&gt; 1481

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1481

```

gtcgggtcgc cgccagtct cgtgccgaca tgcagttcct ggcccgggag gtcgcatcca
60
tccggatgca gatgggagcag ttggccacgc gcgattatct gcgctcggag ctacgcgacg
120
agttgcgctc cctgctcgag gagatcgagg cctcaccggc ctcccactaa ctgaccgggt
180
tcgcgacgag cgagttgtcg catcggggcca acggtgtgta gacaagtcag catgagcacc
240
gagaacccag tggttaaggc cattgccgat gcgttgctgc acgtcaatga ccccgagatc
300
aaacgccccca ttaccgatct caacatgatt gatgagatta ccgtcgacga gcaaggacgc
360
gctttcgtcc gcatcctgct gaccgtcgcc ggggtgtccc tcaagaccga gctgcgtgag
420
caggccaccg aggtgtgctg cagcgttgac ggggtgacca gtgtttccgt cgaactcggc
480
accatgaccg acgaacagcg cgatgctctc aaagttcagc tgcgcggtga cgtccccgaa
540
cgcggt
545

```

&lt;210&gt; 1482

&lt;211&gt; 104

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1482

```

Met Ser Thr Glu Asn Pro Val Val Lys Ala Ile Ala Asp Ala Leu Ser
 1             5             10             15
His Val Asn Asp Pro Glu Ile Lys Arg Pro Ile Thr Asp Leu Asn Met
          20             25             30
Ile Asp Glu Ile Thr Val Asp Glu Gln Gly Arg Ala Phe Val Arg Ile
      35             40             45
Leu Leu Thr Val Ala Gly Cys Pro Leu Lys Thr Glu Leu Arg Glu Gln
      50             55             60
Ala Thr Glu Ala Val Arg Ser Val Asp Gly Val Thr Ser Val Ser Val
65             70             75             80
Glu Leu Gly Thr Met Thr Asp Glu Gln Arg Asp Ala Leu Lys Val Gln
          85             90             95
Leu Arg Gly Asp Val Pro Glu Arg
          100

```

&lt;210&gt; 1483

&lt;211&gt; 625

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1483

```

gtacggcttc gagagggcta cagtgtccga gaggtcacac tggccaaagg aggggtccaa
60

```

ttggaggtaa agctggtgct gctgtggaaa cacaacatgc gcattgagta tgtggctatg  
 120  
 gcatcctggc ccctggagcc tgagggccct cgagtaacac ggggtggaagt gacgatggaa  
 180  
 ggcggctacg acattttgca tgatgtgtcc tgtgcactaa ggcagcccat tcgttcattg  
 240  
 tatcgtaccc atgttatccg gcgtttctgg aacacgctgc agagcatcaa ccagacagac  
 300  
 cagatgcttg cccacettca gtccttctcc tcagtgcctg agcatttcac gcttcctgac  
 360  
 agcaccaaga gcggagtgcc actcttctac atccctccag gctccaccac cccggtgctc  
 420  
 tccctccagc ccagtgggtc tgactcatcc catgcccagt ttgtgccta ctggaagccc  
 480  
 agtgcgtgcc atggatgcaa attcctggca gcgatggctg cacatgcac gcctgggtgct  
 540  
 aatcctggag catgacacac caatcccca gcaattgcac accccgggca gcaatgggag  
 600  
 ctactacgga gagaagacaa cgcgt  
 625

&lt;210&gt; 1484

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1484

Val	Arg	Leu	Arg	Glu	Gly	Tyr	Ser	Val	Arg	Glu	Val	Thr	Leu	Ala	Lys
1				5					10					15	
Gly	Gly	Ser	Gln	Leu	Glu	Val	Lys	Leu	Val	Leu	Leu	Trp	Lys	His	Asn
			20				25						30		
Met	Arg	Ile	Glu	Tyr	Val	Ala	Met	Ala	Ser	Trp	Pro	Leu	Glu	Pro	Glu
		35				40					45				
Gly	Pro	Arg	Val	Thr	Arg	Val	Glu	Val	Thr	Met	Glu	Gly	Gly	Tyr	Asp
	50				55				60						
Ile	Leu	His	Asp	Val	Ser	Cys	Ala	Leu	Arg	Gln	Pro	Ile	Arg	Ser	Leu
65			70						75				80		
Tyr	Arg	Thr	His	Val	Ile	Arg	Arg	Phe	Trp	Asn	Thr	Leu	Gln	Ser	Ile
			85					90					95		
Asn	Gln	Thr	Asp	Gln	Met	Leu	Ala	His	Leu	Gln	Ser	Phe	Ser	Ser	Val
		100					105					110			
Pro	Glu	His	Phe	Thr	Leu	Pro	Asp	Ser	Thr	Lys	Ser	Gly	Val	Pro	Leu
	115					120					125				
Phe	Tyr	Ile	Pro	Pro	Gly	Ser	Thr	Thr	Pro	Val	Leu	Ser	Leu	Gln	Pro
	130				135					140					
Ser	Gly	Ser	Asp	Ser	Ser	His	Ala	Gln	Phe	Ala	Ala	Tyr	Trp	Lys	Pro
145			150						155					160	
Ser	Ala	Val	His	Gly	Cys	Lys	Phe	Leu	Ala	Ala	Met	Ala	Ala	His	Ala
		165					170							175	
Ser	Pro	Gly	Ala	Asn	Pro	Gly	Ala								
		180													

&lt;210&gt; 1485

&lt;211&gt; 2058

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1485

ntatgttcag cgttcaacga tattggctac cactatggtg ccatggtcgt cgatgctgcg  
60  
ctgttctctgc cacagtcacg acccagacta tttatcattg gtgtcagaaa cgatattttt  
120  
gttggcgata ttactttctga atcacctctt aaaatgtggc ataccagaac tttattgaat  
180  
gcctacagca atctgaaaga tgatgccaaag tccaattggg tatgggtggga ccttcctatg  
240  
ccagcccaga gaaaatctgc tttcgccgat ttgattgaag aaaatcctag cagcgttaag  
300  
tggcataccc ggaaggaaac acagcagctc ttggatatga tgactgatgt taacttagct  
360  
aagggttgagg ctgcaaaaaa gctatcgatc gagtctaagg aaaatgttgt agggacaatt  
420  
tataaaagaa ctgcgaccga tagctttgga gttaaagcgc agcgtgctga agtgcggttt  
480  
gatgatgttg ccggttgtct tcgcaccctt ggaggggggt caagtcggca agtcataatg  
540  
gtcgttgata acgggactgt aaaaacgagg ttgatctcaa gtagagaaac tgcaaggctt  
600  
atggggttac ccgacgaata catattgcca aaaaattata atgaggcgta tcacttaacg  
660  
ggtgatggtg ttgtagtgcc ggttgtatcc cacatagcca ctcatatttt tgaccagtg  
720  
atggagcgtg tgtttgagga tgcggcgagg ctgcttaagc aaatcgcata gcatcgtttt  
780  
ggcaggaaga tatgagcgtt attccgtgta aaaaggacct tcagctaaaa aaattgattg  
840  
aatcctatgc agaagccttg aaagttgagg ccataagct aggagagcat ggattaactg  
900  
aagctgaatt ttatgatagc ggctctttc ggggggctat cgagcgaatt cgaggacagt  
960  
tctccgcgac catgcgggag aaaagaaatt tcgttaagca tgttttaaatt tacatgcagg  
1020  
ataacgacta cattgctgat tgggagtcgg ctggtgaatc gaatcgccat gattatatgg  
1080  
taactctcaa ttctgggcgc aaagctgcta ttgagctgaa aggggtgcctt gatggcaata  
1140  
acactaacat ctttgatcgc cccctcagg cagaagaatt tgttatctgg agtgtatgca  
1200  
caaatectgg tgctgacct cagcataatg tttggtctgg gcttcacacc agactaagt  
1260  
ctgaaatcat ttcacgggag caaaggattg atggaatggt catttgggac tgggcttggt  
1320  
gaacagtcgg aaggccatgc cccaaaatag caactgaacc tgagcgggct gtaacatttg  
1380  
ggcgttcaa attgccgcca ccatgtttgt atcttttacc ttcgacgatt ccaagcccaa  
1440  
gaaacaaccc gtctccaaga gctcagcaga ttgaagacgt gcagctaata aaagcgtttc  
1500



acgattgttt tgggtgccgg tctgaagaag ttaatttcgt taactttgat gttggttatt  
 1560  
 atggtaaaga taccgtccgt aaaacgacta tcattcgaaa cggcatgggtg gagcgtgaat  
 1620  
 cggaatgac ggcaataagg cggctttaat ttgtgcatgc ctatgctgca tgaatccgca  
 1680  
 tgatcgtttg aggatcgttt ttgctgaggc cggccagttc tgggtgggctt ttgcttatgt  
 1740  
 catgcacctg catgaaaacc gctacataaa gcgggcaggc gtggcgggga tacgagcgcg  
 1800  
 cgcaacgggg tgaaatgggtg aatatcaggg gcaatctccg gcacgctggc ggcttgaatc  
 1860  
 gggtaggggtg agtgagaggc agcaataaag aagcgccccg cagaatgctg ctggggcgct  
 1920  
 gtgagaggtg gtcttgttgt cgcggtgcgg tgggtcagtc gtagcgattg tcttctgtca  
 1980  
 gccccagcgt gtacggctca aagcggatca cttcttcgcc cagccagtca ttaagctccc  
 2040  
 gcagtcgctt ctgcaggc  
 2058

<210> 1486

<211> 256

<212> PRT

<213> Homo sapiens

<400> 1486

Xaa	Cys	Ser	Ala	Phe	Asn	Asp	Ile	Gly	Tyr	His	Tyr	Gly	Ala	Met	Val
1				5					10					15	
Val	Asp	Ala	Ala	Leu	Phe	Leu	Pro	Gln	Ser	Arg	Pro	Arg	Leu	Phe	Ile
		20						25					30		
Ile	Gly	Val	Arg	Asn	Asp	Ile	Phe	Val	Gly	Asp	Ile	Thr	Ser	Glu	Ser
		35					40					45			
Pro	Ser	Lys	Met	Trp	His	Thr	Arg	Thr	Leu	Leu	Asn	Ala	Tyr	Ser	Asn
		50				55					60				
Leu	Lys	Asp	Asp	Ala	Lys	Ser	Asn	Trp	Val	Trp	Trp	Asp	Leu	Pro	Met
65				70					75				80		
Pro	Ala	Gln	Arg	Lys	Ser	Ala	Phe	Ala	Asp	Leu	Ile	Glu	Glu	Asn	Pro
			85					90					95		
Ser	Ser	Val	Lys	Trp	His	Thr	Arg	Lys	Glu	Thr	Gln	Gln	Leu	Leu	Asp
		100					105						110		
Met	Met	Thr	Asp	Val	Asn	Leu	Ala	Lys	Val	Glu	Ala	Ala	Lys	Lys	Leu
		115				120					125				
Ser	Ile	Glu	Ser	Lys	Glu	Asn	Val	Val	Gly	Thr	Ile	Tyr	Lys	Arg	Thr
	130				135						140				
Arg	Thr	Asp	Ser	Phe	Gly	Val	Lys	Ala	Gln	Arg	Ala	Glu	Val	Arg	Phe
145				150					155					160	
Asp	Asp	Val	Ala	Gly	Cys	Leu	Arg	Thr	Pro	Gly	Gly	Gly	Ser	Ser	Arg
			165					170					175		
Gln	Val	Ile	Met	Val	Val	Asp	Asn	Gly	Thr	Val	Lys	Thr	Arg	Leu	Ile
		180				185						190			
Ser	Ser	Arg	Glu	Thr	Ala	Arg	Leu	Met	Gly	Leu	Pro	Asp	Glu	Tyr	Ile
		195				200					205				
Leu	Pro	Lys	Asn	Tyr	Asn	Glu	Ala	Tyr	His	Leu	Thr	Gly	Asp	Gly	Val

210	215	220
Val Val Pro Val Val Ser His Ile Ala Thr His Ile Phe Asp Pro Val		
225	230	235
Met Glu Arg Val Phe Glu Asp Ala Ala Gly Leu Leu Lys Gln Ile Ala		240
245	250	255

<210> 1487  
 <211> 823  
 <212> DNA  
 <213> Homo sapiens

<400> 1487  
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 60  
 ccgagcaggt gacatttcag ctaaggctgg gaaggatgag gagaagtcag gaactccagg  
 120  
 catcagggaa tgctggggaa aaaaagcact ccaggcccag ggatcagcaa agcacaggat  
 180  
 gcctggggga acacacagcc tcagagcatt tgaggaacag aaaaggcaac gtgactaagc  
 240  
 ttcttggggc ggtgaggtca ggcagggagg tgggtgagag gtcattggggc cgcaggcaaa  
 300  
 cggccctccc tcccagtgcc ccacatgcag gccctggagc accaggagcg gggaggctcc  
 360  
 gtggtgtgtc ttctgcaag tggcctgcct ttgggagcat cagcccttcc tcttggggac  
 420  
 tgggagaggc cggcagttag ggaagaatgg cctcgggtcg tgcgtagaga atgtagggga  
 480  
 cacagggcct ctacaggacc cagatcctga tcttgcaga tctgcacgcc cgtgggaggg  
 540  
 tgctggcggc agaaacgcgt tgccataagc cttctcccca ctgcaggcag gtgtgggtcag  
 600  
 gggacctcct tggagaacaa ggtgggggaa tttggcagct ttctcagcat ggcgtccatc  
 660  
 cccctacat tcttggggca cccactgtag gccaggccct gtgccggatc tgatgataca  
 720  
 gtgatgacta agtcacagtc cctgcctctg agggcccat gatgtgccgg gacagccaag  
 780  
 caaccaata tgttaaaatc cagtgtcagg acccnaggag aag  
 823

<210> 1488  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 1488  
 Met Leu Gly Arg Ser Cys Glu Gly Lys Phe Arg Lys Asp Leu Ser Glu  
 1 5 10 15  
 Gln Val Thr Phe Gln Leu Arg Leu Gly Arg Met Arg Arg Ser Gln Glu  
 20 25 30  
 Leu Gln Ala Ser Gly Asn Ala Gly Glu Lys Lys His Ser Arg Pro Arg  
 35 40 45  
 Asp Gln Gln Ser Thr Gly Cys Leu Gly Glu His Thr Ala Ser Glu His

50                      55                      60  
 Leu Arg Asn Arg Lys Gly Asn Val Thr Lys Leu Pro Gly Ala Val Arg  
 65                      70                      75                      80  
 Ser Gly Arg Glu Val Gly Ala Arg Ser Trp Gly Arg Arg Gln Thr Ala  
                     85                      90                      95  
 Leu Pro Pro Ser Ala Pro His Ala Gly Pro Gly Ala Pro Gly Ala Gly  
                     100                      105                      110  
 Arg Leu Arg Gly Val Ser Ser Cys Lys Trp Pro Ala Phe Gly Ser Ile  
                     115                      120                      125  
 Ser Pro Phe Ser Trp Gly Leu Gly Glu Ala Gly Ser Glu Gly Arg Met  
                     130                      135                      140  
 Ala Leu Gly Arg Ala  
 145

<210> 1489

<211> 342

<212> DNA

<213> Homo sapiens

<400> 1489

nncagttca ccgtcaagct ggccgaggcc ggccaacaca atgtgcgcaa tgcgctggcc  
 60  
 gcgattgcct gcgccgtggg tgccggcatc aaccaggacg ccatcgtagc cggcctcgaa  
 120  
 gccttcgccc cggtcgggcg acgtttgcag cgcaagcagg ccgccagcgg cgcgcccgtc  
 180  
 attgacgaca cccacaaccc caatcccaat tcaatgcgcc cggcgatcga cgtgctggcc  
 240  
 cgcgtaccgg cgccgcgcac cctgggtggtg ggcgacatgg gcgaagtcgg cgcacaggga  
 300  
 aaagaatttc acgaagaaat cggggcttac gcacacacgc gt  
 342

<210> 1490

<211> 114

<212> PRT

<213> Homo sapiens

<400> 1490

Xaa Gln Phe Thr Val Lys Leu Ala Ala Ala Gly Glu His Asn Val Arg  
 1                      5                      10                      15  
 Asn Ala Leu Ala Ala Ile Ala Cys Ala Val Gly Ala Gly Ile Asn Gln  
                     20                      25                      30  
 Asp Ala Ile Val Arg Gly Leu Glu Ala Phe Ala Pro Val Gly Gly Arg  
                     35                      40                      45  
 Leu Gln Arg Lys Gln Ala Ala Ser Gly Ala Pro Val Ile Asp Asp Thr  
                     50                      55                      60  
 His Asn Pro Asn Pro Asn Ser Met Arg Pro Ala Ile Asp Val Leu Ala  
 65                      70                      75                      80  
 Arg Val Pro Ala Pro Arg Ile Leu Val Val Gly Asp Met Gly Glu Val  
                     85                      90                      95  
 Gly Ala Gln Gly Lys Glu Phe His Glu Glu Ile Gly Ala Tyr Ala His  
                     100                      105                      110  
 Thr Arg

<210> 1491  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 1491  
 ncctcgttgt tctcatagag ggctacggca tcgcgttga actgttcgga gtacctggac  
 60  
 atgggggtag attacctttc ttcccagctc gactgggctg gatatcaggt gtccaccaca  
 120  
 tgggggtcag gtcccaactcc caaaggagta gccatcaccc acgagtcggc ggtcaatacg  
 180  
 attgtcgatg tcaacgaacg cctcgggggtg actccgaccg accggatatt ggggatttca  
 240  
 gagctaaact tcgatctatc ggtatacgac atcttcggga tgttcgcgcg gggtgctacc  
 300  
 ttggtgttgc catctccagc agacaaacgt gat  
 333

<210> 1492  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 1492  
 Met Gly Val Asp Tyr Leu Ser Ser Gln Leu Asp Trp Ala Gly Tyr Gln  
 1 5 10 15  
 Val Ser Thr Thr Trp Gly Ser Gly Pro Thr Pro Lys Gly Val Ala Ile  
 20 25 30  
 Thr His Glu Ser Ala Val Asn Thr Ile Val Asp Val Asn Glu Arg Leu  
 35 40 45  
 Gly Val Thr Pro Thr Asp Arg Ile Leu Gly Ile Ser Glu Leu Asn Phe  
 50 55 60  
 Asp Leu Ser Val Tyr Asp Ile Phe Gly Met Phe Ala Arg Gly Ala Thr  
 65 70 75 80  
 Leu Val Leu Pro Ser Pro Ala Asp Lys Arg Asp  
 85 90

<210> 1493  
 <211> 1316  
 <212> DNA  
 <213> Homo sapiens

<400> 1493  
 nggtaccagg gcaaagaagg ctgggcccc gcctcctacc taaagaagaa cagtggggag  
 60  
 cccttgcccc cgaagccagg ccctggctca ccctcccacc cgggtgccct tgacttggat  
 120  
 ggtgtttccc ggcagcagaa cgcggtgggc agggagaagg agctgctcag cagccagagg  
 180  
 gacgggagggt ttgaaggccg cccggtgccc gacggtgacg ccaagcagag atcaccaaag  
 240

atgaggcaga gacccccctcc tcgccgggac atgaccattc ctcgaggcct caacctgccc  
 300  
 aagccgcca tcccgcccca agtggaggaa gagtattaca ccatcgccga attccagaca  
 360  
 accatcccag acggcatcag cttccaggca ggcctgaagg tcgaggatgat cgagaaaaac  
 420  
 ttgagtggct ggtggtacat tcagattgaa gataaggaag ggtgggcccc ggccaccttc  
 480  
 attgacaagt acaagaagac gagcaacgag tcgagaccca actttctggc tcccctgccc  
 540  
 cagcaggatga cccagctccg gctgggggaa gcagcagcgc tggagaacaa cacgggcagc  
 600  
 gaagccacgg gccctccccg gccctgcct gacgcaccgc atggtgtcat ggactcgggg  
 660  
 ttgccatggt ctaaagactg gaagggcagt aaggatgtcc tgaggaaggc atcttcagac  
 720  
 atgtctgctg cagcaggcta cgaggagatc tcagaccccg acatggagga gaagcccagc  
 780  
 ctccctccgc ggaaagaatc catcatcaag tcggaggggg agctgctgga gcgggagcgg  
 840  
 gagcggcaga ggacggagca gctccggggc cccactccca agcctccggg cgtgattttg  
 900  
 ccgatgatgc cagccaaaca catccctcca gcccgggaca gcaggaggcc agagcccaaa  
 960  
 cctgacaaaa gcagactgtt ccagctgaaa aatgacatgg ggctggagtg tggccacaag  
 1020  
 gtcttgccca aggaagtga gaagcccaac ctccggccca tctccaaatc caaaactgac  
 1080  
 ctgccagagg agaagccaga tgccactccc cagaatccct tcttgaagtc cagacctcag  
 1140  
 gttaggccaa aaccagctcc tcccccaaaa acggagccac ctcagggcga agaccaagtc  
 1200  
 gacatctgca acctcaggag taagctcagg cctgccaaat cccaagacaa gtccttggtg  
 1260  
 gatggggagg gccccaggc agtagggggc caagacgtgg ccttcagccg aagctt  
 1316

&lt;210&gt; 1494

&lt;211&gt; 438

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1494

Xaa	Tyr	Gln	Gly	Lys	Glu	Gly	Trp	Ala	Pro	Ala	Ser	Tyr	Leu	Lys	Lys
1			5					10					15		
Asn	Ser	Gly	Glu	Pro	Leu	Pro	Pro	Lys	Pro	Gly	Pro	Gly	Ser	Pro	Ser
			20					25					30		
His	Pro	Gly	Ala	Leu	Asp	Leu	Asp	Gly	Val	Ser	Arg	Gln	Gln	Asn	Ala
			35				40					45			
Val	Gly	Arg	Glu	Lys	Glu	Leu	Leu	Ser	Ser	Gln	Arg	Asp	Gly	Arg	Phe
			50			55				60					
Glu	Gly	Arg	Pro	Val	Pro	Asp	Gly	Asp	Ala	Lys	Gln	Arg	Ser	Pro	Lys
65					70				75					80	
Met	Arg	Gln	Arg	Pro	Pro	Pro	Arg	Arg	Asp	Met	Thr	Ile	Pro	Arg	Gly

```

      85              90              95
Leu Asn Leu Pro Lys Pro Pro Ile Pro Pro Gln Val Glu Glu Glu Tyr
      100              105              110
Tyr Thr Ile Ala Glu Phe Gln Thr Thr Ile Pro Asp Gly Ile Ser Phe
      115              120              125
Gln Ala Gly Leu Lys Val Glu Val Ile Glu Lys Asn Leu Ser Gly Trp
      130              135              140
Trp Tyr Ile Gln Ile Glu Asp Lys Glu Gly Trp Ala Pro Ala Thr Phe
145              150              155              160
Ile Asp Lys Tyr Lys Lys Thr Ser Asn Ala Ser Arg Pro Asn Phe Leu
      165              170              175
Ala Pro Leu Pro His Glu Val Thr Gln Leu Arg Leu Gly Glu Ala Ala
      180              185              190
Ala Leu Glu Asn Asn Thr Gly Ser Glu Ala Thr Gly Pro Ser Arg Pro
      195              200              205
Leu Pro Asp Ala Pro His Gly Val Met Asp Ser Gly Leu Pro Trp Ser
      210              215              220
Lys Asp Trp Lys Gly Ser Lys Asp Val Leu Arg Lys Ala Ser Ser Asp
225              230              235              240
Met Ser Ala Ser Ala Gly Tyr Glu Glu Ile Ser Asp Pro Asp Met Glu
      245              250              255
Glu Lys Pro Ser Leu Pro Pro Arg Lys Glu Ser Ile Ile Lys Ser Glu
      260              265              270
Gly Glu Leu Leu Glu Arg Glu Arg Glu Arg Gln Arg Thr Glu Gln Leu
      275              280              285
Arg Gly Pro Thr Pro Lys Pro Pro Gly Val Ile Leu Pro Met Met Pro
      290              295              300
Ala Lys His Ile Pro Pro Ala Arg Asp Ser Arg Arg Pro Glu Pro Lys
305              310              315              320
Pro Asp Lys Ser Arg Leu Phe Gln Leu Lys Asn Asp Met Gly Leu Glu
      325              330              335
Cys Gly His Lys Val Leu Ala Lys Glu Val Lys Lys Pro Asn Leu Arg
      340              345              350
Pro Ile Ser Lys Ser Lys Thr Asp Leu Pro Glu Glu Lys Pro Asp Ala
      355              360              365
Thr Pro Gln Asn Pro Phe Leu Lys Ser Arg Pro Gln Val Arg Pro Lys
      370              375              380
Pro Ala Pro Ser Pro Lys Thr Glu Pro Pro Gln Gly Glu Asp Gln Val
385              390              395              400
Asp Ile Cys Asn Leu Arg Ser Lys Leu Arg Pro Ala Lys Ser Gln Asp
      405              410              415
Lys Ser Leu Leu Asp Gly Glu Gly Pro Gln Ala Val Gly Gly Gln Asp
      420              425              430
Val Ala Phe Ser Arg Ser
      435

```

&lt;210&gt; 1495

&lt;211&gt; 329

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1495

```

agatctctgt cccgtagagg tgccacctca tcttccatga gagctgtgct ttgctttctt
60

```

ctggaggctg caaggaggat ggccccatc acggcggacc tacatgctgg gagtccggga  
 120  
 gagggcaggg cgcgacatg gggcatgtgg cgatgtgttt caccacccac tcccgcctga  
 180  
 agtgccactg tgagcccaac ccacggtgcc aggctgggct gcactccagg ctctgcagc  
 240  
 agacccacct cctcagcctc ctccccctga aggctgggca tggcctggac aaagggtgtc  
 300  
 ctctctgtgt gtgccatgct gacgtggca  
 329

<210> 1496

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1496

Met	Ala	Gln	Gln	Arg	Arg	Thr	Pro	Phe	Val	Gln	Ala	Met	Pro	Ser	Leu
1			5						10					15	
Gln	Gly	Lys	Glu	Ala	Glu	Glu	Val	Gly	Leu	Leu	Gln	Glu	Pro	Gly	Val
		20						25				30			
Gln	Pro	Ser	Leu	Ala	Pro	Trp	Val	Gly	Leu	Thr	Val	Ala	Leu	Gln	Ala
		35				40					45				
Gly	Val	Gly	Gly	Glu	Thr	His	Arg	His	Met	Pro	His	Val	Arg	Gly	Leu
	50					55				60					
Pro	Ser	Pro	Gly	Leu	Pro	Ala	Cys	Arg	Ser	Ala	Val	Met	Gly	Ala	Ile
65					70					75				80	
Leu	Leu	Ala	Ala	Ser	Arg	Arg	Lys	Gln	Ser	Thr	Ala	Leu	Met	Glu	Asp
			85					90						95	
Glu	Val	Ala	Pro	Leu	Arg	Asp	Arg	Asp							
			100					105							

<210> 1497

<211> 345

<212> DNA

<213> Homo sapiens

<400> 1497

naacttcttg cactcactca ggcgcacggt tggcggccga cttggaagcc gctgcagcac  
 60  
 ttgacgcggg gcgatctcga agcgttcggt cttggcctga cggtcgatgg ctgcggcgtg  
 120  
 ccgttgatcg cgcaatgcg acgggtgggg cagggcgtgc ggccgacacc accgcaagaa  
 180  
 cgcaactcac ggcagatgaa tctgttttga aacgcaagga agggtaatga caggcaccga  
 240  
 caagaagcgg atcccgagc tgctgcgtgt tgagctcact gaacttaccg gcccgatcga  
 300  
 gcagccttac gcgcccgatg cacgtcattc tttcgggcca cgcgt  
 345

<210> 1498

<211> 104

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1498

```

Met Thr Cys Ile Gly Arg Val Arg Leu Leu Asp Arg Ala Gly Lys Phe
 1             5             10             15
Ser Glu Leu Asn Thr Gln Gln Leu Arg Asp Pro Leu Leu Val Gly Ala
      20             25             30
Cys His Tyr Pro Ser Leu Arg Phe Lys Thr Asp Ser Ser Ala Val Ser
      35             40             45
Cys Val Leu Ala Val Val Ser Ala Ala Arg Pro Ala Pro Pro Val Ala
      50             55             60
Phe Ala Arg Ser Thr Ala Arg Arg Ser His Arg Pro Ser Gly Gln Asp
65             70             75             80
Arg Thr Leu Arg Asp Arg Pro Ala Ser Ser Ala Ala Ala Ala Ser Lys
      85             90             95
Ser Ala Ala Asn Arg Ala Pro Glu
      100

```

&lt;210&gt; 1499

&lt;211&gt; 402

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1499

```

-aaatatattc tgccagagtt tgaacacgac accatgctct ggcatttggg catgtcgggg
60
agttttccgtc tatgcgagag caatgaagaa ttacgcaaac atgaccatct aatcattcag
120
tttgaagata tcgaactgcy ttatcatgat cctcgccggt ttggttgcac tctttggctg
180
gatgcacaat cacaagcaa attaatagat acgctggggc cagaaccctt aagcgagaac
240
tttaatgcgg agtattttatt tgaaaaattg aagaataaaa aggttggcac caaagttgca
300
attatggata accatgtggt ggtgggcgta ggcaatattt atgcgaccga aagtctgttt
360
aatctgggga ttcattccagc acaaccggcc tcgactttaa gc
402

```

&lt;210&gt; 1500

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1500

```

Lys Tyr Ile Leu Pro Glu Phe Glu His Asp Thr Met Leu Trp His Leu
 1             5             10             15
Gly Met Ser Gly Ser Phe Arg Leu Cys Glu Ser Asn Glu Glu Leu Arg
      20             25             30
Lys His Asp His Leu Ile Ile Gln Phe Glu Asp Ile Glu Leu Arg Tyr
      35             40             45
His Asp Pro Arg Arg Phe Gly Cys Ile Leu Trp Leu Asp Ala Gln Ser
      50             55             60
Gln Ser Lys Leu Ile Asp Thr Leu Gly Pro Glu Pro Leu Ser Glu Asn

```



```

65          70          75          80
Phe Asn Ala Glu Tyr Leu Phe Glu Lys Leu Lys Asn Lys Lys Val Gly
      85          90          95
Thr Lys Val Ala Ile Met Asp Asn His Val Val Val Gly Val Gly Asn
      100          105          110
Ile Tyr Ala Thr Glu Ser Leu Phe Asn Leu Gly Ile His Pro Ala Gln
      115          120          125
Pro Ala Ser Thr Leu Ser
      130

```

&lt;210&gt; 1501

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1501

```

nnacgcgtgc atgctgcagg catcatccat cgcgatctga agcccaaaa catcttctcg
60
gtgccgagcg cgccgagcg cgacttcgtg aagatcttcg acttcggcg atgccagatg
120
gtcacaccga aggtatcgaa cggcgtgcc gagctgaaga cgagcgcggg aaatctcttc
180
ggcacggtgc cgtacatggc gccggagtgc ttcgaggacg gctcgaccg gctggatgcg
240
cgccgaggaca tctactccac gggcatcatc atgtaccgct gcgtgacggg gacgtcccc
300
ttcaaggcga acaccgtctt cgagatgctc atccatctgc gcgagggccg cccatcaagc
360
tt
362

```

&lt;210&gt; 1502

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1502

```

Xaa Arg Val His Ala Ala Gly Ile Ile His Arg Asp Leu Lys Pro Gln
1      5      10      15
Asn Ile Phe Leu Val Pro Ser Ala Arg Glu Arg Asp Phe Val Lys Ile
      20      25      30
Phe Asp Phe Gly Ala Cys Gln Met Val Thr Pro Lys Val Ser Asn Gly
      35      40      45
Val Pro Glu Leu Lys Thr Ser Ala Gly Asn Leu Phe Gly Thr Val Pro
      50      55      60
Tyr Met Ala Pro Glu Cys Phe Glu Asp Gly Ser His Arg Leu Asp Ala
65      70      75      80
Arg Ala Asp Ile Tyr Ser Thr Gly Ile Ile Met Tyr Arg Cys Val Thr
      85      90      95
Gly Thr Leu Pro Phe Lys Ala Asn Thr Val Phe Glu Met Leu Ile His
      100      105      110
Leu Arg Glu Gly Arg Pro Ser Ser
      115      120

```

<210> 1503  
 <211> 623  
 <212> DNA  
 <213> Homo sapiens

<400> 1503  
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 60  
 gaccgggtac accgcacctg gttgcgccag gtgtctgagg aggtctgaca gttaccgcaa  
 120  
 gggctcatga cgacccctcc tgaacctgt tcaaagggcg acggcttacc attcctcgct  
 180  
 gtgagtcctg aacagcagct tctcgaatat gaccgacgtc atgtctggca cccctacgcc  
 240  
 ccgacgatcg gggcagaccc aatgcttgca gtgacggctg ccaacggagt ctggctgcag  
 300  
 ctgcatgatg gggaaacaccg ccacgaggtc atcgatgcga tggcctcgtg gtggtgccag  
 360  
 attcacggtt accgaaaccc ggtcctcgac gaggccctca accgtcaaag ctcccagttc  
 420  
 agtcacgtca tgtttggcgg actcacccat aaggccgcgg ttgacgccgt catatcccta  
 480  
 gtgcgcctgg ccccgggggc cctcgaccgg atcttctcgg ctgattccgg gtctgtcggc  
 540  
 gtcgaggtga gtctcaaatt ggctcgtcag gtgcaaatcg ctcgcaccgc agcgcgcggc  
 600  
 ggcactttga cgaggacacg cgt  
 623

<210> 1504  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<400> 1504  
 Met Thr Thr Pro Pro Glu His Cys Ser Lys Gly Asp Gly Leu Pro Phe  
 1 5 10 15  
 Leu Ala Val Ser Pro Glu Gln Gln Leu Leu Glu Tyr Asp Arg Arg His  
 20 25 30  
 Val Trp His Pro Tyr Ala Pro Thr Ile Gly Ala Asp Pro Met Leu Ala  
 35 40 45  
 Val Thr Ala Ala Asn Gly Val Trp Leu Gln Leu His Asp Gly Glu His  
 50 55 60  
 Arg His Glu Val Ile Asp Ala Met Ala Ser Trp Trp Cys Gln Ile His  
 65 70 75 80  
 Gly Tyr Arg Asn Pro Val Leu Asp Glu Ala Leu Asn Arg Gln Ser Ser  
 85 90 95  
 Gln Phe Ser His Val Met Phe Gly Gly Leu Thr His Lys Ala Ala Val  
 100 105 110  
 Asp Ala Val Ile Ser Leu Val Arg Leu Ala Pro Gly Pro Leu Asp Arg  
 115 120 125  
 Ile Phe Leu Ala Asp Ser Gly Ser Val Gly Val Glu Val Ser Leu Lys  
 130 135 140  
 Leu Ala Arg Gln Val Gln Ile Ala Arg Thr Ala Ala Arg Gly Gly Thr

```
<210> 1505
<211> 556
<212> DNA
<213> Homo sapiens
```

```
<210> 1506
<211> 169
<212> PRT
<213> Homo sapiens
```

1244

130                      135                      140  
 Gly Gln Leu Ala Asp Gly Ile Asp Gln Phe Thr Gly Asn Leu Val Gly  
 145                      150                      155                      160  
 Tyr Arg Thr Glu Ile Arg Gln Tyr Ala  
                          165

<210> 1507

<211> 667

<212> DNA

<213> Homo sapiens

<400> 1507

agatctctta agatgtgctc attatcatga gaacagcgtg gaggaaacca cccccaggat  
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 ccagttacct ccacttgctc tgccttggc acgtggggct tatggggatt acaattcaag  
 120  
 gtgagacttg ggtggggaca cagtgggaaca tgaagtgtgc cagctgggt ggatgacgcc  
 180  
 ctctccccc cgccaccgag agctgcaggc cacatgattc cttttgggta gcactcgga  
 240  
 aagggcagaa tgtacaggaa cagagtgaga ttcgcagggc ctggggctga gggaggggac  
 300  
 gcactagagg aaggcaaagg ggagcctcct ggggtgtggg agcactttct gtcttggtt  
 360  
 tgggtggtggc tgcacagtgg cccacacccg tcagagctca cctgcctgca cccaggccct  
 420  
 ccgtgcaccc tggcagccca gatgactgca ccagcccagg ggaggtggag gaatgccaca  
 480  
 cgcaccggtta cctggggacc gggggctctc ggtgatcatc ccgagctcca agacagaagc  
 540  
 tggactacag ccgtgctgag tggaggggtt tgggtggctgg gtgcccgcct cctattgctc  
 600  
 ctgcagactc tggggctctc ggcgcccca gtggggcaat gtgggctgct gcagggaaact  
 660  
 cacgcgt  
 667

<210> 1508

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1508

Met Tyr Arg Asn Arg Val Arg Phe Ala Gly Pro Gly Ala Glu Gly Gly  
 1                      5                      10                      15  
 Asp Ala Leu Glu Glu Gly Lys Gly Glu Pro Pro Gly Cys Gly Glu His  
                          20                      25                      30  
 Phe Leu Ser Trp Phe Trp Trp Trp Leu His Ser Gly Pro His Pro Ser  
                          35                      40                      45  
 Glu Leu Thr Cys Leu His Pro Gly Pro Pro Cys Thr Leu Ala Ala Gln  
                          50                      55                      60  
 Met Thr Ala Pro Ala Gln Gly Arg Trp Arg Asn Ala Thr Arg Thr Gly  
 65                      70                      75                      80  
 Thr Trp Gly Pro Gly Val Leu Gly Asp His Pro Glu Leu Gln Asp Arg

<210> 1511  
<211> 633

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1511

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120
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240
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300
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420
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480
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540
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633

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&lt;210&gt; 1512

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1512

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Ala Gly Thr Gly Val Lys Ala Met Ala Leu Gly Pro Gly Trp Val His
1           5           10           15
Thr Glu Phe His Ser Arg Ala Asn Val Thr Gly Asn His Leu Pro Asp
20           25           30
Phe Phe Trp Ile Asp Ala Glu Val Leu Val Arg Glu Ala Leu Asn Asp
35           40           45
Leu Asp His Asp Lys Val Val Ser Ile Pro Thr Pro Leu Trp Lys Phe
50           55           60
Phe Ile Ala Val Ala Thr His Thr Pro Arg Ser Ala Met Arg Phe Leu
65           70           75           80
Ser Arg Thr Leu Ser Ser Ser Arg Asp Lys Asp Asp His Pro Arg His
85           90           95
Thr Pro Gly Gly Glu Ala
100

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&lt;210&gt; 1513

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1513

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 60  
 ttggctgtcc aatctcgtaa tgcccttctg aatgacttgc tgggcctgcc tcctgacacg  
 120  
 gctgtttcgc aggaaccgcc actcccgtc cttgcggatc tgactctcca ggctgtgctc  
 180  
 ttctgggac ttcatgacgg gctgggtaaa atagccgggc gctccagtcg cagaaccccg  
 240  
 tctgcaccgt ggcgagatg aaacttttgt gtccagcagc atcgtccgcg tcgtccgcag  
 300  
 tctgctctgg gcccttgctg aacatcttcc gtgtccgggg gaactgggtg gagtgagggg  
 360  
 tgtactgcgc ccagcgggg cctgtgggtgc ccggccggcc g  
 401

<210> 1514

<211> 108

<212> PRT

<213> Homo sapiens

<400> 1514

Met	Phe	Asp	Lys	Gly	Pro	Glu	Gln	Thr	Ala	Asp	Asp	Ala	Asp	Asp	Ala
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Ala	Gly	His	Lys	Ser	Phe	Ile	Ser	Ala	Thr	Val	Gln	Thr	Gly	Phe	Cys
			20					25					30		
Asp	Trp	Ser	Ala	Arg	Leu	Phe	Tyr	Pro	Ala	Arg	His	Glu	Asp	Pro	Arg
		35					40				45				
Arg	Ala	Arg	Pro	Gly	Glu	Ser	Asp	Pro	Gln	Gly	Ala	Gly	Val	Ala	Val
	50					55					60				
Pro	Ala	Lys	Gln	Pro	Cys	Gln	Glu	Ala	Gly	Pro	Ala	Ser	His	Ser	Glu
65					70				75					80	
Gly	His	Tyr	Glu	Ile	Gly	Arg	Pro	Asn	Ile	Ser	Glu	Gln	Glu	Pro	Arg
				85				90						95	
Arg	Pro	Leu	Cys	Gly	Glu	Ile	Pro	Pro	Leu	His	Ala				
			100					105							

<210> 1515

<211> 720

<212> DNA

<213> Homo sapiens

<400> 1515

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 120  
 aactacgagc ctgacctgac cgacgatgcg acgtcgggtcc cgctcgccgt cgctattgac  
 180  
 gatcccggcc cgcctacgcc tattgcgcgc cgccacgaca tcagcgaatc gggcatctat  
 240  
 gagaccatg tcaaagggct aaccgcctt caccctctcg ttctgagca tcttcgcagc  
 300  
 acctatgccg ggcttgcta tccggctgtt atcgaacacc tcaagtcaat cggagtaaca  
 360

gccatcgaac tactaccggt ccagcagttc gtctccgaac cattcatcgt tgggcgcggc  
 420  
 ttatccgatt actgggggta caacaccctg ggggtctttg cgccgcatgc tgcctactgc  
 480  
 tccgtcggct cgatgggaac ccaggtgcgc gaggttcaagg acatgggtgac gtctttccac  
 540  
 gaagccggca tcgaggtttt ctcgatgtc gtctacaacc aactgggtga gggcggccat  
 600  
 gaaggaccga ctctgtcttt ccgcggcatc gatcacgagt cttattaccg cctcaccaac  
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 720

<210> 1516

<211> 240

<212> PRT

<213> Homo sapiens

<400> 1516

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Asp	Pro	Tyr	Ala	Arg	Ala	Ile	Thr	Ala	Gly	Val	Asp	Tyr	His	Gly	Pro
			20					25				30			
Ile	Met	Asp	His	Thr	Pro	Glu	Ser	Asn	Tyr	Glu	Pro	Asp	Leu	Thr	Asp
		35					40					45			
Asp	Ala	Thr	Ser	Val	Pro	Leu	Ala	Val	Val	Ile	Asp	Asp	Pro	Gly	Pro
	50					55				60					
Pro	Thr	Pro	Ile	Ala	Arg	Arg	His	Asp	Ile	Ser	Glu	Ser	Gly	Ile	Tyr
65					70				75					80	
Glu	Thr	His	Val	Lys	Gly	Leu	Thr	Arg	Leu	His	Pro	Leu	Val	Pro	Glu
			85					90					95		
His	Leu	Arg	Ser	Thr	Tyr	Ala	Gly	Leu	Ala	Tyr	Pro	Ala	Val	Ile	Glu
		100					105					110			
His	Leu	Lys	Ser	Ile	Gly	Val	Thr	Ala	Ile	Glu	Leu	Leu	Pro	Val	Gln
	115					120					125				
Gln	Phe	Val	Ser	Glu	Pro	Phe	Ile	Val	Gly	Arg	Gly	Leu	Ser	Asp	Tyr
	130					135				140					
Trp	Gly	Tyr	Asn	Thr	Leu	Gly	Phe	Phe	Ala	Pro	His	Ala	Ala	Tyr	Cys
145					150				155					160	
Ser	Val	Gly	Ser	Met	Gly	Thr	Gln	Val	Arg	Glu	Phe	Lys	Asp	Met	Val
			165					170					175		
Thr	Ser	Phe	His	Glu	Ala	Gly	Ile	Glu	Val	Phe	Leu	Asp	Val	Val	Tyr
		180					185					190			
Asn	His	Thr	Gly	Glu	Gly	Gly	His	Glu	Gly	Pro	Thr	Leu	Ser	Phe	Arg
	195					200					205				
Gly	Ile	Asp	His	Glu	Ser	Tyr	Tyr	Arg	Leu	Thr	Asn	Asp	His	Arg	Asn
	210					215				220					
Asp	Tyr	Asp	Val	Thr	Gly	Cys	Gly	Asn	Ser	Val	Asp	Thr	Ser	His	Pro
225					230					235					240

<210> 1517

<211> 497

<212> DNA

<213> Homo sapiens



&lt;400&gt; 1517

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 120  
 tccttttcca tcgggctgca agtactgttt ccattcctcc tggcaggctt tgggaccgtg  
 180  
 gctgctggca tgggtgttga catcgtgcag cactgggaag tcttccagaa ggtgacagag  
 240  
 gtcttcatcc tagtgctgc gctgctgggg ctcaaaggga acctggaaat gaccctggca  
 300  
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 360  
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 420  
 tccatcgcag ccgtcgtctt tggctggatc cctgatggcc acttcagtat tccgcacgcc  
 480  
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 497

&lt;210&gt; 1518

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1518

Xaa	Arg	Val	Lys	Gly	Val	Arg	Glu	Glu	Asp	Ala	Leu	Leu	Glu	Asn	Gly
1				5					10					15	
Ser	Gln	Ser	Asn	Glu	Ser	Asp	Asp	Val	Ser	Thr	Asp	Arg	Gly	Pro	Ala
			20					25					30		
Pro	Pro	Ser	Pro	Leu	Lys	Glu	Thr	Ser	Phe	Ser	Ile	Gly	Leu	Gln	Val
		35					40					45			
Leu	Phe	Pro	Phe	Leu	Leu	Ala	Gly	Phe	Gly	Thr	Val	Ala	Ala	Gly	Met
	50					55					60				
Val	Leu	Asp	Ile	Val	Gln	His	Trp	Glu	Val	Phe	Gln	Lys	Val	Thr	Glu
65					70					75				80	
Val	Phe	Ile	Leu	Val	Pro	Ala	Leu	Leu	Gly	Leu	Lys	Gly	Asn	Leu	Glu
			85						90				95		
Met	Thr	Leu	Ala	Ser	Arg	Leu	Ser	Thr	Ala	Ala	Asn	Ile	Gly	His	Met
		100						105					110		
Asp	Thr	Pro	Lys	Glu	Leu	Trp	Arg	Met	Ile	Thr	Gly	Asn	Met	Ala	Leu
		115					120					125			
Ile	Gln	Val	Gln	Ala	Pro	Val	Val	Gly	Phe	Leu	Ala	Ser	Ile	Ala	Ala
		130					135				140				
Val	Val	Phe	Gly	Trp	Ile	Pro	Asp	Gly	His	Phe	Ser	Ile	Pro	His	Ala
145					150					155				160	
Phe	Leu	Leu	Cys	Gly											
			165												

&lt;210&gt; 1519

&lt;211&gt; 2076

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 1519  
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120  
cttacaaaaa ttgaaggagt gctctctggg gatccacttg atctgaaaat gtttgaggct  
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720  
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1080  
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1140  
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1320  
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1440  
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1560

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 1680  
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 1800  
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 1860  
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 1920  
 atcattgttc ttgtcaatgc ctttgtgtct atcacagtgg agaacttctt ccttgacatg  
 1980  
 gtcctttgga aagtgtgtgt caaccgagac aaacaaggag agtatcgggt cagcaccaca  
 2040  
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 2076

<210> 1520

<211> 692

<212> PRT

<213> Homo sapiens

<400> 1520

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Pro	Glu	Glu	Asn	Val	Cys	Asn	Glu	Met	Leu	Val	Lys	Ser	Gln	Phe	Val
			20					25					30		
Ala	Cys	Met	Ala	Thr	Cys	His	Ser	Leu	Thr	Lys	Ile	Glu	Gly	Val	Leu
		35					40					45			
Ser	Gly	Asp	Pro	Leu	Asp	Leu	Lys	Met	Phe	Glu	Ala	Ile	Gly	Trp	Ile
	50					55				60					
Leu	Glu	Glu	Ala	Thr	Glu	Glu	Glu	Thr	Ala	Leu	His	Asn	Arg	Ile	Met
65					70					75				80	
Pro	Thr	Val	Val	Arg	Pro	Pro	Lys	Gln	Leu	Leu	Pro	Glu	Ser	Thr	Pro
			85					90						95	
Ala	Gly	Asn	Gln	Glu	Met	Glu	Leu	Phe	Glu	Leu	Pro	Ala	Thr	Tyr	Glu
		100					105						110		
Ile	Gly	Ile	Val	Arg	Gln	Phe	Pro	Phe	Ser	Ser	Ala	Leu	Gln	Arg	Met
	115					120						125			
Ser	Val	Val	Ala	Arg	Val	Leu	Gly	Asp	Arg	Lys	Met	Asp	Ala	Tyr	Met
	130					135					140				
Lys	Gly	Ala	Pro	Glu	Ala	Ile	Ala	Gly	Leu	Cys	Lys	Pro	Glu	Thr	Val
145				150					155					160	
Pro	Val	Asp	Phe	Gln	Asn	Val	Leu	Glu	Asp	Phe	Thr	Lys	Gln	Gly	Phe
			165					170						175	
Arg	Val	Ile	Ala	Leu	Ala	His	Arg	Lys	Leu	Glu	Ser	Lys	Leu	Thr	Trp
		180					185						190		
His	Lys	Val	Gln	Asn	Ile	Ser	Arg	Asp	Ala	Ile	Glu	Asn	Asn	Met	Asp
	195					200						205			
Phe	Met	Gly	Leu	Ile	Ile	Met	Gln	Asn	Lys	Leu	Lys	Gln	Glu	Thr	Pro
	210					215						220			
Ala	Val	Leu	Glu	Asp	Leu	His	Lys	Ala	Asn	Ile	Arg	Thr	Val	Met	Val

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225          230          235          240
Thr Gly Asp Ser Met Leu Thr Ala Val Ser Val Ala Arg Asp Cys Gly
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Met Ile Leu Pro Gln Asp Lys Val Ile Ile Ala Glu Ala Leu Pro Pro
          260          265          270
Lys Asp Gly Lys Val Ala Lys Ile Asn Trp His Tyr Ala Asp Ser Leu
          275          280          285
Thr Gln Cys Ser His Pro Ser Ala Ile Asp Pro Glu Ala Ile Pro Val
          290          295          300
Lys Leu Val His Asp Ser Leu Glu Asp Leu Gln Met Thr Arg Tyr His
305          310          315          320
Phe Ala Met Asn Gly Lys Ser Phe Ser Val Ile Leu Glu His Phe Gln
          325          330          335
Asp Leu Val Pro Lys Leu Met Leu His Gly Thr Val Phe Ala Arg Met
          340          345          350
Ala Pro Asp Gln Lys Thr Gln Leu Ile Glu Ala Leu Gln Asn Val Asp
          355          360          365
Tyr Phe Val Gly Met Cys Gly Asp Gly Ala Asn Asp Cys Gly Ala Leu
          370          375          380
Lys Arg Ala His Gly Gly Ile Ser Leu Ser Glu Leu Glu Ala Ser Val
385          390          395          400
Ala Ser Pro Phe Thr Ser Lys Thr Pro Ser Ile Ser Cys Val Pro Asn
          405          410          415
Leu Ile Arg Glu Gly Arg Ala Ala Leu Ile Thr Ser Phe Cys Val Phe
          420          425          430
Lys Phe Met Ala Leu Tyr Ser Ile Ile Gln Tyr Phe Ser Val Thr Leu
          435          440          445
Leu Tyr Ser Ile Leu Ser Asn Leu Gly Asp Phe Gln Phe Leu Phe Ile
          450          455          460
Asp Leu Ala Ile Ile Leu Val Val Val Phe Thr Met Ser Leu Asn Pro
465          470          475          480
Ala Trp Lys Glu Leu Val Ala Gln Arg Pro Pro Ser Gly Leu Ile Ser
          485          490          495
Gly Ala Leu Leu Phe Ser Val Leu Ser Gln Ile Ile Ile Cys Ile Gly
          500          505          510
Phe Gln Ser Leu Gly Phe Phe Trp Val Lys Gln Gln Pro Trp Tyr Glu
          515          520          525
Val Trp His Pro Lys Ser Asp Ala Cys Asn Thr Thr Gly Ser Gly Phe
          530          535          540
Trp Asn Ser Ser His Val Asp Asn Glu Thr Glu Leu Asp Glu His Asn
545          550          555          560
Ile Gln Asn Tyr Glu Asn Thr Thr Val Phe Phe Ile Ser Ser Phe Gln
          565          570          575
Tyr Leu Ile Val Ala Ile Ala Phe Ser Lys Gly Lys Pro Phe Arg Gln
          580          585          590
Pro Cys Tyr Lys Asn Tyr Phe Phe Val Phe Ser Val Ile Phe Leu Tyr
          595          600          605
Ile Phe Ile Leu Phe Ile Met Leu Tyr Pro Val Ala Ser Val Asp Gln
          610          615          620
Val Leu Gln Ile Val Cys Val Pro Tyr Gln Trp Arg Val Thr Met Leu
625          630          635          640
Ile Ile Val Leu Val Asn Ala Phe Val Ser Ile Thr Val Glu Asn Phe
          645          650          655
Phe Leu Asp Met Val Leu Trp Lys Val Val Phe Asn Arg Asp Lys Gln

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 240  
 aaggagatcg tggaccctct gtacggcata gctgaggtgg agattcccaa catccagaag  
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 420  
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<210> 1524

<211> 175

<212> PRT

<213> Homo sapiens

<400> 1524

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Cys	Phe	Gln	Gly	Gln	His	Gly	Thr	Asp	Ala	Glu	Arg	Arg	His	Lys	Lys
		20						25					30		
Leu	Pro	Leu	Thr	Ala	Leu	Ala	Gln	Asn	Met	Gln	Glu	Ala	Ser	Thr	Gln
		35					40					45			
Leu	Glu	Asp	Ser	Leu	Leu	Gly	Lys	Met	Leu	Glu	Thr	Cys	Gly	Asp	Ala
		50				55					60				
Glu	Asn	Gln	Leu	Ala	Leu	Glu	Leu	Ser	Gln	His	Glu	Val	Phe	Val	Glu
65					70					75				80	
Lys	Glu	Ile	Val	Asp	Pro	Leu	Tyr	Gly	Ile	Ala	Glu	Val	Glu	Ile	Pro
			85					90						95	
Asn	Ile	Gln	Lys	Gln	Arg	Lys	Gln	Leu	Ala	Arg	Leu	Val	Leu	Asp	Trp
			100					105					110		
Asp	Ser	Val	Arg	Ala	Arg	Trp	Asn	Gln	Ala	His	Lys	Ser	Ser	Gly	Thr
		115					120					125			
Asn	Phe	Gln	Gly	Leu	Pro	Ser	Lys	Ile	Asp	Thr	Leu	Lys	Glu	Gly	Met
		130				135					140				
Asp	Glu	Ala	Gly	Asn	Lys	Val	Glu	Gln	Cys	Lys	Asp	Gln	Leu	Ala	Ala
145					150					155				160	
Asp	Met	Tyr	Asn	Phe	Met	Ala	Lys	Glu	Gly	Glu	Tyr	Gly	Lys	Phe	
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<210> 1525

<211> 294

<212> DNA

<213> Homo sapiens

<400> 1525

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 294

<210> 1526

<211> 98

<212> PRT

<213> Homo sapiens

<400> 1526

Val	His	Glu	Arg	Met	Asp	Leu	Ile	Arg	Gln	Ser	Val	Asp	Ala	Arg	Ile
1				5				10					15		
Asn	Val	Asp	Tyr	Trp	Ser	Gly	Leu	Leu	Val	Asp	Tyr	Thr	Ser	Gln	His
		20					25					30			
Gly	Val	Asp	Val	Leu	Val	Lys	Gly	Leu	Arg	Ser	Ser	Leu	Asp	Tyr	Glu
		35				40					45				
Tyr	Glu	Leu	Pro	Met	Ala	Gln	Met	Asn	Arg	Arg	Leu	Ser	Gly	Ile	Asp
50					55				60						
Thr	Val	Phe	Leu	Leu	Thr	Asp	Glu	Lys	Tyr	Gly	Tyr	Ile	Ser	Ser	Ser
65					70				75					80	
Leu	Cys	Lys	Gln	Val	Ala	Gln	Phe	Gly	Gly	Glu	Val	Thr	Gly	Met	Leu
			85					90						95	

Arg Ile

<210> 1527

<211> 371

<212> DNA

<213> Homo sapiens

<400> 1527

tgtacaaacc cgcctatgag caagtgcaaa ccaacatgga aatgctcaag gccggacgca  
 60  
 gtttcaagga atacgccgag atggcctgga agattcccga gcattacaaa aacaaccgct  
 120  
 acttcgccct ggtgcacggg gttggcatga ccggcgagta cccttgggtg gtgcaccgcg  
 180  
 aagacattga cgcgctgggt tacgacgggtg tgttcgaggc cggcatgacc atctgtgtgg  
 240  
 aaagctacat cggccacgac gacggcgggc aaggcgtgaa gctcgaagaa cagatctaca  
 300  
 tccacgaaca cagcatcgag ttgctctccg attatccgtt cgacccacgc ctgttgccgc  
 360  
 gctgaacgcg t  
 371

<210> 1528

<211> 109

<212> PRT

<213> Homo sapiens

<400> 1528

```

Met Glu Met Leu Lys Ala Gly Arg Ser Phe Lys Glu Tyr Ala Glu Met
 1           5           10           15
Ala Trp Lys Ile Pro Glu His Tyr Lys Asn Asn Arg Tyr Phe Ala Leu
 20           25           30
Val His Gly Val Gly Met Thr Gly Glu Tyr Pro Trp Val Val His Arg
 35           40           45
Glu Asp Ile Asp Ala Leu Gly Tyr Asp Gly Val Phe Glu Ala Gly Met
 50           55           60
Thr Ile Cys Val Glu Ser Tyr Ile Gly His Asp Asp Gly Gly Glu Gly
 65           70           75           80
Val Lys Leu Glu Glu Gln Ile Tyr Ile His Glu His Ser Ile Glu Leu
 85           90           95
Leu Ser Asp Tyr Pro Phe Asp Pro Arg Leu Leu Pro Arg
100           105

```

<210> 1529

<211> 609

<212> DNA

<213> Homo sapiens

<400> 1529

```

naccgctggt gctcaccctc cgtgtgactc gcgctctgtc cggctcaggg ctgcccctcc
60
gtgggacttg cgctctgtcc ggctcagggc tcgcccctccg tgggacttgc gctctgtccg
120
gctcagggct cgcccctcgt gggacttgcg ctctgtccgg ctcagggctc gccctccgtg
180
ggacttgccg tctgtccggc tcagggctcg cctccgtgg gacttgccgt ctgtccggct
240
cagggctcgc cctccgtggg acttgccgtc tgtccggctc agggctcgcc ctccgtggga
300
tttgcgctct gtctggctca ggctgcgcag ggcaatggag gaacctcccg agcaggccca
360
gcggctcctt ccaccagcc cccatctccg gccggccatt tgtgaggccc tctgccactg
420
aggtgcactg tttccaattc ctcatcaca agctctacct tccacgagcc cagagcatga
480
acgcattcgg ccattggtct caccactctg cgaggagcac agcctcttct ccaccgtcca
540
atagegtgtt cctcctttcc caggcctcac agaattgctt gtccgcatcc tcccagcatt
600
ccattcacg
609

```

<210> 1530

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1530

```

Leu Ala Leu Cys Pro Ala Gln Gly Ser Pro Ser Val Gly Leu Ala Leu

```



1		5		10		15									
Cys	Pro	Ala	Gln	Gly	Ser	Pro	Ser	Val	Gly	Leu	Ala	Leu	Cys	Pro	Ala
		20						25					30		
Gln	Gly	Ser	Pro	Ser	Val	Gly	Leu	Ala	Leu	Cys	Pro	Ala	Gln	Gly	Ser
		35					40					45			
Pro	Ser	Val	Gly	Leu	Ala	Leu	Cys	Pro	Ala	Gln	Gly	Ser	Pro	Ser	Val
		50				55				60					
Gly	Leu	Ala	Leu	Cys	Pro	Ala	Gln	Gly	Ser	Pro	Ser	Val	Gly	Leu	Ala
65				70					75				80		
Leu	Cys	Pro	Ala	Gln	Gly	Ser	Pro	Ser	Val	Gly	Phe	Ala	Leu	Cys	Leu
			85					90				95			
Ala	Gln	Ala	Ala	Gln	Gly	Asn	Gly	Gly	Thr	Ser	Arg	Ala	Gly	Pro	Ala
		100						105				110			
Ala	Pro	Ser	Thr	Gln	Pro	Pro	Ser	Pro	Ala	Gly	His	Leu			
		115					120					125			

&lt;210&gt; 1531

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1531

```

accggtcgcc ggcttgctga gggtaacctt ctggccacag ttggtgatgg tgataggtcc
60
agcgttggac tgggacgccg acgctgaaaa agaagctgac gagtccttgg gggcgcccg
120
acattcgcca agcatgagga cggggagcat cgagaccgag acagctcggc gaaggaattt
180
cggggtggca ggcattggca aactagcttt ctgtgatcgg cgtgcgcggc cgggcaacaa
240
cagggcgctc tcaggtggtc ttccggctcg atttcgtctc cgttcccggc accttcccag
300
tgcgcatggc caggtgggtc aagtcggggc ggatcagtca taccgctgag ctcagctccg
360
gcttttcacc ggattccagc gctggtgtgg tcaccagcaa cctgacgaga ggatttttagc
420
accccttcg cataccgcta tccaggcct ccacgacagc ggcaccgatg acgatcgct
480
tcaccgagcg cggcgttttc ggcagcttcc acatggggat cagaccatat tgatgcactg
540
gcgatccctt catacgcgag ccgccgatat ggcccccgag tgaggcccct cagttcgcgc
600
tgacgcatgc cgctctgcgc agcctgcaaa cgctttcccg caacctcacc acacgtttgc
660
cgggttcggg gctggcgagc tgagccgtgt cacaagttca cgagctgggt caccgctccg
720
cgagag
726

```

&lt;210&gt; 1532

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1532

Met Val Ile Gly Pro Ala Leu Asp Trp Asp Ala Asp Ala Glu Lys Glu  
 1 5 10 15  
 Ala Asp Glu Ser Leu Gly Ala Pro Ala His Ser Ala Ser Met Arg Thr  
 20 25 30  
 Gly Ser Ile Glu Thr Ala Thr Ala Arg Arg Arg Asn Phe Gly Val Ala  
 35 40 45  
 Gly Met Ala Lys Leu Ala Phe Cys Asp Arg Arg Ala Arg Pro Gly Asn  
 50 55 60  
 Asn Arg Ala Ser Ser Gly Gly Leu Arg Ala Arg Leu Arg Leu Arg Ser  
 65 70 75 80  
 Arg His Leu Pro Ser Ala His Gly Gln Val Val Gln Val Gly Ala Asp  
 85 90 95  
 Gln Ser Tyr Arg Cys Ala Gln Leu Arg Leu Phe Thr Gly Phe Gln Arg  
 100 105 110  
 Trp Cys Gly His Gln Gln Pro Asp Ala Arg Ile Leu Ala Pro Pro Ser  
 115 120 125  
 His Thr Ala Ile Gln Gly Leu His Asp Ser Gly Thr Asp Asp Asp Arg  
 130 135 140  
 Val His Arg Ala Arg Arg Phe Arg Gln Leu Pro His Gly Asp Gln Thr  
 145 150 155 160  
 Ile Leu Met His Trp Arg Ser Leu His Thr Arg Ala Ala Asp Met Ala  
 165 170 175  
 Pro Glu

&lt;210&gt; 1533

&lt;211&gt; 364

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1533

natatgctgg tcgatcatgt gcatcagatc gtccagtggc cggagcgcgg ctggctggcg  
 60  
 gagattattc acagcgaacg ggcgaccggc ggtgcgccgc ttaacgtcct gctgacgctg  
 120  
 gttaaaatgc acgtcggctt gccgttgacg gcggtcggtc ttatcggcga agacagcgat  
 180  
 ggcgattaca ttatggcgat gctcgaccag taccacgtca atcgccagcg ggtacagcgc  
 240  
 accacgtttg cccccacgtc gatgtcgacg gtgatgaccg atcccactgg gcagcgcacc  
 300  
 tttttccatt cgctgccgc caatcgctg ctgatctcc ccgccttga tcgactcgac  
 360  
 gcgt  
 364

&lt;210&gt; 1534

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1534

Xaa Met Leu Val Asp His Val His Gln Ile Val Gln Trp Pro Glu Arg

```

      1             5             10             15
Gly Trp Leu Ala Glu Ile Ile His Ser Glu Arg Ala Thr Gly Gly Ala
      20             25             30
Pro Leu Asn Val Leu Leu Thr Leu Val Lys Met His Val Gly Leu Pro
      35             40             45
Leu Gln Ala Val Gly Leu Ile Gly Glu Asp Ser Asp Gly Asp Tyr Ile
      50             55             60
Met Ala Met Leu Asp Gln Tyr His Val Asn Arg Gln Arg Val Gln Arg
      65             70             75             80
Thr Thr Phe Ala Pro Thr Ser Met Ser Gln Val Met Thr Asp Pro Thr
      85             90             95
Gly Gln Arg Thr Phe Phe His Ser Pro Ala Ala Asn Arg Leu Leu Asp
      100            105            110
Leu Pro Ala Phe Asp Arg Leu Asp Ala
      115            120

```

&lt;210&gt; 1535

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1535

```

gaattcgggg ggctccggga atgaagtttc catttcgcaa gccttctgaa gcaaataccgc
60
caatccctgg ggcccgcggt gcgtgccggc cagcggccag tcctggcccg gaatgatcca
120
ctcgatatct tcggcagaca acgccagcag accgggccta tcgccgcggc ccatggctgc
180
aaaaaaaactc ttcacagtct ggacattccc ttgtgtgctc atcgaaatct ctccatgtcc
240
tttacctggg atcgtgtccg atctcatcgg acgcgttgag gacctgctgg tgaggacggg
300
gtgtcgggtga ttcagccgat atcgactttg catggcgatg tcccagctgc cggagccgtt
360
actggccac
369

```

&lt;210&gt; 1536

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1536

```

Met Gln Ser Arg Tyr Arg Leu Asn His Arg His Pro Val Leu Thr Ser
1             5             10             15
Arg Ser Ser Thr Arg Pro Met Arg Ser Asp Thr Ile Pro Gly Lys Gly
      20             25             30
His Gly Glu Ile Ser Met Ser Thr Gln Gly Asn Val Gln Thr Val Lys
      35             40             45
Ser Phe Phe Ala Ala Met Gly Arg Gly Asp Arg Pro Gly Leu Leu Ala
      50             55             60
Leu Ser Ala Glu Asp Ile Glu Trp Ile Ile Pro Gly Gln Asp Trp Pro
      65             70             75             80
Leu Ala Gly Thr His Arg Gly Pro Gln Gly Leu Ala Asp Leu Leu Gln

```

				85					90					95
Lys	Ala	Cys	Glu	Met	Glu	Thr	Ser	Phe	Pro	Glu	Pro	Pro	Glu	Phe
				100				105					110	

<210> 1537  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<400> 1537  
 ccactcgcgg cgctcctga gccctctcgt gtgtcaggac gccagcatcc tgttcgtggt  
 60  
 ctcggggctg ctgcacgtgt accagcggaa gatcggcagc caggaggaca cctgcttggt  
 120  
 cctcacgcgc cccggggaga tgggtgggcca gctggccgtg ctcaccgagg agacctcgtc  
 180  
 ggctgtggtgg agacactgac ccaccaggcc cgggcgacca cgggtgcatgc cgttcgggac  
 240  
 tcagaattgg ccaagctgcc ggcaggagcc ctcacgtcca tcaagcgag gtac  
 294

<210> 1538  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 1538  
 Pro Leu Ala Ala Pro Pro Glu Pro Ser Arg Val Ser Gly Arg Gln His  
 1 5 10 15  
 Pro Val Arg Val Leu Gly Ala Ala Ala Arg Val Pro Ala Glu Asp Arg  
 20 25 30  
 Gln Pro Gly Gly His Leu Leu Val Pro His Ala Pro Arg Gly Asp Gly  
 35 40 45  
 Gly Pro Ala Gly Arg Ala His Arg Gly Asp Leu Val Gly Val Val Glu  
 50 55 60  
 Thr Leu Thr His Gln Ala Arg Ala Thr Thr Val His Ala Val Arg Asp  
 65 70 75 80  
 Ser Glu Leu Ala Lys Leu Pro Ala Gly Ala Leu Thr Ser Ile Lys Arg  
 85 90 95  
 Arg Tyr

<210> 1539  
 <211> 1015  
 <212> DNA  
 <213> Homo sapiens

<400> 1539  
 acgcgttcgg gcgtcaggca cacgcatctc aacagatgtg gctgacaccc aaggcagtcg  
 60  
 gcctcagtgc cctgtcaccc acctagaacc tgttcacagc atgtcatccg ggctgctctg  
 120  
 gccttgactg gacatgatta tttatcetta cacaccgtgg ctgctctaca ggccaagaaa  
 180

caggctgctc agccagggtc aggagaaggt gggtcaggct ccccggggac ctcaggccct  
 240  
 gacgcaccc taggcctcct ctgtcggggc agcctggctc agcagagccc  
 300  
 gggacacacg gctgaggcca cccaggctgg gccatcttgc ccctgttttg tgccccctac  
 360  
 tcagttctcc ttctgtcctg gctcaggctc aggccagtca agaggggtggc tgagaagcag  
 420  
 gaggagcctc agagaccctc ccctcgaaag cactggggct tccacctcac aagcggcagg  
 480  
 ttcgcttttg gagctgctgg tccatcgccc aggcctggcc aggggcaggc gaggatcctg  
 540  
 gttgccgatc catcgccag gcctggccca ggagccggtg aggaacctgg ggctgttggtg  
 600  
 caggggtcgc cgtctccagc tctctgccgt ggtgagggga ttgtgctgtg tgcacaccac  
 660  
 ctggctgcat cgaatccac catggcccag aggggtggacc tgtggctcct tggggggcca  
 720  
 gcacccccag tctaattgggt gccctgcca ctctcctgag tccccgtgca gagtcccccc  
 780  
 caacacctca gccttcacct ttctcagtta atcaaaagat tccaaaaaaa gcaaaccat  
 840  
 cagaacggct tctccaccg agtggtcagg ataaataatc atgtccagtc aaggccagag  
 900  
 cagcccgat gacatgctat gaacaggttt taggtgggtg acagggcact gaggccgact  
 960  
 gccttgggtg tcagccacat ctgttgagat gcgtgtgct gacgcccga cgcgt  
 1015

&lt;210&gt; 1540

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1540

His	Pro	Arg	Gln	Ser	Ala	Ser	Val	Pro	Cys	His	Pro	Pro	Arg	Thr	Cys
1				5					10					15	
Ser	Gln	His	Val	Ile	Arg	Ala	Ala	Leu	Ala	Leu	Thr	Gly	His	Asp	Tyr
			20					25					30		
Leu	Ser	Leu	His	Thr	Val	Ala	Ala	Leu	Gln	Ala	Lys	Lys	Gln	Ala	Ala
		35					40					45			
Gln	Pro	Gly	Ser	Gly	Glu	Gly	Gly	Ser	Gly	Ser	Pro	Gly	Thr	Ser	Gly
	50					55					60				
Pro	Asp	Ala	Ser	Trp	Pro	His	Pro	Arg	Pro	Pro	Leu	Ser	Gly	Gln	Pro
65					70					75				80	
Gly	Ser	Ala	Glu	Pro	Gly	Thr	His	Gly							
					85										

&lt;210&gt; 1541

&lt;211&gt; 1482

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1541

cgccgatcac ggggagcccc tcgactgcct cccagaacaa agtgggaaag ggaagcttag  
60  
cccgccgctg ccgcctccga gcagcccgcc aggactctgg ctactggaga tgggcgcccc  
120  
gctatcgagg cgacgggtgc cggcggaccc gtccctggcc ctggacgcgc tgcccccgga  
180  
gctgctggtg caggtgctga gccacgtgcc ggccacgctc cttggacacg cgatgccgcc  
240  
cagtgtgccg cgcctggcgc gacatagtgg acgggcccac tgggaggctg ctgcaactgg  
300  
cccgcgaccg cagcgcggag ggccgagcac tctacgcagt ggctcaacgc tgccctgcca  
360  
acaacgaaga caaagaggag ttcccgtgtg gcgccctggc gcgctactga ctgcgcgcgc  
420  
ccttcggccg caatctcatc ttcaactcct gcggagagca gggcttcaga ggctgggagg  
480  
tggagcatgg cgggaacggc tgggcatag aaaagaacct aacaccggtg cctggggctc  
540  
cttcgcagac ctgcttcgtg acctctttcg aatgggtgctc caagaggcag cttgtggacc  
600  
tggatgatga aggggtgtgg caggagctgc tggacagcgc ccagattgag atctgtgtgg  
660  
ctgactgggtg gggcgctcga gagaactgcg gctgcgtcta ccagctccgg gtccgccttc  
720  
tggatgtgta tgaaaaggaa gtggtcaagt tctcagcctc acctgacctg gtccttcagt  
780  
ggactgagag gggctgccga caggtctccc acgtcttcac caactttggc aagggcattc  
840  
gctacgtatc ttttgagcag tacgggagag acgtgagttc ctgggtgggg cactatggcg  
900  
cccttgtagc ccactccagt gtgagggta ggatccgtct gtcctagcga ctggactact  
960  
gcctgacgtt gtcagtcaag accagccttg cagccagggtg cagtggctca cacctgtggg  
1020  
atctcccccac tttggccttc caaaatgttg cgattatagg cgtgagccac tgtggctggc  
1080  
ctgaaatctt ctagtatcca cattcataaa gtaaaaagaa aataaaaagg catagaatgt  
1140  
caagctaacc aggcgtccgc tacttcagaa gagggtactg tcgcatgggg agtctgtaac  
1200  
catgcttttc acttccactg catctctcgc tggctcaaaa cacgacaggt gtgtccattg  
1260  
gacaacagag agtgggaatt ccaaaagtat gggcactagg aaaagacttc ttccatcaag  
1320  
cttaattggt ttgttattca tttaatgact ttccctgctg ttacctaatt acaaattgga  
1380  
tggaactgtg tttttttctg ctttgttttt tcagtttgct gtttctgtag ccatattgta  
1440  
ttctgtgtca aataaagtcc agttggattc tggaaaaaaa aa  
1482

&lt;210&gt; 1542

&lt;211&gt; 57

&lt;212&gt; PRT

<213> Homo sapiens

<400> 1542

```

Lys Gly Ile Glu Cys Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu Glu
 1             5             10             15
Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe His Phe His Cys
      20             25             30
Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Arg
      35             40             45
Glu Trp Glu Phe Gln Lys Tyr Gly His
 50             55

```

<210> 1543

<211> 311

<212> DNA

<213> Homo sapiens

<400> 1543

```

gctagcgatg ctactttaag gtatgcgaag ttggatgctg acgttgccctc ctatcggttg
60
gagtcaaacg gacgaacaag cgttcgaggt agctttaaat gcgggcgacg ccagaaagtt
120
accaaagtgc gtgccgcgcc ttatgtttct cgaatggctc acgcgccgag gctacttgct
180
ccacggctcg agccgagccg acctcgtttg ttttgaacct cgagcaccca aagacttcag
240
ccctgacgag ttcagcaaac gcaccgccgt tttcgctctc tcagatgggg tgtggccccc
300
cncnccnc c
311

```

<210> 1544

<211> 96

<212> PRT

<213> Homo sapiens

<400> 1544

```

Met Arg Ser Trp Met Leu Thr Leu Pro Pro Ile Gly Trp Ser Gln Thr
 1             5             10             15
Asp Glu Gln Ala Phe Glu Val Ala Leu Asn Ala Gly Asp Ala Arg Lys
      20             25             30
Leu Pro Lys Ser Val Pro Arg Leu Met Phe Leu Glu Trp Leu Thr Arg
      35             40             45
Arg Gly Tyr Leu Leu His Gly Ser Ser Arg Ala Asp Leu Val Cys Phe
 50             55             60
Glu Pro Arg Ala Pro Lys Asp Phe Ser Pro Asp Glu Phe Ser Lys Arg
65             70             75             80
Thr Ala Val Phe Ala Ser Ser Asp Gly Val Trp Pro Pro Xaa Xaa Xaa
      85             90             95

```

<210> 1545

<211> 362

<212> DNA

<213> Homo sapiens

&lt;400&gt; 1545

ccatgggtgcg gccgtctggt aacgataggc aaatccttgc catgccacca attcttcctt  
 60  
 caacagtagt tggcgaatcc ttcgatgggc aagtcctgtg agcttgctca tctgacggat  
 120  
 cgtctctgtc tcaagcacct cgctgtttc caggttcaag gcctggatag tgcgagtgtc  
 180  
 gtactggctg atcacttcca ccgagtgggc tgggtagccc cttgccattc gctttatgat  
 240  
 ctcaaccata gatgcatttg gcatgttcca gagcttgtae tccttaacga tctctctggc  
 300  
 gtcgtagaaa accttcacgc tategtcagg atgggtcact gtggtgatgt accgtccaga  
 360  
 ac  
 362

&lt;210&gt; 1546

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1546

Met	Val	Lys	Ser	Cys	Glu	Leu	Ala	His	Leu	Thr	Asp	Arg	Leu	Cys	Leu
1				5					10					15	
Lys	His	Leu	Ala	Cys	Phe	Gln	Val	Gln	Gly	Leu	Asp	Ser	Ala	Ser	Val
		20						25					30		
Val	Leu	Val	Asp	His	Phe	His	Arg	Val	Val	Trp	Val	Ala	Pro	Cys	His
	35					40					45				
Ser	Leu	Tyr	Asp	Leu	Asn	His	Arg	Cys	Ile	Trp	His	Val	Pro	Glu	Leu
	50				55					60					
Val	Leu	Leu	Asn	Asp	Leu	Ser	Gly	Val	Val	Glu	Asn	Leu	His	Ala	Ile
65					70					75				80	
Val	Arg	Met	Gly	His	Cys	Gly	Asp	Val	Pro	Ser	Arg				
			85					90							

&lt;210&gt; 1547

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1547

cgcggtgcca caccggaaga cccggccagc tcacgcctgg gtgaaagttt ctgggcgttc  
 60  
 ctgccgcgtt cgggtgtggt cagcgccgtg tcggcgtgga acctggagcg cgagcgctg  
 120  
 cgaaactcg gctgcccggc ctggcactgg aagaacgccg tgctcagtgc ctggatgtac  
 180  
 agcgtggtgt tgtggggggg gatgattgtc tgggtgggag cggcggtgat tccgttcctg  
 240  
 atcattcagg gtgtctacgg gttctcgttg ctggaagtgg tcaactacgt cgagcactac  
 300  
 gggcttaaag gccagaagtt gcccaacggt cgttatgaac ggtgttcgcc tcggcactcg  
 360



tggaacagca accggattgt caccaatata tttctgttcc aacttcagcg gcattccgac  
420

caccatgcc

429

<210> 1548

<211> 143

<212> PRT

<213> Homo sapiens

<400> 1548

Arg	Val	Ala	Thr	Pro	Glu	Asp	Pro	Ala	Ser	Ser	Arg	Leu	Gly	Glu	Ser
1				5				10					15		
Phe	Trp	Ala	Phe	Leu	Pro	Arg	Ser	Val	Trp	Phe	Ser	Ala	Val	Ser	Ala
		20						25				30			
Trp	Asn	Leu	Glu	Arg	Glu	Arg	Leu	Arg	Lys	Leu	Gly	Leu	Pro	Ala	Trp
	35					40					45				
His	Trp	Lys	Asn	Ala	Val	Leu	Ser	Ala	Trp	Met	Tyr	Ser	Val	Val	Leu
	50					55				60					
Trp	Gly	Val	Met	Ile	Val	Trp	Leu	Gly	Ala	Ala	Val	Ile	Pro	Phe	Leu
65				70				75					80		
Ile	Ile	Gln	Gly	Val	Tyr	Gly	Phe	Ser	Leu	Leu	Glu	Val	Val	Asn	Tyr
		85				90						95			
Val	Glu	His	Tyr	Gly	Leu	Lys	Arg	Gln	Lys	Leu	Pro	Asn	Gly	Arg	Tyr
		100				105						110			
Glu	Arg	Cys	Ser	Pro	Arg	His	Ser	Trp	Asn	Ser	Asn	Arg	Ile	Val	Thr
	115					120					125				
Asn	Ile	Phe	Leu	Phe	Gln	Leu	Gln	Arg	His	Ser	Asp	His	His	Ala	
	130					135					140				

<210> 1549

<211> 443

<212> DNA

<213> Homo sapiens

<400> 1549

gtcgacaggc tccaggggtc tgttttgtag tgcacccgct gtggtgcaac atgcgtctgg  
60  
gcacaccagc gtcgcccgtt tctgttgta gtctttcttc tctgactcca ggggtattgg  
120  
gtctttctgc cagcgcccat gcaactttgg cagcctggcc tgtctgctgg taagtggggc  
180  
agaatccctg cactccacca ttcttgggca aactccctc taggattttg gtctcccttt  
240  
tctctctggt ctttgaccac cgctaccag caaactctc catctagacc agccagcatt  
300  
ggttttcttc actccccag ctgccgctg ggaggcgcca ctgcaaactt ccctggggtc  
360  
tcccagctgc tcagagatcc ccatgccctt ccctgatcag ctccctgccc ggttctcatt  
420  
ccgacgcggc tgcattggata ttc  
443

<210> 1550

<211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 1550  
 Met Arg Thr Gly Gln Gly Ala Asp Gln Gly Arg Ala Trp Gly Ser Leu  
 1 5 10 15  
 Ser Ser Trp Glu Thr Pro Gly Lys Phe Ala Val Ala Pro Pro Thr Arg  
 20 25 30  
 Gln Leu Gly Glu Trp Lys Lys Pro Met Leu Ala Gly Leu Asp Gly Gly  
 35 40 45  
 Val Cys Trp Val Ala Val Val Lys Asp Gln Arg Glu Lys Gly Asp Gln  
 50 55 60  
 Asn Pro Arg Gly Ser Val Ala Gln Glu Trp Trp Ser Ala Gly Ile Leu  
 65 70 75 80  
 Pro His Leu Pro Ala Asp Arg Pro Gly Cys Gln Ser Cys Met Gly Ala  
 85 90 95  
 Gly Arg Lys Thr Gln Tyr Pro Trp Ser Gln Arg Gly Lys Thr Thr  
 100 105 110  
 Gly Asn Gly Arg Arg Trp Cys Ala Gln Thr His Val Ala Pro Gln Arg  
 115 120 125  
 Val His Tyr Lys Thr Glu Pro Trp Ser Leu Ser  
 130 135

<210> 1551  
 <211> 306  
 <212> DNA  
 <213> Homo sapiens

<400> 1551  
 ccatggatac cccacctctg gcactcaaca tgacttggct gccacacacc aggaaacctc  
 60  
 agaggagcag ccagctggcc aagcaccctt gcccttggcc tgcgggctcc acaaaagctg  
 120  
 gaggagcaaa cgcagctcac ctctttttct gtccactgct tcagggccta cccctgtgct  
 180  
 ttggagatgg aacaaaagtg agagagctcc ctgacacacc ctcccagggc gaggatggca  
 240  
 gtccttctc ccatcttggtc ctaacacagc ctcccagga gaccaggggc atccnnnnc  
 300  
 ccnnnc  
 306

<210> 1552  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 1552  
 Met Asp Thr Pro Pro Leu Ala Leu Asn Met Thr Trp Leu Pro His Thr  
 1 5 10 15  
 Arg Lys Pro Gln Arg Ser Ser Gln Leu Ala Lys His Pro Cys Pro Cys  
 20 25 30  
 Pro Ala Gly Ser Thr Lys Ala Gly Gly Ala Asn Ala Ala His Leu Phe

```

      35              40              45
Phe Cys Pro Leu Leu Gln Gly Leu Pro Leu Cys Phe Gly Asp Gly Thr
  50              55              60
Lys Val Arg Glu Leu Pro Asp Thr Pro Ser Gln Gly Glu Asp Gly Ser
  65              70              75              80
Ser Phe Leu His Leu Val Leu Thr Gln Pro Pro Gln Glu Thr Arg Gly
              85              90              95
Ile Pro Xaa Pro Xaa
      100

```

&lt;210&gt; 1553

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1553

```

atcctgcaga atgatggcgt ggtcaccagc ccctattccc ggccacgcaa ggcggggccac
  60
acgctactca tcctgggggg ccagaccttc atgtgtgaca agatctacca ggtggaccac
  120
aaggccaagg agatcatccc caaggccgac ctgccagacc cccggaagga gttcagcgcc
  180
tcagcgatcg gctgcaaggt ctatgtgacg gggggcaggg gctccgagaa cgggggtctcc
  240
aaggatgtct ggggtgtacga caccgtacat gaggaatggt ccaaggcggc gcccatgctg
  300
attgcccgtt ttggccatgg ctcagctgag ctggagaact gcctctatgt ggtgggggga
  360
cacacatccc tggcaggggt cttcccggcc tcgccttctg tctccctgaa acaagtggag
  420
aaatacgacc ctgggggcaa caagtggatg atgggtggccc ccttgcgagg tggcgtcagc
  480
aatgccgcag tggtgagtgc caagctgaag ctctttgttt ttggaggaac cagcatccac
  540
cgggacatgg tgtccaaggt ccagtgtat gaccctcgg agaacagggt gacgatcaag
  600
gccgagtgcc cccagccttg gcggtacaca gccgctgccg tcctgggcag ccagatc
  657

```

&lt;210&gt; 1554

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1554

```

Ile Leu Gln Asn Asp Gly Val Val Thr Ser Pro Tyr Ser Arg Pro Arg
  1              5              10              15
Lys Ala Gly His Thr Leu Leu Ile Leu Gly Gly Gln Thr Phe Met Cys
      20              25              30
Asp Lys Ile Tyr Gln Val Asp His Lys Ala Lys Glu Ile Ile Pro Lys
      35              40              45
Ala Asp Leu Pro Ser Pro Arg Lys Glu Phe Ser Ala Ser Ala Ile Gly
      50              55              60
Cys Lys Val Tyr Val Thr Gly Gly Arg Gly Ser Glu Asn Gly Val Ser

```

```

65          70          75          80
Lys Asp Val Trp Val Tyr Asp Thr Val His Glu Glu Trp Ser Lys Ala
          85          90          95
Ala Pro Met Leu Ile Ala Arg Phe Gly His Gly Ser Ala Glu Leu Glu
          100          105          110
Asn Cys Leu Tyr Val Val Gly Gly His Thr Ser Leu Ala Gly Val Phe
          115          120          125
Pro Ala Ser Pro Ser Val Ser Leu Lys Gln Val Glu Lys Tyr Asp Pro
          130          135          140
Gly Ala Asn Lys Trp Met Met Val Ala Pro Leu Arg Asp Gly Val Ser
          145          150          155          160
Asn Ala Ala Val Val Ser Ala Lys Leu Lys Leu Phe Val Phe Gly Gly
          165          170          175
Thr Ser Ile His Arg Asp Met Val Ser Lys Val Gln Cys Tyr Asp Pro
          180          185          190
Ser Glu Asn Arg Trp Thr Ile Lys Ala Glu Cys Pro Gln Pro Trp Arg
          195          200          205
Tyr Thr Ala Ala Ala Val Leu Gly Ser Gln Ile
          210          215

```

&lt;210&gt; 1555

&lt;211&gt; 328

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1555

```

acgcgtggga gctcgggaga gaggactctg cttctggggt ttgaagggtga gcgtgattct
60
ggaggagcct gccttgccgc gagcgtgtgt tgtggagagg atgcaggaca tgagtgatcc
120
tgtaagggtg atcgagtgtg cctcgtgaag tctggaagtc agcgagtgtg ggccgtggag
180
gtgagccacc ggtttgtgat ttgaaactga gtgagagtgc tgtggagcgc gaaatatgtg
240
tgtgtgtaga gtggaggtga gcgaatttgt gtgcatgtga gacggacgca atggcagagt
300
gtagcatcct gtgttgggat tgggattn
328

```

&lt;210&gt; 1556

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1556

```

Met Leu His Ser Ala Ile Ala Ser Val Ser His Ala His Lys Phe Ala
1          5          10          15
His Leu His Ser Thr His Thr His Ile Ser Arg Ser Thr Ala Leu Ser
          20          25          30
Leu Ser Phe Lys Ser Gln Thr Gly Gly Ser Pro Pro Arg Pro Thr Leu
          35          40          45
Ala Asp Phe Gln Thr Ser Arg Gly Thr Leu Asp His Pro Tyr Arg Ile
          50          55          60
Thr His Val Leu His Pro Leu His Asn Thr Arg Ser Pro Gln Gly Arg

```

```

65              70              75              80
Leu Leu Gln Asn His Ala His Leu Gln Thr Pro Glu Ala Glu Ser Ser
              85              90              95
Leu Pro Ser Ser His Ala
              100

```

<210> 1557  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1557
gtgcacagac ttttcgagcg ggccattaag tggtttacgt ctgggatcgg ctccgctttc
60
tcgcattttt cggatcaggt caaattctgt gctcggcatt gacaggaaat tgacgtgtat
120
cagtcgattc tttgcagtgt ctggacggca ggctgaatag gctgaaagca ggacaactac
180
gaccatgccg caccatgtgg atcgtctacc gttttggcct tgccgccatt gccttgatcg
240
ccctgattgc gctgttcgtg tgccagtacc ggctatcggc caggctggcg cgccggaagc
300
gaagctcgat gggcagcagg cgcattgagga acccgcgccc attgaatcgt gaggcgctgg
360
cggagcgcgg cccgttcaaa tgcgacgcgt
390

```

<210> 1558  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1558
Met Ala Pro Gly Ser Ser Cys Ala Cys Cys Pro Ser Ser Phe Ala Ser
1      5      10      15
Gly Ala Pro Ala Trp Pro Ile Ala Gly Thr Gly Thr Arg Thr Ala Gln
      20      25      30
Ser Gly Arg Ser Arg Gln Trp Arg Gln Gly Gln Asn Gly Arg Arg Ser
      35      40      45
Thr Trp Cys Gly Met Val Val Val Val Leu Leu Ser Ala Tyr Ser Ala
      50      55      60
Cys Arg Pro Asp Thr Ala Lys Asn Arg Leu Ile His Val Asn Phe Leu
65      70      75      80
Ser Met Pro Ser Thr Glu Phe Asp Leu Ile Arg Lys Met Arg Glu Ser
      85      90      95
Gly Ala Asp Pro Arg Arg Lys Pro Leu Asn Gly Pro Leu Glu Lys Ser
      100      105      110
Val His

```

<210> 1559  
 <211> 556  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 1559

accggtggcg acggtatcgg tggcgcgctcg atccttgccct cggaatcctt cgctgcagag  
 60  
 ggtgagtcga agcgacccag cgtccaggtg ggcgacccgt tcatggagaa gctgctcatc  
 120  
 gagtgcaccc ttgacctctt caacgccggg gtagttgagg ccttgacagga tttegggtgcc  
 180  
 gccggaatct cctgtgccac ctccgagctg gccagtgtg ggcacgggtg catgcacgtc  
 240  
 gagctcgacc gcgttccgct gcgcgacccg aacctcgccc ctgaagagat cctcatgagc  
 300  
 gagtcccagg agcggatggc cgcggtggtg cgccccgac agcttgaccg cttcatggag  
 360  
 atctgcgccc attgggggtgt cgctgccact gtcattggcg aggtcaccga caccggtcga  
 420  
 cttcacattg attggcaggg cgagcggatt gtcgacgtcg atccgcgac ggttgctcac  
 480  
 gacggaccgg ttctcgacat gccggccgcc cgtccgtggt ggattgatga gctcaacgag  
 540  
 aacgacgcta acgcgt  
 556

&lt;210&gt; 1560

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1560

Thr	Gly	Gly	Asp	Gly	Ile	Gly	Gly	Ala	Ser	Ile	Leu	Ala	Ser	Glu	Ser	1	5	10	15
Phe	Ala	Ala	Glu	Gly	Glu	Ser	Lys	Arg	Pro	Ser	Val	Gln	Val	Gly	Asp	20	25	30	
Pro	Phe	Met	Glu	Lys	Leu	Leu	Ile	Glu	Cys	Thr	Leu	Asp	Leu	Phe	Asn	35	40	45	
Ala	Gly	Val	Val	Glu	Ala	Leu	Gln	Asp	Phe	Gly	Ala	Ala	Gly	Ile	Ser	50	55	60	
Cys	Ala	Thr	Ser	Glu	Leu	Ala	Ser	Ala	Gly	Asp	Gly	Gly	Met	His	Val	65	70	75	80
Glu	Leu	Asp	Arg	Val	Pro	Leu	Arg	Asp	Pro	Asn	Leu	Ala	Pro	Glu	Glu	85	90	95	
Ile	Leu	Met	Ser	Glu	Ser	Gln	Glu	Arg	Met	Ala	Ala	Val	Val	Arg	Pro	100	105	110	
Asp	Gln	Leu	Asp	Arg	Phe	Met	Glu	Ile	Cys	Ala	His	Trp	Gly	Val	Ala	115	120	125	
Ala	Thr	Val	Ile	Gly	Glu	Val	Thr	Asp	Thr	Gly	Arg	Leu	His	Ile	Asp	130	135	140	
Trp	Gln	Gly	Glu	Arg	Ile	Val	Asp	Val	Asp	Pro	Arg	Thr	Val	Ala	His	145	150	155	160
Asp	Gly	Pro	Val	Leu	Asp	Met	Pro	Ala	Ala	Arg	Pro	Trp	Trp	Ile	Asp	165	170	175	
Glu	Leu	Asn	Glu	Asn	Asp	Ala	Asn	Ala								180	185		

<210> 1561  
 <211> 466  
 <212> DNA  
 <213> Homo sapiens

<400> 1561  
 acgcgtgaaa ggtttgagag aagagagatg ccgctattga atctgctgga gttttacatc  
 60  
 ccaagatgaa gacagcattc agaattgatg tgatttcctt gaatgtggct taggaaatgt  
 120  
 ggacacttaa aactctcact tgaaattggg cacaggtttg atgtagagat aaggacgggg  
 180  
 tgcggaatgg agaccattt tgctattgat tcatctgacc gataaggcca tagtgcagtt  
 240  
 aggtgatatt cgaaagcttc ttgatgctc tttatgtata tgttgggaagg aactaccagg  
 300  
 cgttgcttta aattcccaat gtgttgtttc gttactacta atttaatacc gtaagctcta  
 360  
 ggtaaagtgc catgttggtg aactctgact gttctctttg gaattgaacg ttttgcaccc  
 420  
 tcctcctgtg gctttaggtc tgacattgta tttgacctt actagt  
 466

<210> 1562  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 1562  
 Met Ser Asp Leu Lys Pro Gln Glu Glu Asp Ala Lys Arg Ser Ile Pro  
 1 5 10 15  
 Lys Arg Thr Val Arg Val Gln Gln His Gly Thr Leu Pro Arg Ala Tyr  
 20 25 30  
 Gly Ile Lys Leu Val Val Thr Lys Gln His Ile Gly Asn Leu Lys Gln  
 35 40 45  
 Arg Leu Val Val Pro Ser Asn Ile Tyr Ile Lys Ser Ile Lys Glu Ala  
 50 55 60  
 Phe Glu Tyr His Leu Thr Ala Leu Trp Pro Tyr Arg Ser Asp Glu Ser  
 65 70 75 80  
 Met Thr Lys Trp Val Ser Ile Pro His Pro Val Leu Ile Ser Thr Ser  
 85 90 95  
 Asn Leu Cys Pro Ile Ser Ser Glu Ser Phe Lys Cys Pro His Phe Leu  
 100 105 110  
 Ser His Ile Gln Gly Asn His Ile Asn Ser Glu Cys Cys Leu His Leu  
 115 120 125  
 Gly Met  
 130

<210> 1563  
 <211> 434  
 <212> DNA  
 <213> Homo sapiens

<400> 1563

ctgggggggtg tgttcggcct gctgtcgggtg tacttgccgc gttggctgca tgaaacaccg  
 60  
 atcttcgctg agatgcagca gcgcaaaacc ctggctgccg agttgccatt gcgcgcggta  
 120  
 ttgcgtgacc accgtggcgc catcgtgctg tcgatgctgt tgacgtgggt gctgtcggcg  
 180  
 ggtgtggttg tggatcctct gatgaccccg accgtgctgc aaaccgtcta ccacttcagc  
 240  
 ccgacgggtg cgctgcaagc caacagcctg gcgatcgta cgctgagcct gggctgcatt  
 300  
 gcgtccggcg cgctggctga ccgttttggg gccggctcgc ttttggtcac cggttggcgt  
 360  
 tgctgctggc cacttcctgg acgctgtatc acagcctgat ggcccagacg gaatggttga  
 420  
 ataagtgtac gcgt  
 434

<210> 1564  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 1564  
 Leu Gly Gly Val Phe Gly Leu Leu Ser Val Tyr Leu Pro Arg Trp Leu  
 1 5 10 15  
 His Glu Thr Pro Ile Phe Ala Glu Met Gln Gln Arg Lys Thr Leu Ala  
 20 25 30  
 Ala Glu Leu Pro Leu Arg Ala Val Leu Arg Asp His Arg Gly Ala Ile  
 35 40 45  
 Val Leu Ser Met Leu Leu Thr Trp Leu Leu Ser Ala Gly Val Val Val  
 50 55 60  
 Val Ile Leu Met Thr Pro Thr Val Leu Gln Thr Val Tyr His Phe Ser  
 65 70 75 80  
 Pro Thr Val Ala Leu Gln Ala Asn Ser Leu Ala Ile Val Thr Leu Ser  
 85 90 95  
 Leu Gly Cys Ile Ala Ser Gly Ala Leu Ala Asp Arg Phe Gly Ala Gly  
 100 105 110  
 Arg Val Leu Val Thr Gly Trp Arg Cys Cys Trp Pro Leu Pro Gly Arg  
 115 120 125  
 Cys Ile Thr Ala  
 130

<210> 1565  
 <211> 373  
 <212> DNA  
 <213> Homo sapiens

<400> 1565  
 ccatggctcg agcccttggt tcaacaagag ccgtctactg acgctaacc accatgagcc  
 60  
 agaggggtgag cggttctggc acctactgga ccatgaaagc aataaagagg acaagggagc  
 120  
 ctgcattcgg ccatttcttc ccaagaatca ccataaagg tgtcaaaatc aaggaccctg  
 180



atccggtgat tctcgaagtc atcgatgagc agaacaagtt tacccccgag ggagaaaagc  
 240  
 ggggtggtgct cttgatgctc gacaacctct accgtcccag taccacccgt gcattggcga  
 300  
 acggggggcgt cccttatctg cggtcgaaga gtgtcactgt tgacctcgta gacagccggg  
 360  
 acaacacggg tac  
 373

<210> 1566  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 1566  
 Met Ser Gln Arg Val Ser Gly Ser Gly Thr Tyr Trp Thr Met Lys Ala  
 1 5 10 15  
 Ile Lys Arg Thr Arg Glu Pro Ala Phe Gly His Phe Phe Pro Arg Ile  
 20 25 30  
 Thr Ile Lys Val Val Lys Ile Lys Asp Pro Asp Pro Val Ile Leu Glu  
 35 40 45  
 Val Ile Asp Glu Gln Asn Lys Phe Thr Pro Glu Gly Glu Lys Arg Val  
 50 55 60  
 Val Leu Leu Met Leu Asp Asn Leu Tyr Arg Pro Ser Thr His Arg Ala  
 65 70 75 80  
 Leu Ala Asn Gly Gly Val Pro Tyr Leu Arg Ser Lys Ser Val Thr Val  
 85 90 95  
 Asp Leu Val Asp Ser Arg Asp Asn Thr Gly  
 100 105

<210> 1567  
 <211> 917  
 <212> DNA  
 <213> Homo sapiens

<400> 1567  
 agcttttttcg accgctgaag gagtgggata cccgctcccc agacactccc tttctagggg  
 60  
 aagccgctgc actcctgggg gaccagttt gatgcctcca ggaggataag tctgaagccg  
 120  
 gggtgggaag ggagcggaga ggcccaaaca gagcagcagg cagcgccctc tgctggcacc  
 180  
 ctggagacag cttcggctgc ggggcccctg ctttctagtc ctccccagct ttcaggacac  
 240  
 cttgacaacc tggggtcctt gcagaagtgg cccggctgtc cccaagtct cctgaagcta  
 300  
 tctgggtagg gtgggaggca gtgtgtgag ccacaaatgc aaagcagagg ggacagatgt  
 360  
 tgggactcaa agacatgagg tagagctggc cccatgggta ggtgccacca ccagagccca  
 420  
 tgaggcttcg tgttctagaa ggtgggtggg tagtgccgca ctgagggcgt gtccgggagg  
 480  
 gagcatgtgt caccagggct caggaaacag catgagtcac gacgcggggg tgtttaaggc  
 540

attcgtgccca cagcggggac ctccggagcta tgccttgata aggcaagtga gggtacatgt  
 600  
 acgatgatgc ggtttgtgct gcagactgga aaaaagcagg ggctttgtcc tctcctgacc  
 660  
 ccctcacact ctgccttcac ggtaggctcc tgagaggggg gtctccaagg aggggtgtcag  
 720  
 tactgcagct tcagctggcg tggatggggg gcttacagga gcagcagggc tgagggagat  
 780  
 gacagcagta cgaatcgtgg ctctcctgag gcctggggtt cctcatatgt aaaatggggg  
 840  
 ttgcattaga ccataccctt ggctgtgtt taggcaaata gggatgaaag tggggccaag  
 900  
 ggctgaagag ctgggtc  
 917

<210> 1568  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 1568  
 Met Gly Pro Ala Leu Pro His Val Phe Glu Ser Gln His Leu Ser Pro  
 1 5 10 15  
 Leu Leu Cys Ile Cys Gly Ser Gln His Cys Leu Pro Pro Tyr Pro Asp  
 20 25 30  
 Ser Phe Arg Arg Leu Gly Gly Gln Pro Gly His Phe Cys Arg Asp Pro  
 35 40 45  
 Arg Leu Ser Arg Cys Pro Glu Ser Trp Gly Gly Leu Glu Gly Arg Gly  
 50 55 60  
 Pro Ala Ala Glu Ala Val Ser Arg Val Pro Ala Glu Gly Ala Ala Cys  
 65 70 75 80  
 Cys Ser Val Trp Ala Ser Pro Leu Pro Ser Gln Pro Gly Phe Arg Leu  
 85 90 95  
 Ile Leu Leu Glu Ala Ser Asn Trp Val Pro Gln Glu Cys Ser Gly Phe  
 100 105 110  
 Pro

<210> 1569  
 <211> 379  
 <212> DNA  
 <213> Homo sapiens

<400> 1569  
 ggagggcctg tgattctact gcaggcaggc acccccaca acctcacatg ccgggccttc  
 60  
 aatgcgaagc ctgctgccac catcatctgg ttccgggacg ggacgcagca ggagggcgct  
 120  
 gtggccagca cggaattgct gaaggatggg aagagggaga ccaccgtgag ccaactgctt  
 180  
 attaacccca cggacctgga catagggcgt gtcttcactt gccgaagcat gaacgaagcc  
 240  
 atccctagtg gcaaggagac ttccatcgag ctggatgtgc accaccctcc tacagtgacc  
 300

ctgtccattg agccacagac ggtgcaggag ggtgagcgtg ttgtctttac ctgccaggcc  
 360  
 acagccaacc cggagatct  
 379

<210> 1570  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 1570  
 Gly Gly Pro Val Ile Leu Leu Gln Ala Gly Thr Pro His Asn Leu Thr  
 1 5 10 15  
 Cys Arg Ala Phe Asn Ala Lys Pro Ala Ala Thr Ile Ile Trp Phe Arg  
 20 25 30  
 Asp Gly Thr Gln Gln Glu Gly Ala Val Ala Ser Thr Glu Leu Leu Lys  
 35 40 45  
 Asp Gly Lys Arg Glu Thr Thr Val Ser Gln Leu Leu Ile Asn Pro Thr  
 50 55 60  
 Asp Leu Asp Ile Gly Arg Val Phe Thr Cys Arg Ser Met Asn Glu Ala  
 65 70 75 80  
 Ile Pro Ser Gly Lys Glu Thr Ser Ile Glu Leu Asp Val His His Pro  
 85 90 95  
 Pro Thr Val Thr Leu Ser Ile Glu Pro Gln Thr Val Gln Glu Gly Glu  
 100 105 110  
 Arg Val Val Phe Thr Cys Gln Ala Thr Ala Asn Pro Glu Ile  
 115 120 125

<210> 1571  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 1571  
 tgcgcacttt tccgctcccc atgggtcccc tggncgttga tcatgccccca gatgttcac  
 60  
 atcggcatct tcttcttcct gccaagcggc caagccgtgc tccagtcttt ccagatggaa  
 120  
 gatgcgttcg gcatgtcgac cgaatgggtc ggattggaca acttccgcaa cctgctggat  
 180  
 gacccacact acctgaattc cttccagcgc accgccgtgt tctcgggtgct ggtggcaggg  
 240  
 gtcgggatcg ccgtgtcact ggggtctggcg atctttgccg accccatcac tccgtcgcca  
 300  
 tgtgtacaag acacactgct gatcgtgccc tacgccgtgg caccatgat cgccggc  
 357

<210> 1572  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 1572.  
 Cys Ala Leu Phe Arg Ser Arg Trp Val Pro Trp Xaa Leu Ile Met Pro

```

      1           5           10           15
Gln Met Phe Ile Ile Gly Ile Phe Phe Phe Leu Pro Ser Gly Gln Ala
      20           25           30
Val Leu Gln Ser Phe Gln Met Glu Asp Ala Phe Gly Met Ser Thr Glu
      35           40           45
Trp Val Gly Leu Asp Asn Phe Arg Asn Leu Leu Asp Asp Pro Thr Tyr
      50           55           60
Leu Asn Ser Phe Gln Arg Thr Ala Val Phe Ser Val Leu Val Ala Gly
      65           70           75           80
Val Gly Ile Ala Val Ser Leu Gly Leu Ala Ile Phe Ala Asp Pro Ile
      85           90           95
Thr Pro Ser Pro Cys Val Gln Asp Thr Leu Leu Ile Val Pro Tyr Ala
      100           105           110
Val Ala Pro Met Ile Ala Gly
      115

```

&lt;210&gt; 1573

&lt;211&gt; 337

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1573

```

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60
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120
cttttcaagg ctccatcttt ctaataaact ggccattttt ggaattgggtt ataacacccg
180
ttggaaagag gatatccgtt accattatgc tgagatcagc tcccagggtgc cccttggtcaa
240
gcgacttcgg gagtacttca actctgagaa gcctgaagga cggatcatta tgacccgagt
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gcagaaaatg aactggaaaa atgtttacta caaattt
337

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&lt;210&gt; 1574

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1574

```

Met Gln Asn Ile Val Gln Ile Leu Glu Ser Val Gln Leu Lys Trp Glu
      1           5           10           15
Leu Phe Gln Ser Trp Thr Asp Phe Ser Arg Leu His Leu Ser Asn Lys
      20           25           30
Leu Ala Ile Phe Gly Ile Gly Tyr Asn Thr Arg Trp Lys Glu Asp Ile
      35           40           45
Arg Tyr His Tyr Ala Glu Ile Ser Ser Gln Val Pro Leu Gly Lys Arg
      50           55           60
Leu Arg Glu Tyr Phe Asn Ser Glu Lys Pro Glu Gly Arg Ile Ile Met
      65           70           75           80
Thr Arg Val Gln Lys Met Asn Trp Lys Asn Val Tyr Tyr Lys Phe
      85           90           95

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<210> 1575  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 1575  
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 120  
 gaccaggccc gtgcgattct gggcgacgat ctactcatcg gcttgccgc tcagactccc  
 180  
 gcccatgtgg aggccgccct gtcccagggg cgtgacatcg tcgactatct gggagttggg  
 240  
 gccctgcatg gtactggaac caaacctgag gctggggagc tcggcctggc tgagattcgt  
 300  
 gatgtcgtca acgccagccc gtggccgggt tgcgtcatcg gtggggtgag cgcacccgat  
 360  
 gctcaagacg tagccccggg gggatgtgac ggctgagcg tcgtctcggc gatttgccgg  
 420  
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 471

<210> 1576  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 1576  
 Xaa Arg Val Arg Glu Ile Cys Val Ser Gly Gly Val Pro Leu Ile Ile  
 1 5 10 15  
 Asp Asp Arg Val His Leu Val Ala Glu Ile Gly Ala Asp Gly Val His  
 20 25 30  
 Val Gly Gln Ser Asp Met Pro Val Asp Gln Ala Arg Ala Ile Leu Gly  
 35 40 45  
 Asp Asp Leu Leu Ile Gly Leu Ser Ala Gln Thr Pro Ala His Val Glu  
 50 55 60  
 Ala Ala Leu Ser Gln Gly Arg Asp Ile Val Asp Tyr Leu Gly Val Gly  
 65 70 75 80  
 Ala Leu His Gly Thr Gly Thr Lys Pro Glu Ala Gly Glu Leu Gly Leu  
 85 90 95  
 Ala Glu Ile Arg Asp Val Val Asn Ala Ser Pro Trp Pro Val Cys Val  
 100 105 110  
 Ile Gly Gly Val Ser Ala Ser Asp Ala Gln Asp Val Ala Arg Val Gly  
 115 120 125  
 Cys Asp Gly Leu Ser Val Val Ser Ala Ile Cys Arg Ser Thr Asp Pro  
 130 135 140  
 Lys Ser Ser Ala Arg Glu Leu Ala Glu Ala Trp Arg Thr  
 145 150 155

<210> 1577  
 <211> 287  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 1577

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120  
ttgcgcgttg ccggggcagg cttccccgct cgcgccagc gcgcgcgcgg cgatctggtg  
180  
atcgagctgg agccgatgct gccgcaggcg cccgacaagc aactgcacgc gctgatcgag  
240  
cagctcgacg tggcgctcgg gaagagcgcg acacgccatt ttccgga  
287

&lt;210&gt; 1578

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1578

Leu	Val	Leu	Gln	Arg	Pro	Ile	Ser	Ala	Leu	Arg	Met	Leu	Ile	Gly	Gly
1			5						10				15		
Pro	Leu	Arg	Ile	Pro	His	Pro	Ala	Gly	Leu	Arg	Thr	Val	Ala	Leu	Glu
			20					25					30		
Pro	Gly	Val	Ala	His	Ala	Arg	Thr	Leu	Arg	Val	Ala	Gly	Ala	Gly	Phe
			35				40					45			
Pro	Ala	Arg	Gly	Gln	Arg	Ala	Ala	Gly	Asp	Leu	Val	Ile	Glu	Leu	Glu
			50				55				60				
Pro	Met	Leu	Pro	Gln	Ala	Pro	Asp	Lys	Gln	Leu	His	Ala	Leu	Ile	Glu
				70					75					80	
Gln	Leu	Asp	Val	Ala	Leu	Gly	Lys	Ser	Ala	Thr	Arg	His	Phe	Pro	
			85						90					95	

&lt;210&gt; 1579

&lt;211&gt; 2829

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1579

ngggcgggg agcggacttc ctctctgag ggccgtgccg cgctgccaga tttgttcttc  
60  
cgcccccgcc tccgcggctc ggaggcgagc ggaaggtgcc ccggggccga ggcccgtagc  
120  
ggggcgggcg ggagcccccg cagtccgggg tcgccggcga gggccatgtc gctgttgggg  
180  
gacccgctac aggccctgcc gccctcgccc gccccacgg ggccgctgct cgccccctcg  
240  
gccggcgcgga ccctcaaccg cctgcgggag ccgctgctgc ggaggctcag cgagctcctg  
300  
gatcaggcgc ccgagggccg gggctggagg agactggcgg agctggcggg gagtcgcggg  
360  
cgctccgcc tcagttgcct agacctggag cagtgttctc ttaaggtact ggagcctgaa  
420  
ggaagcccca gcctgtgtct gctgaagtta atgggtgaaa aaggttgac agtcacagaa  
480

ttgagtgtt tctgcaggc tatggaacac actgaagttc ttcagcttct cagccccca  
540  
ggaataaaga ttactgtaaa cccagagtca aaggcagtct tggctggaca gtttgtgaaa  
600  
ctgtgttgcc gggcaactgg acatcctttt gttcaatatc agtggttcaa aatgaataaa  
660  
gagattccaa atggaaatac atcagagctt atttttaatg cagtgcattgt aaaagatgca  
720  
ggcttttatg tctgtcgagt taataacaat ttcacctttg aattcagcca gtggtcacag  
780  
ctggatgttt gcgacatccc agagagcttc cagagaagtg ttgatggcgt ctctgaatcc  
840  
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900  
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960  
ccattaacac atgagaccaa aaagctatac atggtgcctt atgcggattt ggaacaccaa  
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ggaacctact ggtgtcatgt atataatgat cgagacagtc aagatagcaa gaaggtagaa  
1080  
atcatcatag gaagaacaga tgaggcagtg gagtgcactg aagatgaatt aaataatctt  
1140  
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1200  
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1320  
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1920  
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2040  
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2100

gcaataaag gcacacctga agaaactggc agctacttgg tatcaaagga tcttcccaag  
 2160  
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 2220  
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 2280  
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 2340  
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 2400  
 ggagcagggc attatcactc attgcaagac ccattccatg gtgtttacca ttcacatcct  
 2460  
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 2520  
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 2580  
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 2700  
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 2820  
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 2829

<210> 1580

<211> 824

<212> PRT

<213> Homo sapiens

<400> 1580

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Pro	Thr	Gly	Pro	Leu	Leu	Ala	Pro	Pro	Ala	Gly	Ala	Thr	Leu	Asn	Arg
			20					25					30		
Leu	Arg	Glu	Pro	Leu	Leu	Arg	Arg	Leu	Ser	Glu	Leu	Leu	Asp	Gln	Ala
			35				40					45			
Pro	Glu	Gly	Arg	Gly	Trp	Arg	Arg	Leu	Ala	Glu	Leu	Ala	Gly	Ser	Arg
			50				55				60				
Gly	Arg	Leu	Arg	Leu	Ser	Cys	Leu	Asp	Leu	Glu	Gln	Cys	Ser	Leu	Lys
65					70					75				80	
Val	Leu	Glu	Pro	Glu	Gly	Ser	Pro	Ser	Leu	Cys	Leu	Leu	Lys	Leu	Met
				85					90					95	
Gly	Glu	Lys	Gly	Cys	Thr	Val	Thr	Glu	Leu	Ser	Asp	Phe	Leu	Gln	Ala
			100					105					110		
Met	Glu	His	Thr	Glu	Val	Leu	Gln	Leu	Leu	Ser	Pro	Pro	Gly	Ile	Lys
			115				120					125			
Ile	Thr	Val	Asn	Pro	Glu	Ser	Lys	Ala	Val	Leu	Ala	Gly	Gln	Phe	Val
			130				135					140			
Lys	Leu	Cys	Cys	Arg	Ala	Thr	Gly	His	Pro	Phe	Val	Gln	Tyr	Gln	Trp
145					150					155				160	
Phe	Lys	Met	Asn	Lys	Glu	Ile	Pro	Asn	Gly	Asn	Thr	Ser	Glu	Leu	Ile



[illegible]

595                      600                      605  
 Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu  
 610                      615                      620  
 Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp  
 625                      630                      635                      640  
 Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser  
 645                      650                      655  
 Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu  
 660                      665                      670  
 Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu  
 675                      680                      685  
 Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu  
 690                      695                      700  
 Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly  
 705                      710                      715                      720  
 Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro  
 725                      730                      735  
 Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser  
 740                      745                      750  
 Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro  
 755                      760                      765  
 Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp  
 770                      775                      780  
 Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg  
 785                      790                      795                      800  
 Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser  
 805                      810                      815  
 Asp Arg Leu Arg Ile Ser Glu Lys  
 820

&lt;210&gt; 1581

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1581

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 60  
 cgggtgcccc aggtggctga cgcttggtc gattcgggct cgatgccctt cgcccagtg  
 120  
 ggatacccg atgtgccccg ttcgaaggag aagttcgagt cccactaccc gggtgacttc  
 180  
 atctgtgagg ccatcgacca gaccgcggg tggttttaca ccatgatggc cgtcgggaacc  
 240  
 ctggtgtttg acgagtcctc gtaccgcaat gtgctgtgtc tgggccacat cttggccgag  
 300  
 gacggctgca agatgagcaa gcaccttggc aacatcctgt tgcctatccc gctcatggat  
 360  
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 420  
 cgacgc  
 426

&lt;210&gt; 1582

<211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 1582  
 Asp Pro His Arg Pro Phe Ile Asp Glu Val Thr Phe Thr Arg Glu Gly  
 1 5 10 15  
 His Thr Tyr His Arg Val Pro Glu Val Ala Asp Ala Trp Leu Asp Ser  
 20 25 30  
 Gly Ser Met Pro Phe Ala Gln Trp Gly Tyr Pro His Val Pro Gly Ser  
 35 40 45  
 Lys Glu Lys Phe Glu Ser His Tyr Pro Gly Asp Phe Ile Cys Glu Ala  
 50 55 60  
 Ile Asp Gln Thr Arg Gly Trp Phe Tyr Thr Met Met Ala Val Gly Thr  
 65 70 75 80  
 Leu Val Phe Asp Glu Ser Ser Tyr Arg Asn Val Leu Cys Leu Gly His  
 85 90 95  
 Ile Leu Ala Glu Asp Gly Arg Lys Met Ser Lys His Leu Gly Asn Ile  
 100 105 110  
 Leu Leu Pro Ile Pro Leu Met Asp Ser His Gly Ala Asp Ala Leu Arg  
 115 120 125  
 Trp Phe Met Ala Ala Asp Gly Ser Pro Trp Ser Ala Arg Arg  
 130 135 140

<210> 1583  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<400> 1583  
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 ggggggttctg aggaaatggg gtcaatggat gaggcaggtt ataggaagga tttgggggct  
 120  
 cctaaggga taggttcagg gagtaaggca ggtttcaggg atggtttagg gagttctggg  
 180  
 gaaatgggggt caatggatga ggcagattat aggaaggatt tgggagctcc tgaggaaatg  
 240  
 ggttcaggca gttacacaga ttacaggaat ggtttaggca gttctggaaa aatcagttca  
 300  
 ggggatgagg caggttataa gaatgtttta ggggggttctg ggaggaatcc attagggagc  
 360  
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 420  
 ggttctaggc aaggctttgg gggaactagt  
 450

<210> 1584  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 1584  
 Xaa Arg Val Lys Gly Tyr Gly Asp Gly Ser Gly Ser Lys Glu Gly Phe

```

      1           5           10           15
Arg Asp Gly Leu Gly Gly Ser Glu Glu Met Gly Ser Met Asp Glu Ala
      20           25           30
Gly Tyr Arg Lys Asp Leu Gly Ala Pro Lys Gly Ile Gly Ser Gly Ser
      35           40           45
Lys Ala Gly Phe Arg Asp Gly Leu Gly Ser Ser Gly Glu Met Gly Ser
      50           55           60
Met Asp Glu Ala Asp Tyr Arg Lys Asp Leu Gly Ala Pro Glu Glu Met
      65           70           75           80
Gly Ser Gly Ser Tyr Thr Asp Tyr Arg Asn Gly Leu Gly Ser Ser Gly
      85           90           95
Lys Ile Ser Ser Gly Asp Glu Ala Gly Tyr Lys Asn Val Leu Gly Gly
      100          105          110
Ser Gly Arg Asn Pro Leu Gly Ser Glu Ala Gly Ser Arg Gly Ser Leu
      115          120          125
Glu Asp Ser Gly Tyr Ile Leu Ser Trp Asn Glu Ala Gly Ser Arg Gln
      130          135          140
Gly Phe Gly Gly Thr Ser
      145          150

```

&lt;210&gt; 1585

&lt;211&gt; 596

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1585

```

tgatcatctg taattcttgt ccgtgggcgt ttgaactgag aatgtcttaa gaagttggga
60
tctaattccga gctgctgctg gcaaagttgg gtgaggtctg cagagagtgc gtccatctgt
120
ggcagctgca gggcaagctg gggaggaagc gcagggtggt gcacaggttg catcataatg
180
gaaggaaaga gggcaggtc cagagaaacc ggctctccc aaaaagttat caaacttg
240
tttagaaata cgctttttta ggaacgacag agaaataaag attcaccata caacttcagt
300
aaccctccta taacggtttt agaagatattc agaattgatc cacagcccac ctctttagaa
360
cattacaaat ctgatgcattc attcagtaaa aggtcttcta gaacgagatt tactgactac
420
cagcttaggg ttctgcaaga cttttttgac acaaacgctt acccaaaaga tgatgaaata
480
gaacaactct ccaactgttct caatctgcct acccgggtta ttgttgatg gttccagaat
540
gctcgtcaga aagcacgaaa gagttatgag aatcaagcag aaacccttc acgcgt
596

```

&lt;210&gt; 1586

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1586

Met Glu Gly Lys Ser Gly Arg Ser Arg Glu Thr Gly Leu Ser Gln Lys

```

      1           5           10           15
Val Ile Lys His Trp Phe Arg Asn Thr Leu Phe Lys Glu Arg Gln Arg
      20           25           30
Asn Lys Asp Ser Pro Tyr Asn Phe Ser Asn Pro Pro Ile Thr Val Leu
      35           40           45
Glu Asp Ile Arg Ile Asp Pro Gln Pro Thr Ser Leu Glu His Tyr Lys
      50           55           60
Ser Asp Ala Ser Phe Ser Lys Arg Ser Ser Arg Thr Arg Phe Thr Asp
      65           70           75           80
Tyr Gln Leu Arg Val Leu Gln Asp Phe Phe Asp Thr Asn Ala Tyr Pro
      85           90           95
Lys Asp Asp Glu Ile Glu Gln Leu Ser Thr Val Leu Asn Leu Pro Thr
      100          105          110
Arg Val Ile Val Val Trp Phe Gln Asn Ala Arg Gln Lys Ala Arg Lys
      115          120          125
Ser Tyr Glu Asn Gln Ala Glu Thr Pro Ser Arg
      130          135

```

&lt;210&gt; 1587

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1587

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tgtacacaca gtgatttggg gtcctttttc ctaaaacagc ttctttatca ggactttgga
60
attctgggtg agatagaaac actgaaaaca gggcggaagt tttttcttct ggcttcttag
120
tccacggagg gtcacagctg gagaggatat gccgtggcat tctccctggg agaccacaca
180
tgttcccgac agctcagacc ccagaccgca tgtgctcctg acagctcaga cccagaccg
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360
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420
gaccccagac cgcggtgct cctgacagct cagaccccag accgcgggtg ctctgacag
480
ctcagacccc agaccacgcg t
501

```

&lt;210&gt; 1588

&lt;211&gt; 86

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1588

```

Ser Thr Glu Gly Ser Ala Trp Arg Gly Tyr Ala Val Ala Phe Ser Leu
1           5           10           15
Gly Asp His Thr Cys Ser Arg Gln Leu Arg Pro Gln Thr Ala Cys Ala
20          25          30
Pro Asp Ser Ser Asp Pro Arg Pro Arg Val Leu Leu Thr Ala Gln Thr

```

```

      35              40              45
Pro Asp Arg Arg Cys Ser Arg Gln Leu Arg Pro Gln Thr Ala Gly Ala
      50              55              60
Pro Asp Ser Ser Asp Pro Arg Pro Arg Val Leu Pro Thr Ala Gln Thr
65              70              75              80
Pro Asp Arg Gly Cys Ser
      85

```

&lt;210&gt; 1589

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1589

```

aagcttgctg gggacaccct ttttacgggg cctcgtgggg gaggagttac ctgcattgac
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tccaccgggt ccactaacgc cgacatggct gctttcgtgc gagcaggggg aacgtctttc
120
tgcctactcg ttgctgacca ccaagagggc gggcgtggac gggtcacgcg cagttggcag
180
gatgtccccg gtacgagttt ggcatctca gcgttggtgc ccaatgatcg tccgtcgcat
240
gactggggct ggctgtcgat ggttgcgggg ctcgctggtg tcaaggatcat caaggaggtc
300
ggtggggctg accgttcccc agtgacgctg aagtggccca atgatgtgct cgtggatctg
360
gacactgacc agggcggaag agtggtcgga attctctcag aacgcgt
407

```

&lt;210&gt; 1590

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1590

```

Lys Leu Ala Gly Asp Thr Leu Phe Thr Gly Pro Arg Gly Gly Gly Val
1      5      10      15
Thr Cys Ile Asp Ser Thr Gly Ser Thr Asn Ala Asp Met Ala Ala Phe
      20      25      30
Val Arg Ala Gly Gly Thr Ser Phe Cys Leu Leu Val Ala Asp His Gln
      35      40      45
Glu Gly Gly Arg Gly Arg Phe Thr Arg Ser Trp Gln Asp Val Pro Gly
      50      55      60
Thr Ser Leu Ala Ile Ser Ala Leu Val Pro Asn Asp Arg Pro Ser Gln
65      70      75      80
Asp Trp Gly Trp Leu Ser Met Val Ala Gly Leu Ala Val Val Lys Val
      85      90      95
Ile Lys Glu Val Gly Gly Ala Asp Arg Ser Arg Val Thr Leu Lys Trp
      100     105     110
Pro Asn Asp Val Leu Val Asp Leu Asp Thr Asp Gln Gly Gly Lys Val
      115     120     125
Cys Gly Ile Leu Ser Glu Arg
      130     135

```

<210> 1591  
 <211> 424  
 <212> DNA  
 <213> Homo sapiens

<400> 1591  
 agatctctct ccctgagata acccaggctt tagaaccaaa gagctgagag accctgtccc  
 60  
 ttcagagagg cacttgcacc tagaggagtc tctgggaagc agatggggat atgggacaga  
 120  
 cgcattcttga aaaagccccc agatgcctcc ctatggagga cctcaccac ccacatcacc  
 180  
 agtagggagc ttgggactta ccctaaccac aggggggtga ctgttgcgt ccctgcacag  
 240  
 aacgtccagc gagtcctgac tttccagccg ctgcgcttca tccaggagca cgtcctgac  
 300  
 cctgtctttg acctcagcgg cccagcagt ctggcccagc ctgtccagta ctcccttgac  
 360  
 tgtgggatcc ctggctgctc acgcccctga ggaccctcg gatctgctcc agcacgtgaa  
 420  
 attt  
 424

<210> 1592  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 1592  
 Met Gly Ile Trp Asp Arg Arg Ile Leu Lys Lys Pro Pro Asp Ala Ser  
 1 5 10 15  
 Leu Trp Arg Thr Ser Pro Thr His Ile Thr Ser Arg Glu Leu Gly Thr  
 20 25 30  
 Tyr Pro Asn His Arg Gly Val Thr Val Val Val Pro Ala Gln Asn Val  
 35 40 45  
 Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln Glu His Val  
 50 55 60  
 Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro  
 65 70 75 80  
 Val Gln Tyr Ser Leu Asp Cys Gly Ile Pro Gly Cys Ser Arg Pro  
 85 90 95

<210> 1593  
 <211> 1678  
 <212> DNA  
 <213> Homo sapiens

<400> 1593  
 cttgaatcta aaataaatga aataaacaca gaaattaacc agttgattga aaagaaaatg  
 60  
 atgagaaatg agccattga aggcaaactc tcaactgtata ggcaacaggc atctatcatt  
 120  
 tcccgtaaaa aagaagccaa agctgaggaa cttcaggagg ccaaggagaa gttagccagc  
 180

ctagagagag aagcatcagt aaagagaaat cagacccgtg aatttgatgg tactgaagtt  
240  
ttaaaggagg atgagttcaa acgatatgtc aataaacttc gaagcaagag tacagttttc  
300  
aaaaagaagc atcacataat agctgaactt aaagctgaat tcgggtctttt gcagaggact  
360  
gaagaacttc ttaagcaacg tcatgaaaat attcaacaac aactgcaaac tatggaggag  
420  
aaaaagggtg tatctggata tagttacacc caagaagagc tagaaagagt atctgcactg  
480  
aagagtgaag ttgatgaaat gaaaggacga acattggatg atatgtctga aatgggtgaaa  
540  
aaactgtatt cattgggtatc tgaaaagaag tcagctcttg cctcagttat aaaagagcta  
600  
cgacagttgc gtcaaaaata tcaagaactg acccaggagt gtgatgaaaa gaaatcccag  
660  
tatgatagct gtgcagcagg cctcgaaagc aatcgggtcca aattagaaca ggaagttaga  
720  
agactccgtg aagaatgtct tcaagaagaa agtagatacc attatacaaa ttgtatgatt  
780  
aagaacctag aagttcaact tcgtcgtgct actgatgaga tgaaggcata tatctctttc  
840  
gatcaacaag aaaaaagaaa ggcaattagg gaacagtata ccaaaaatac tgctgaacaa  
900  
gaaaaccttg gaaagaaact tcgggaaaaa caaaaagtta tacgagaaaag tcatgggtcca  
960  
aatatgaaac aagcaaaaaat gtggcgtgat ttggaacaat taatggaatg taagaaacag  
1020  
tgctttctga aacaacaaag ccaaacttcc attgggtcagg taattcagga ggggtggggag  
1080  
gaccggctaa tactgtgaat tcttgtgtca tcggttggggg ttttacttga taccactagc  
1140  
tataagccta atctcataat gtatttcttt ttgaaaactg atttgtttag cattttgttt  
1200  
tcagaagagc cattctttat taagttttca tagaaaataa tgtaaggta gatttagttt  
1260  
gaatgttttt tcatatgaaa aagaggcttt tattcttttc catagtttag acatcactgg  
1320  
cgtcttctga gttttatgag acaggaaact aagtttacta tctgtaaatg taaacatatg  
1380  
tccattaaga aacatgtagt ttttttttag aatgtaataa cccagtggct tactgttttt  
1440  
cttaatctct tttaaaaaaa ctttagaaga atcttttagg aactaatatc tcttgttctg  
1500  
aagaaacatt tatctgacgt tcagcagttc ctacagtttt acttcagttt atttttcttc  
1560  
tgtaaaatgc aagaaaattt aatattttga ctaacatgtc ttttctgttt gtatcattta  
1620  
aaggcaata aacttggtac gtatttcata tctattttaa aaatgaaaaa aaaaaaaa  
1678

&lt;210&gt; 1594

&lt;211&gt; 365

&lt;212&gt; PRT



&lt;213&gt; Homo sapiens

&lt;400&gt; 1594

```

Leu Glu Ser Lys Ile Asn Glu Ile Asn Thr Glu Ile Asn Gln Leu Ile
 1           5           10           15
Glu Lys Lys Met Met Arg Asn Glu Pro Ile Glu Gly Lys Leu Ser Leu
 20           25           30
Tyr Arg Gln Gln Ala Ser Ile Ile Ser Arg Lys Lys Glu Ala Lys Ala
 35           40           45
Glu Glu Leu Gln Glu Ala Lys Glu Lys Leu Ala Ser Leu Glu Arg Glu
 50           55           60
Ala Ser Val Lys Arg Asn Gln Thr Arg Glu Phe Asp Gly Thr Glu Val
 65           70           75           80
Leu Lys Gly Asp Glu Phe Lys Arg Tyr Val Asn Lys Leu Arg Ser Lys
 85           90           95
Ser Thr Val Phe Lys Lys Lys His His Ile Ile Ala Glu Leu Lys Ala
100          105          110
Glu Phe Gly Leu Leu Gln Arg Thr Glu Glu Leu Leu Lys Gln Arg His
115          120          125
Glu Asn Ile Gln Gln Gln Leu Gln Thr Met Glu Glu Lys Lys Gly Ile
130          135          140
Ser Gly Tyr Ser Tyr Thr Gln Glu Glu Leu Glu Arg Val Ser Ala Leu
145          150          155          160
Lys Ser Glu Val Asp Glu Met Lys Gly Arg Thr Leu Asp Asp Met Ser
165          170          175
Glu Met Val Lys Lys Leu Tyr Ser Leu Val Ser Glu Lys Lys Ser Ala
180          185          190
Leu Ala Ser Val Ile Lys Glu Leu Arg Gln Leu Arg Gln Lys Tyr Gln
195          200          205
Glu Leu Thr Gln Glu Cys Asp Glu Lys Lys Ser Gln Tyr Asp Ser Cys
210          215          220
Ala Ala Gly Leu Glu Ser Asn Arg Ser Lys Leu Glu Gln Glu Val Arg
225          230          235          240
Arg Leu Arg Glu Glu Cys Leu Gln Glu Glu Ser Arg Tyr His Tyr Thr
245          250          255
Asn Cys Met Ile Lys Asn Leu Glu Val Gln Leu Arg Arg Ala Thr Asp
260          265          270
Glu Met Lys Ala Tyr Ile Ser Ser Asp Gln Gln Glu Lys Arg Lys Ala
275          280          285
Ile Arg Glu Gln Tyr Thr Lys Asn Thr Ala Glu Gln Glu Asn Leu Gly
290          295          300
Lys Lys Leu Arg Glu Lys Gln Lys Val Ile Arg Glu Ser His Gly Pro
305          310          315          320
Asn Met Lys Gln Ala Lys Met Trp Arg Asp Leu Glu Gln Leu Met Glu
325          330          335
Cys Lys Lys Gln Cys Phe Leu Lys Gln Gln Ser Gln Thr Ser Ile Gly
340          345          350
Gln Val Ile Gln Glu Gly Gly Glu Asp Arg Leu Ile Leu
355          360          365

```

&lt;210&gt; 1595

&lt;211&gt; 559

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1595

accggtcccg ctcacaggcc cacacctgct tctcctcctg gggcagggca gcctggtggg  
 60  
 gcatggcccg ggagccgccc acttggcgag gaacaggctc catagcgacc tcagaacact  
 120  
 ggtgctgggg ccagccagg gagagcatct tcccgtggg accttccccg gggcggtca  
 180  
 tcccttgag atgtagggtg cagctgagat ggtggcgcc ccattcctgc tgttcgccag  
 240  
 cctgggctgg ggggtactagg atcaccttg ggctgatgag gagcccgggt cttgggcagt  
 300  
 taccaagtgg ggggtcacag tctggaaagt ggtggaacca agggagcggc ctcgcccagg  
 360  
 ccacactctc aaatactggc cctcgacaaa aggcagctgg gctctcaaga cagggccacc  
 420  
 tcctctctgc tgggcccgcg ccgctggaga gcaagtggga actgacccta tcttctgtcc  
 480  
 cagcttgag agccagcatc aaggtcaggc ctcacttgcc caagaaagag gagtgaggag  
 540  
 gccactgga ggaacgcgt  
 559

&lt;210&gt; 1596

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1596

Met	Leu	Ala	Leu	Gln	Ala	Gly	Thr	Glu	Asp	Arg	Val	Ser	Ser	His	Leu
1				5					10					15	
Leu	Ser	Thr	Gly	Ala	Gly	Pro	Ala	Glu	Arg	Arg	Trp	Pro	Cys	Leu	Glu
		20						25					30		
Ser	Pro	Ala	Ala	Phe	Cys	Arg	Gly	Pro	Val	Phe	Glu	Ser	Val	Ala	Trp
	35						40					45			
Ala	Arg	Pro	Leu	Pro	Trp	Phe	His	His	Phe	Pro	Asp	Cys	Asp	Pro	Pro
	50					55					60				
Leu	Gly	Asn	Cys	Pro	Arg	Pro	Gly	Leu	Leu	Ile	Ser	Pro	Arg	Val	Ile
65					70					75				80	
Leu	Val	Pro	Pro	Ala	Gln	Ala	Gly	Glu	Gln	Gln	Glu	Trp	Gly	Arg	His
				85					90					95	
His	Leu	Ser	Cys	Thr	Leu	His	Leu	Gln	Gly	Met	Ser	Arg	Pro	Gly	Glu
		100						105					110		
Gly	Pro	Ser	Gly	Lys	Met	Leu	Ser	Leu	Ala	Gly	Pro	Gln	His	Gln	Cys
	115						120					125			
Ser	Glu	Val	Ala	Met	Glu	Pro	Val	Pro	Arg	Gln	Val	Gly	Gly	Ser	Pro
	130					135					140				
Ala	Met	Pro	His	Gln	Ala	Ala	Leu	Pro	Gln	Glu	Glu	Lys	Gln	Val	Trp
145				150						155				160	
Ala	Cys	Glu	Arg	Asp	Arg										
				165											

&lt;210&gt; 1597

&lt;211&gt; 609

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1597

tcgtcaacgg aaacttcggc cttegggcct acccataatc cttgggacct tgaacgggta  
 60  
 ccgggtgggt ccgggtgggtg ttcagcagct agcttggtt cctttcaggc cccgttggt  
 120  
 ttgggcactg ataccggggg ctcgatccgc caacctggag cggtgaccgg caccgtcggg  
 180  
 atcaagccga cctacgggtc gacctccga tacggcgta tcgctatggc ttcattcttg  
 240  
 gataactctg ggccttcgc ccgtaccgtc cttgacgccg cgttgctcca tcaggccatt  
 300  
 gccggtcacg acgctatgga ccagaccacg attaatcagc ccaccccggc ggtcgttgag  
 360  
 gctgcgcggc aggcagacgt ttccgggggtg cgcattggcg ttgtcacgga gttgagcggg  
 420  
 cagggttacg accctcaggt cgaggcccg ttccacgagg ctgtcgagat gctaatagag  
 480  
 gcgggggctg aggtcgttga ggtctcttgc ccgaactttg acctgcctt acctgcttat  
 540  
 taccttattc agcctgccga ggtgtctagc aacctggctc gttacgacgc catgcgttac  
 600  
 ggcttacgc  
 609

&lt;210&gt; 1598

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1598

Ser	Ser	Thr	Glu	Thr	Ser	Ala	Phe	Gly	Pro	Thr	His	Asn	Pro	Trp	Asp
1				5					10					15	
Leu	Glu	Arg	Val	Pro	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Ala	Ala	Ser	Leu
			20					25					30		
Ala	Ser	Phe	Gln	Ala	Pro	Leu	Ala	Leu	Gly	Thr	Asp	Thr	Gly	Gly	Ser
			35					40					45		
Ile	Arg	Gln	Pro	Gly	Ala	Val	Thr	Gly	Thr	Val	Gly	Ile	Lys	Pro	Thr
			50					55				60			
Tyr	Gly	Ser	Thr	Ser	Arg	Tyr	Gly	Val	Ile	Ala	Met	Ala	Ser	Ser	Leu
						70				75				80	
Asp	Thr	Pro	Gly	Pro	Cys	Ala	Arg	Thr	Val	Leu	Asp	Ala	Ala	Leu	Leu
					85				90					95	
His	Gln	Ala	Ile	Ala	Gly	His	Asp	Ala	Met	Asp	Gln	Thr	Thr	Ile	Asn
				100				105					110		
Gln	Pro	Thr	Pro	Ala	Val	Val	Glu	Ala	Ala	Arg	Gln	Ala	Asp	Val	Ser
				115				120				125			
Gly	Val	Arg	Ile	Gly	Val	Val	Thr	Glu	Leu	Ser	Gly	Gln	Gly	Tyr	Asp
				130				135				140			
Pro	Gln	Val	Glu	Ala	Arg	Phe	His	Glu	Ala	Val	Glu	Met	Leu	Ile	Glu
						150				155				160	
Ala	Gly	Ala	Glu	Val	Val	Glu	Val	Ser	Cys	Pro	Asn	Phe	Asp	Leu	Ala



130

&lt;210&gt; 1601

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1601

```

gccggccgcc ccgtttccgc agattctgga ggagtgccga tggccgagtt catctacacc
60
atgcacaacg tccgaaaggc ggtgggtgac aaagttatcc ttgacaatgt cacgctgtcg
120
ttcttcccg ggcgcaagat tgggtgtgtc ggaccgaatg gcgctggcaa atcgacgatg
180
ctcaagctca tggctggtct cgataagccc aataacggcg atgccaactt ggctaaaggc
240
gccaccgtcg gaatcttgct tcaggagccc ccgctcaccg aggacaaaac tgttcgcgag
300
aacgtcgaag aggccgtcgg cgacatcaaa gccaaagtgg cacgggttcga ggaagtctcc
360
gccgagatgg ccaaccctga cgccgacttt gacgccctga tggcggagat gggtagctg
420
cagaccgagc tcgataacgc caacgcg
447

```

&lt;210&gt; 1602

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1602

```

Met Ala Glu Phe Ile Tyr Thr Met His Asn Val Arg Lys Ala Val Gly
1      5      10      15
Asp Lys Val Ile Leu Asp Asn Val Thr Leu Ser Phe Phe Pro Gly Ala
20     25     30
Lys Ile Gly Val Val Gly Pro Asn Gly Ala Gly Lys Ser Thr Met Leu
35     40     45
Lys Leu Met Ala Gly Leu Asp Lys Pro Asn Asn Gly Asp Ala Asn Leu
50     55     60
Ala Lys Gly Ala Thr Val Gly Ile Leu Leu Gln Glu Pro Pro Leu Thr
65     70     75     80
Glu Asp Lys Thr Val Arg Glu Asn Val Glu Glu Ala Val Gly Asp Ile
85     90     95
Lys Ala Lys Leu Ala Arg Phe Glu Glu Val Ser Ala Glu Met Ala Asn
100    105    110
Pro Asp Ala Asp Phe Asp Ala Leu Met Ala Glu Met Gly Glu Leu Gln
115    120    125
Thr Glu Leu Asp Asn Ala Asn Ala
130    135

```

&lt;210&gt; 1603

&lt;211&gt; 540

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1603

acgcgtaagc tcaccgaagc catgatggca atgctgctgg aactgcatta cagcaagcag  
 60.  
 gaaatccttg aggcgtaacct caacgaggtc ttcgtcggtc aggatggcca gcgcgccgtg  
 120  
 cacgggtttg gcttggccag tcagttcttc tttggccagc ctttgtccga gctgaagttg  
 180  
 catcaagtcg cgttggttggc cgggatgggc aaggggcccg cctattacaa cccgcggcgc  
 240  
 aatccggaac gtgcgctcga gcgtcgtaac ctggtgctgg atgtgctgga acagcagggg  
 300  
 gtagccactg ccgaacaagt cgctgccgca aagaaaatgc cgctgggtgt aaccactcgc  
 360  
 ggcaagctgg cggacagctc cttcccaggc tttatcgacc tggtaaacy ccagttgcgt  
 420  
 gaagattacc gcgacgaaga cttgaccgaa gaaggcctgc ggattttcac cagtttcgac  
 480  
 ccgattctgc agatgaaagc cgaagcatcg gtgaacgaca cattcaagcg cctgaccggc  
 540

&lt;210&gt; 1604

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1604

Thr	Arg	Lys	Leu	Thr	Glu	Ala	Met	Met	Ala	Met	Leu	Leu	Glu	Leu	His
1				5					10					15	
Tyr	Ser	Lys	Gln	Glu	Ile	Leu	Glu	Ala	Tyr	Leu	Asn	Glu	Val	Phe	Val
			20					25					30		
Gly	Gln	Asp	Gly	Gln	Arg	Ala	Val	His	Gly	Phe	Gly	Leu	Ala	Ser	Gln
		35				40						45			
Phe	Phe	Phe	Gly	Gln	Pro	Leu	Ser	Glu	Leu	Lys	Leu	His	Gln	Val	Ala
	50				55						60				
Leu	Leu	Val	Gly	Met	Val	Lys	Gly	Pro	Ser	Tyr	Tyr	Asn	Pro	Arg	Arg
65					70					75				80	
Asn	Pro	Glu	Arg	Ala	Leu	Glu	Arg	Arg	Asn	Leu	Val	Leu	Asp	Val	Leu
			85						90					95	
Glu	Gln	Gln	Gly	Val	Ala	Thr	Ala	Glu	Gln	Val	Ala	Ala	Ala	Lys	Lys
			100					105						110	
Met	Pro	Leu	Gly	Val	Thr	Thr	Arg	Gly	Lys	Leu	Ala	Asp	Ser	Ser	Phe
		115					120					125			
Pro	Gly	Phe	Ile	Asp	Leu	Val	Lys	Arg	Gln	Leu	Arg	Glu	Asp	Tyr	Arg
		130				135					140				
Asp	Glu	Asp	Leu	Thr	Glu	Glu	Gly	Leu	Arg	Ile	Phe	Thr	Ser	Phe	Asp
145					150					155				160	
Pro	Ile	Leu	Gln	Met	Lys	Ala	Glu	Ala	Ser	Val	Asn	Asp	Thr	Phe	Lys
			165					170						175	
Arg	Leu	Thr	Gly												
			180												

&lt;210&gt; 1605

&lt;211&gt; 427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1605

```

acgcgttggg gcggtcgggc gcacgcagtc cgtccaagag gtacaggcca gcgttgccgc
60
cattctttgc gggcgggata tgcactggga tattgcggcc catcgctgt gaccacacat
120
cgcagcgctg gacccaccag cccacctggg cccactcgca cgtgccagta ctgtccgcac
180
gcaagaaatc gcggtgagct gcgtgcgcct gctgggtgcc gcctgccact acggcaagac
240
ccagcgctac ggcgactgcc atgatgaccg aaaggacgcg acccctaata gatgcagtca
300
tctttctcct tcacaaagta tttggtaatt gtcacttagc tttatcgctc ggaatctgtg
360
aaccgttaac atcccgacgc ggaagctaac tagcaagcag tctaatgcac tcccgggcca
420
aatgttg
427

```

&lt;210&gt; 1606

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1606

```

Met Thr Ala Ser Ile Arg Gly Arg Val Leu Ser Val Ile Met Ala Val
1      5      10     15
Ala Val Ala Leu Gly Leu Ala Val Val Ala Gly Gly Thr Gln Gln Ala
20     25     30
His Ala Ala His Arg Asp Phe Leu Arg Ala Asp Ser Thr Gly Thr Cys
35     40     45
Glu Trp Asp Gln Val Gly Trp Trp Val Gln Arg Cys Asp Val Trp Ser
50     55     60
Gln Ala Met Gly Arg Asn Ile Pro Val Gln Ile Pro Pro Ala Lys Asn
65     70     75     80
Gly Gly Asn Ala Gly Leu Tyr Leu Leu Asp Gly Leu Arg Ala Thr Asp
85     90     95
Arg Thr Asn Ala
100

```

&lt;210&gt; 1607

&lt;211&gt; 396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1607

```

gcacggctcc gctcgcggcc gccgtgatgg tacataccgg cgcgaccgtg atcgattctt
60
tgccgcaagg caatttactt ccacgtcacg gccgatgcga tgaagatgac gattcgctca
120
cggatgggac tgatcccgta cgaggcgatc gtgggcggga cgatgatgat cgtggcgacg
180

```

ttgctgtacg gattcatttt gtagcataaa taaggagggg ttcgatgaac aggaaaaccc  
 240  
 tttctgttgg caccgattc gttcaaggaa agcatgacgg caaaagaagt ctgtatcgcg  
 300  
 atggaaaaag gactgagccg cgtctacccc gacgcccggg ttatccatgt gccgatggcg  
 360  
 gacggaggcg aaggcacggg gcagtcgctg gtcgac  
 396

<210> 1608

<211> 56

<212> PRT

<213> Homo sapiens

<400> 1608

Thr	Gly	Lys	Pro	Phe	Leu	Leu	Ala	Pro	Asp	Ser	Phe	Lys	Glu	Ser	Met
1				5				10					15		
Thr	Ala	Lys	Glu	Val	Cys	Ile	Ala	Met	Glu	Lys	Gly	Leu	Ser	Arg	Val
		20					25					30			
Tyr	Pro	Asp	Ala	Arg	Phe	Ile	His	Val	Pro	Met	Ala	Asp	Gly	Gly	Glu
		35				40					45				
Gly	Thr	Val	Gln	Ser	Leu	Val	Asp								
	50					55									

<210> 1609

<211> 505

<212> DNA

<213> Homo sapiens

<400> 1609

acgcgtagat gccacagcgc caggacacac gccaccgcgg agccgaggat gatccacatg  
 60  
 ggctcgactc acatggacgc catggattcg gcagtgagga gcaggccgcg agcttcgcac  
 120  
 gcggcccgac tgcgtagtcg cgctcatctca gtgcacatct gttcttcccc gtcctatgagg  
 180  
 ttcgcggcgt aggacatcgt tacgtccagc atggtggcga tctcagcaat gtcacagccg  
 240  
 gccttgtgga gggcgaggag ccgagcgcgc gtgcttcctg ctggcacgat gcgttcacgt  
 300  
 gctgcgttga tgtcgtcgat actgatatgc aggatgcgcc cggggtcgaa gacggggaat  
 360  
 ggggtgaatt ggacgggtccc ccctggccag cgagtcgttg gacgattcga ctggggacat  
 420  
 gcgcgagcag ggcgacgaca cgccacggaa cgcggcattc atggacgagg gaacggacat  
 480  
 ggagcgagaa aaagcgggcg tcgac  
 505

<210> 1610

<211> 129

<212> PRT

<213> Homo sapiens



&lt;400&gt; 1610

```

Met Pro Arg Ser Val Ala Cys Arg Arg Pro Ala Arg Ala Cys Pro Gln
 1           5           10           15
Ser Asn Arg Pro Thr Thr Arg Trp Pro Gly Gly Thr Val Gln Phe Thr
      20           25           30
Pro Phe Pro Val Phe Asp Pro Gly Arg Ile Leu His Ile Ser Ile Asp
      35           40           45
Asp Ile Asn Ala Ala Arg Glu Arg Ile Val Pro Ala Gly Ser Thr Arg
      50           55           60
Ala Arg Leu Leu Ala Leu His Lys Ala Gly Cys Asp Ile Ala Glu Ile
65           70           75           80
Ala Thr Met Leu Asp Val Thr Met Ser Tyr Ala Ala Asn Leu Met Ser
      85           90           95
Gly Glu Glu Gln Met Cys Thr Glu Met Thr Arg Leu Arg Ser Arg Ala
      100          105          110
Ala Cys Glu Ala Arg Gly Leu Leu Ser Thr Ala Glu Ser Met Ala Ser
      115          120          125
Met

```

&lt;210&gt; 1611

&lt;211&gt; 532

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1611

```

acgcgtgctg cgtttacagt tgcgtctatt gatttaggtg cgcattccaga atttttagga
60
aaaaatgata ttcaattagg caaaaaagaa tctgtagagg atactgcgaa agtattaggt
120
agaatgttcg atgggtattga attccgtggt ttttcacaac aagctggtga agatttagcg
180
aagttctctg gtgtaccggg gtggaatgga ttaacagacg attggcatcc tacacaaatg
240
ttagctgatt ttatgacaat aaaagagaat tttggatata tagaaggaat aaacttaact
300
tacgttgagg atggacgtaa taatattgag cattcattaa tggtagcagg tgctatgtta
360
ggtgttaatg taagaatttg tacacctaaa tcattaaatc caaaagaggc atatgttgat
420
attgcaaaag aaaaagcgag tcaatatggt ggttcagtca tgattacgga taatattgca
480
gaagcagttg aaaatacaga tgctatatat acagatgttt gggtatcgac gg
532

```

&lt;210&gt; 1612

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1612

```

Thr Arg Ala Ala Phe Thr Val Ala Ser Ile Asp Leu Gly Ala His Pro
 1           5           10           15
Glu Phe Leu Gly Lys Asn Asp Ile Gln Leu Gly Lys Lys Glu Ser Val

```

20 25 30  
 Glu Asp Thr Ala Lys Val Leu Gly Arg Met Phe Asp Gly Ile Glu Phe  
 35 40 45  
 Arg Gly Phe Ser Gln Gln Ala Gly Glu Asp Leu Ala Lys Phe Ser Gly  
 50 55 60  
 Val Pro Gly Trp Asn Gly Leu Thr Asp Asp Trp His Pro Thr Gln Met  
 65 70 75 80  
 Leu Ala Asp Phe Met Thr Ile Lys Glu Asn Phe Gly Tyr Leu Glu Gly  
 85 90 95  
 Ile Asn Leu Thr Tyr Val Gly Asp Gly Arg Asn Asn Ile Ala His Ser  
 100 105 110  
 Leu Met Val Ala Gly Ala Met Leu Gly Val Asn Val Arg Ile Cys Thr  
 115 120 125  
 Pro Lys Ser Leu Asn Pro Lys Glu Ala Tyr Val Asp Ile Ala Lys Glu  
 130 135 140  
 Lys Ala Ser Gln Tyr Gly Gly Ser Val Met Ile Thr Asp Asn Ile Ala  
 145 150 155 160  
 Glu Ala Val Glu Asn Thr Asp Ala Ile Tyr Thr Asp Val Trp Val Ser  
 165 170 175  
 Thr

&lt;210&gt; 1613

&lt;211&gt; 584

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1613

nnacgcgttc agccgagaaa tatgctgctt ttgcctgcc acctcacaaa tgctacggca  
 60  
 cagggcgctcc aggttttgcg cctcctggta cgttgctaca cacttgctca cctcccagcg  
 120  
 gtatcaatac aacttgcgaa atgcagacaa ggcccaggcc taagacatgg tagacataca  
 180  
 tatatacaag gaattcacta tatattgggt gaaaggagat cttcccgctc ctgttcttcc  
 240  
 tctgccgcat cctgtgaagc gttcagggag gtcgacatgg ataattgtgcg tatgcctggc  
 300  
 acggtaaagt gtcgcgggct tgtagatgcg tgtgaacggt ttcgtgactt gaagaggtcg  
 360  
 aagctgatgt gttcgcgtga gtcgatgca gcgcgctgcg ttgcgtgect tgtgggtcgat  
 420  
 cgtcgccccg atccgataga atgcggagtt gtattttcgt agtactgctc gacaatgcc  
 480  
 gtgggcgagg cgatgagttc ctcatctgcg tctttctcga ggtcttggtc catgtccata  
 540  
 aacataccaa agctggatgg gtcatacgac ggcgagcat gcat  
 584

&lt;210&gt; 1614

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1614

```

Xaa Arg Val Gln Pro Arg Asn Met Leu Leu Phe Ala Cys His Leu Thr
 1           5           10           15
Asn Ala Thr Ala Gln Gly Val Gln Val Leu Arg Leu Leu Val Arg Cys
 20           25           30
Tyr Thr Leu Ala His Leu Pro Ala Val Ser Ile Gln Leu Ala Lys Cys
 35           40           45
Arg Gln Gly Pro Gly Leu Arg His Gly Arg His Thr Tyr Ile Gln Gly
 50           55           60
Ile His Tyr Ile Leu Gly Glu Arg Arg Ser Ser Arg Ser Cys Ser Ser
 65           70           75           80
Ser Ala Ala Ser Cys Glu Ala Phe Arg Glu Val Asp Met Asp Asn Val
 85           90           95
Arg Met Pro Gly Thr Val Lys Cys Arg Gly Leu Val Asp Ala Cys Glu
100           105           110
Arg Phe Arg Asp Leu Lys Arg Ser Lys Leu Met Cys Ser Arg Glu Leu
115           120           125
Asp Ala Ala Arg Cys Val Ala Cys Leu Val Val Asp Arg Arg Pro Asp
130           135           140
Pro Ile Glu Cys Gly Val Val Phe Ser
145           150

```

&lt;210&gt; 1615

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1615

```

gccggcttgc ccgacgcgtc tatgggtgat gttctgtcct ctgtcgtcgg gccgtggggc
60
tcgggtgcttg tcagtgcctg tgatcatcatt tccctgcttg gggctctact ggcttggatc
120
ctactgtgcg gtgagacgat gcaggtgccg ggtgaggacg gcacatgcc gaaactgttc
180
ggacggatca acaaacatga ggctccagct cccgctttgt ggatcaccaa catcgtctcc
240
cagatatgcc ttgtcatgac ggtgttgtgg gacggtgctt acttggcgat ggcgacctg
300
gctgccgccc tcatcctggt gccgtacctg ctgtcagccg cattcgccct gaagatggtg
360
atc
363

```

&lt;210&gt; 1616

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1616

```

Ala Gly Leu Pro Asp Ala Ser Met Gly Asp Val Leu Ser Ser Val Val
 1           5           10           15
Gly Pro Trp Gly Ser Val Leu Val Ser Ala Gly Val Ile Ile Ser Leu
 20           25           30
Leu Gly Ala Leu Leu Ala Trp Ile Leu Leu Cys Gly Glu Thr Met Gln

```

```

      35              40              45
Val Pro Gly Glu Asp Gly Thr Met Pro Lys Leu Phe Gly Arg Ile Asn
      50              55              60
Lys His Glu Ala Pro Ala Pro Ala Leu Trp Ile Thr Asn Ile Val Ser
      65              70              75              80
Gln Ile Cys Leu Val Met Thr Val Leu Trp Asp Gly Ala Tyr Leu Ala
      85              90              95
Met Ala Thr Leu Ala Ala Ala Leu Ile Leu Val Pro Tyr Leu Leu Ser
      100              105              110
Ala Ala Phe Ala Leu Lys Met Val Ile
      115              120

```

&lt;210&gt; 1617

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1617

```

accggtgact acctgtggga gaagaagggc atcgttccca tcctcaagat tgataagggc
60
ctggctgacg agggctgcca cgttcgtctc atgaagccga ttcccgccct cgacgagttg
120
gtgcaccgcg ccgtcgagga gaagcacatc ttcggtacca aggagcgctc tgtcatcctg
180
gatgacgaca aagctggcat cgaaaagatt gtcgaccagc agttcgaact ggccgaacag
240
gtgcgcgctg cgggtcttgt gccgatcctc gaaccgcgagg tcgacatcca cgctccacat
300
aaggagaagg ctgaggaaag gctgcacaac ctcattccgc agcacatcga ctctctgccg
360
ctcgacgcca agatcatggt gaagctgacg atcccagagt ccgaagacct gtatgccgac
420
ctcattgcgg atccgaaggt cctacgc
447

```

&lt;210&gt; 1618

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1618

```

Thr Gly Asp Tyr Leu Trp Glu Lys Lys Gly Ile Val Pro Ile Leu Lys
1      5      10      15
Ile Asp Lys Gly Leu Ala Asp Glu Gly Cys His Val Arg Leu Met Lys
20     25     30
Pro Ile Pro Gly Leu Asp Glu Leu Val His Arg Ala Val Glu Glu Lys
35     40     45
His Ile Phe Gly Thr Lys Glu Arg Ser Val Ile Leu Asp Asp Asp Lys
50     55     60
Ala Gly Ile Glu Lys Ile Val Asp Gln Gln Phe Glu Leu Ala Glu Gln
65     70     75     80
Val Arg Ala Ala Gly Leu Val Pro Ile Leu Glu Pro Glu Val Asp Ile
85     90     95
His Ala Pro His Lys Glu Lys Ala Glu Glu Arg Leu His Asn Leu Ile

```

```

          100          105          110
Arg Glu His Ile Asp Ser Leu Pro Leu Asp Ala Lys Ile Met Leu Lys
          115          120          125
Leu Thr Ile Pro Ser Ser Glu Asp Leu Tyr Ala Asp Leu Ile Ala Asp
          130          135          140
Pro Lys Val Leu Arg
145

```

<210> 1619  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1619
nnggtaccga aaccctgtgc gctaccgcat aaaatcaaag gaactagtat gcataacgta
60
acaacaaatg gtgcctccat tcccgccctt ggccttggca ctttccgtat gcccggcgaa
120
gatgtgcttc gcatcgctcc ttacgcgctc aaggetggtt ttcgccatgt cgataccgcg
180
cagatttatg gcaatgaagt cgaggctcgg gaagcaattg cgacttccgg cgttcagcgt
240
ggcgacatct ttctgaccac aaaagtctgg gtagataatt ataagcatga tgctttcatc
300
gcatctgtcg atgaaagcct taccaagctt aagaccgact atgtcgatct gctgc
355

```

<210> 1620  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1620
Xaa Val Pro Lys Pro Val Ser Leu Pro His Lys Ile Lys Gly Thr Ser
1      5      10      15
Met His Asn Val Thr Thr Asn Gly Ala Ser Ile Pro Ala Leu Gly Leu
20     25     30
Gly Thr Phe Arg Met Pro Gly Glu Asp Val Leu Arg Ile Val Pro Tyr
35     40     45
Ala Leu Lys Ala Gly Phe Arg His Val Asp Thr Ala Gln Ile Tyr Gly
50     55     60
Asn Glu Val Glu Val Gly Glu Ala Ile Ala Thr Ser Gly Val Gln Arg
65     70     75     80
Gly Asp Ile Phe Leu Thr Thr Lys Val Trp Val Asp Asn Tyr Lys His
85     90     95
Asp Ala Phe Ile Ala Ser Val Asp Glu Ser Leu Thr Lys Leu Lys Thr
100    105    110
Asp Tyr Val Asp Leu Leu
115

```

<210> 1621  
 <211> 386  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 1621

gcgcgccatg gagcgcccc gggcgcgcc aggatgctcc aggccaagtg aagcgggtccg  
 60  
 gctgggggtcg gcgggacccg cgggccatgt acggcgacat attcaacgcc acggggcggg  
 120  
 cccccgaggc ggcggtaggc agcgcgctgg ccccaggagc cacggtcaag gcagaaggcg  
 180  
 ctttgccgct ggagctggcc actgcgcgcg gtatgagggg cggcgcggcc acaaagcccc  
 240  
 acctgcccac ctacctgtg ctcttcttcc tgctgtgtgt ctggggggcg ctggggggcg  
 300  
 tcttcacggg ttgccagctg cgccattcgg ccttcgccgc gctgccccac gaccgcttcg  
 360  
 ctgcgcgacgc ccgcgcgccc ggaagg  
 386

&lt;210&gt; 1622

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1622

Met	Glu	Ala	Pro	Arg	Val	Ala	Pro	Gly	Cys	Ser	Arg	Pro	Ser	Glu	Ala
1				5				10					15		
Val	Arg	Leu	Gly	Ser	Ala	Gly	Pro	Ala	Gly	His	Val	Arg	Arg	His	Ile
		20					25					30			
Gln	Arg	His	Gly	Ala	Gly	Pro	Arg	Gly	Gly	Gly	Arg	Gln	Arg	Ala	Gly
		35				40					45				
Pro	Arg	Ser	His	Gly	Gln	Gly	Arg	Arg	Arg	Phe	Ala	Ala	Gly	Ala	Gly
		50				55				60					
His	Cys	Ala	Arg	Tyr	Glu	Gly	Arg	Arg	Gly	His	Lys	Ala	Arg	Pro	Ala
65				70					75					80	
His	Leu	Pro	Ala	Ala	Leu	Leu	Pro	Ala	Ala	Ala	Leu	Gly	Gly	Ala	Arg
			85					90					95		
Arg	Pro	Leu	His	Arg	Leu	Pro	Ala	Ala	Pro	Phe	Gly	Leu	Arg	Arg	Ala
		100					105						110		
Ala	Pro	Arg	Pro	Leu	Arg	Ser	Arg	Pro	Arg	Ala	Arg	Lys			
		115					120					125			

&lt;210&gt; 1623

&lt;211&gt; 314

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1623

nctgggtgcc agagcctcgt cgggggtccag ccccagggcc ttgcgagtc agacacttgg  
 60  
 ggcccttgct tgtggttttt ctgggagctt tgggccgagg gttccccgga cccttcctg  
 120  
 aacttttccg cagtttcaga ggagagtctg caagtgagag ctgcagtgac tgtgccttgt  
 180  
 gcttggcacc caagcagggc atgggagtct taagtgggac cagggcctca aggacaacag  
 240

agagccgcat ggcagggtac acacctggat aaaagtgggt gggggaagcc cactgctgca  
300

ccccgggcat tgct  
314

<210> 1624

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1624

Met	Pro	Gly	Val	Gln	Trp	Ala	Ser	Pro	Thr	His	Phe	Tyr	Pro	Gly
1			5					10					15	
Val	Tyr	Pro	Ala	Met	Arg	Leu	Ser	Val	Val	Leu	Glu	Ala	Leu	Val
		20					25					30		Pro
Leu	Lys	Thr	Pro	Met	Pro	Cys	Leu	Gly	Ala	Lys	His	Lys	Ala	Gln
	35					40					45			Ser
Leu	Gln	Leu	Ser	Leu	Ala	Asp	Ser	Pro	Leu	Lys	Leu	Arg	Lys	Ser
	50					55					60			Ser
Gly	Lys	Gly	Pro	Gly	Asn	Pro	Arg	Pro	Lys	Ala	Pro	Arg	Lys	Thr
65					70				75					80
Ser	Lys	Gly	Pro	Lys	Cys	Leu	Thr	Arg	Lys	Gly	Pro	Gly	Ala	Gly
			85					90					95	Pro
Arg	Arg	Gly	Ser	Gly	His	Gln								
			100											

<210> 1625

<211> 619

<212> DNA

<213> Homo sapiens

<400> 1625

acgcgtactc agcagcaagt tctgctgagc cccaaatcca cacagactga gcctggacca  
60  
gggctggggc ctccttatcc aagccaatcc agggaaacac tgtgctgact tcaaggcaga  
120  
agggacaaga aagcatgact gtgcacaaat tggctttgca gccatctcca ccaggtagcc  
180  
ctgggagcac ctgggaagaa gccgggccat gcagggagcc caacctcacc ctgcattcag  
240  
aaccgggcct tggaatggcc tgatctgagc cctagcaccc ctgggaagcc gccaccttt  
300  
cttctggcct ctgggaagaa gatgggaatt ttaaggccat gggagaagac actcctggat  
360  
tctttcagct tctccacca cccctgctc cagatgtaat ctgggaagac tggggagtca  
420  
ggggcacagt gagttggagc aggggattgg agggtttggt ggacagcctt ccagggcacc  
480  
tcaggagctg aattatttaa gccagctgcc cgtgggcccc gctcccagcc cttcctgttt  
540  
acacagactc cgtccatagc agacaccttc ccagagcctg ggtgacaata ggctgggtgt  
600  
gttttctgca atcttatag  
619

<210> 1626  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 1626  
 Met Asp Gly Val Cys Val Asn Arg Lys Gly Trp Glu Arg Gly Pro Arg  
   1                  5                  10                  15  
 Ala Ala Gly Leu Asn Asn Ser Ala Pro Glu Val Pro Trp Lys Ala Val  
                   20                  25                  30  
 Pro Gln Thr Leu Gln Ser Pro Ala Pro Thr His Cys Ala Pro Asp Ser  
           35                  40                  45  
 Pro Val Phe Pro Asp Tyr Ile Trp Ser Arg Gly Trp Val Glu Lys Leu  
   50                  55                  60  
 Lys Glu Ser Arg Ser Val Phe Ser His Gly Leu Lys Ile Pro Ile Phe  
 65                  70                  75                  80  
 Phe Pro Glu Ala Arg Arg Lys Val Gly Gly Phe Pro Gly Val Leu Gly  
                   85                  90                  95  
 Leu Arg Ser Gly His Ser Lys Ala Arg Phe  
           100                  105

<210> 1627  
 <211> 481  
 <212> DNA  
 <213> Homo sapiens

<400> 1627  
 naccggtgcg ttgtgcccacat gccttgctcga acaaggccat ataggccgta ccgacgtgag  
 60  
 gatcaccagt gggcgagggg gcaacgcgcg tgcgcgcggg atgcaaata gtcacgatga  
 120  
 cacgaagtct atcgggatcc gctgacagac tccggtaaag ttcccgccat ggcagaacct  
 180  
 actggaaacc cggtgagtc cagctcggac ttcatcctc aggttggttc gcgcggacatc  
 240  
 caacaggaca cctacggcgg gcgcgtccag acccggttcc cacctgagcc taacggctac  
 300  
 ctccacattg gccacgcgaa ggccatcgtc accgatttcg gcgttgccga ggatttcggc  
 360  
 ggcacctgca acctgagact tgatgatact aatccaggca ccgaggaaac cgagtatgtc  
 420  
 gagtcgatcg ttgcagacat tgagtgggta gggtactccc cggcccacgt tgtccacgcg  
 480  
 t  
 481

<210> 1628  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 1628  
 Met Ala Glu Pro Thr Gly Asn Pro Ala Glu Ser Ser Ser Asp Phe Ile



1	5	10	15
His Gln Val Val Arg Ala Asp Ile Gln Gln Asp Thr Tyr Gly Gly Arg			
20	25	30	
Val Gln Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu His Ile Gly			
35	40	45	
His Ala Lys Ala Ile Val Thr Asp Phe Gly Val Ala Glu Asp Phe Gly			
50	55	60	
Gly Thr Cys Asn Leu Arg Leu Asp Asp Thr Asn Pro Gly Thr Glu Glu			
65	70	75	80
Thr Glu Tyr Val Glu Ser Ile Val Ala Asp Ile Glu Trp Leu Gly Tyr			
85	90	95	
Ser Pro Ala His Val Val His Ala			
100			

&lt;210&gt; 1629

&lt;211&gt; 4519

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1629

```

ccaaattgct gggaatgtcc aaagtgtctac caggaggaca gctcggagaa agcccagaag
60
cggaaaatgg aagagagtga cgaagaagct gtgcaagcca aagtcttgcg gcccttgcgg
120
agctgcgatg agcctctcac gccccgcct cattcaccca cttccatgct gcagctcatc
180
catgaccccg tttcccccg gggatatgtg actcgggtcat cccctggggc tggccccagc
240
gaccaccaca gtgccagccg cgatgagcgc ttcaaacggc ggcagttgct gcggctgcag
300
gccacagagc gcaccatggt acgggaaaag gagaacaatc ccagcggcaa aaaggagctg
360
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420
accaaagagc tccacgggac atccattgtg cccaagctgc aggccatcac ggctctctct
480
gccaaccttc gccattcccc ccgtgtgcta gtgcagcact gccagccccg aacccccagc
540
cgtgggggatg aggaggggct ggggggagag gaggaggaag aggaggagga ggaggaggaa
600
gatgacagtg cagaggaggg ggggtgcagcc aggtgaatg gccggggcag ttgggctcag
660
gatggagacg aaagctggat gcagcgggag gtctggatgt ctgtcttccg ctacctcagc
720
cgcagagaac tttgtgaatg tatgcgagtg tgcaagacgt ggtataaatg gtgctgcgac
780
aagagacttt ggacaaaaat tgacttgagt aggtgtaagg ccattgtgcc ccaggccctc
840
agtggcatca tcaagaggca gccagtcagc cttgacctca gttggaccaa catctctaaa
900
aagcaactga catggctcgt caataggctg ccaggactga aagacctcct cctagcaggc
960
tgctcctggg ctgcagtctc tgccctcagc acctccagct gcccccttct caggaccctt
1020

```

gatcttcgggt gggcagtagg aatcaaggac cctcaaattc gggacttgct tactccaccg  
1080  
gctgataaac caggtcagga caatcgcagc aagctccgga acatgaccga cttccggctg  
1140  
gcaggccttg acatcacaga tgccacgctt cgcctcataa ttcgccacat gcccctcctg  
1200  
tctcgactcg acctcagtca ctgcagccac cttacagatc agtcctccaa tctactcact  
1260  
gctgtcgggt cttccactcg ctactctctc acagagctca atatggcagg ttgcaataaa  
1320  
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1380  
cgaggatgca agcagatcac tcgaaaagcc tgcgagcact tcattctcaga cttgtccatc  
1440  
aacagcctct actgcctgtc tgacgagaag ctgatacaga agatcagcta agacacaccc  
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1620  
gcccctctc tacaggtggg gcagagaggg tgggtggacac caggcttatc tgctgtctcc  
1680  
tctccctcct aaggaaaagg gagtagcaga ttgatctgag gggaaagcac aggtgtgtct  
1740  
gtcgaggegc ctgctcgctt actcgctgc caggaggccg ggctctcagt ttgggggtgtt  
1800  
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1860  
gtgcctggtt ctgagcaaac tcccaggga gaaaacggcc ctgtctccat ggccaggttc  
1920  
ttgtggtgtc cagtgcgct ctctctcca tcacactctc cgggcttgcg caggaggggc  
1980  
cagcagcccc aggagtcca gaccgtgcc gatcacactg gtgctgttga gatctccaa  
2040  
acctcagtc cttaactgtg ctctccctcc tttctctcc cttgagcttg gttctgccc  
2100  
gcactcgtgc ttgttcacat aattaggtt cccacccag cctaccgac ttacttgcta  
2160  
gtctctatga ggtccttatt gcacttattg gggttgaagc tcttcagagg agctggaact  
2220  
gtctaccca gggacacacc catttcgttg ctacccaagt ggattctgag acaggcacca  
2280  
tctccttgtt cccctctct cttttgcctc ccactgactg ccttttcca tgtgtcttca  
2340  
ttctgcctga agaaggctt cccaggatgc acgtcctcag agggagcagc ctatctcccc  
2400  
caagctggag gcggcagagg actgggcaa gccccaacct gcctccagc caggctcctc  
2460  
caggcctctg gtttagcgga gcccctgag ccaggcctg tgtctagccc cagtggctca  
2520  
ctgaactttc agggcagtca gggggtcctg cttagaagcc agtcaccagc cctctgcctg  
2580  
cagccatgga aggggggtgtg cacgtgcctc tgtgtgtgtg gctgagtgtt ttctgcgct  
2640

gtgtgtggag ggagggaggg aggggagcat ggtgtctccc gctccaccgc cctttgttga  
2700  
gccccatcag ctgccccctt ttacttttga ttgaacggcc tgtccaaaga tcctctctct  
2760  
agggcagcag agagcttttt gcacttttaa aaaaaaaga aagaaagaaa ggtcggaatt  
2820  
tcttttgggt caatatTTTT aagtgtgtga ggagatgctc agtagcagca gcctatggca  
2880  
agagcttata aatgattgat gcaaatttgc actctgctcc ccctctgtaa ggatactgat  
2940  
agcacaacct cttcccccca ccccgccccg ccttttgggtc gtccatccct gtccctttct  
3000  
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4260

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<210> 1630

<211> 496

<212> PRT

<213> Homo sapiens

<400> 1630

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			20					25					30		
Ala	Lys	Val	Leu	Arg	Pro	Leu	Arg	Ser	Cys	Asp	Glu	Pro	Leu	Thr	Pro
			35				40					45			
Pro	Pro	His	Ser	Pro	Thr	Ser	Met	Leu	Gln	Leu	Ile	His	Asp	Pro	Val
	50					55					60				
Ser	Pro	Arg	Gly	Met	Val	Thr	Arg	Ser	Ser	Pro	Gly	Ala	Gly	Pro	Ser
	65				70					75				80	
Asp	His	His	Ser	Ala	Ser	Arg	Asp	Glu	Arg	Phe	Lys	Arg	Arg	Gln	Leu
				85					90					95	
Leu	Arg	Leu	Gln	Ala	Thr	Glu	Arg	Thr	Met	Val	Arg	Glu	Lys	Glu	Asn
			100					105					110		
Asn	Pro	Ser	Gly	Lys	Lys	Glu	Leu	Ser	Glu	Val	Glu	Lys	Ala	Lys	Ile
	115					120						125			
Arg	Gly	Ser	Tyr	Leu	Thr	Val	Thr	Leu	Gln	Arg	Pro	Thr	Lys	Glu	Leu
	130					135					140				
His	Gly	Thr	Ser	Ile	Val	Pro	Lys	Leu	Gln	Ala	Ile	Thr	Ala	Ser	Ser
	145				150					155				160	
Ala	Asn	Leu	Arg	His	Ser	Pro	Arg	Val	Leu	Val	Gln	His	Cys	Pro	Ala
				165					170					175	
Arg	Thr	Pro	Gln	Arg	Gly	Asp	Glu	Glu	Gly	Leu	Gly	Gly	Glu	Glu	Glu
			180					185					190		
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asp	Ser	Ala	Glu	Glu	Gly	Gly
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Ala	Ala	Arg	Leu	Asn	Gly	Arg	Gly	Ser	Trp	Ala	Gln	Asp	Gly	Asp	Glu
	210					215					220				
Ser	Trp	Met	Gln	Arg	Glu	Val	Trp	Met	Ser	Val	Phe	Arg	Tyr	Leu	Ser
	225				230					235				240	
Arg	Arg	Glu	Leu	Cys	Glu	Cys	Met	Arg	Val	Cys	Lys	Thr	Trp	Tyr	Lys
				245					250					255	
Trp	Cys	Cys	Asp	Lys	Arg	Leu	Trp	Thr	Lys	Ile	Asp	Leu	Ser	Arg	Cys
				260				265					270		
Lys	Ala	Ile	Val	Pro	Gln	Ala	Leu	Ser	Gly	Ile	Ile	Lys	Arg	Gln	Pro
	275					280						285			
Val	Ser	Leu	Asp	Leu	Ser	Trp	Thr	Asn	Ile	Ser	Lys	Lys	Gln	Leu	Thr

290 295 300  
 Trp Leu Val Asn Arg Leu Pro Gly Leu Lys Asp Leu Leu Leu Ala Gly  
 305 310 315 320  
 Cys Ser Trp Ser Ala Val Ser Ala Leu Ser Thr Ser Ser Cys Pro Leu  
 325 330 335  
 Leu Arg Thr Leu Asp Leu Arg Trp Ala Val Gly Ile Lys Asp Pro Gln  
 340 345 350  
 Ile Arg Asp Leu Leu Thr Pro Pro Ala Asp Lys Pro Gly Gln Asp Asn  
 355 360 365  
 Arg Ser Lys Leu Arg Asn Met Thr Asp Phe Arg Leu Ala Gly Leu Asp  
 370 375 380  
 Ile Thr Asp Ala Thr Leu Arg Leu Ile Ile Arg His Met Pro Leu Leu  
 385 390 395 400  
 Ser Arg Leu Asp Leu Ser His Cys Ser His Leu Thr Asp Gln Ser Ser  
 405 410 415  
 Asn Leu Leu Thr Ala Val Gly Ser Ser Thr Arg Tyr Ser Leu Thr Glu  
 420 425 430  
 Leu Asn Met Ala Gly Cys Asn Lys Leu Thr Asp Gln Thr Leu Ile Tyr  
 435 440 445  
 Leu Arg Arg Ile Ala Asn Val Thr Leu Ile Asp Leu Arg Gly Cys Lys  
 450 455 460  
 Gln Ile Thr Arg Lys Ala Cys Glu His Phe Ile Ser Asp Leu Ser Ile  
 465 470 475 480  
 Asn Ser Leu Tyr Cys Leu Ser Asp Glu Lys Leu Ile Gln Lys Ile Ser  
 485 490 495

<210> 1631  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 1631  
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 120  
 ccatgttgac tctcgcgacg agcttgttga gttgcttggc ttttcgaaag acgacattac  
 180  
 caaccaagtt cagcaagctg tggg'gcctt ggggtttaccg ccactagaag atgaaaacgc  
 240  
 acaaggtgaa gatccggcgt cgcaggtccc gccagtcacc gacgaggacc ccactgcttt  
 300  
 cttcgatcaa gttccagatg tgcctctaga  
 330

<210> 1632  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 1632  
 Met Gln Cys Gln Asn Pro Asn Thr Arg Ala Ser Asp Met Ala Gly Trp  
 1 5 10 15  
 Lys Thr Leu Gln Thr Leu Phe His Val Asp Ser Arg Asp Glu Leu Val

```

                20                25                30
Glu Leu Leu Gly Phe Ser Lys Asp Asp Ile Thr Asn Gln Val Gln Gln
                35                40                45
Ala Val Gly Ala Leu Gly Leu Pro Pro Leu Glu Asp Glu Asn Ala Gln
                50                55                60
Gly Glu Asp Pro Ala Ser Gln Val Pro Pro Val Thr Asp Glu Asp Pro
65                70                75                80
Thr Ala Phe Phe Asp Gln Val Pro Asp Val Pro Leu
                85                90

```

&lt;210&gt; 1633

&lt;211&gt; 259

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1633

```

ngggggacgt tggtatcaa tcttgctgga gctttcgtac tggcgacttt gctcgagctg
60
ctcgccacg ctggccctgg cccaggggtt cgtcgagcgg tgcggctatg catcggtacc
120
ggattgtag gtggatttac gacttattcc gccctcacgg tggaaaccgg ccaacgtgtg
180
atgtcagggc agtggttatg gggattgcc tatcttttga cgagtgtcgt ggcaggtgca
240
ttgttggcat gggcatga
259

```

&lt;210&gt; 1634

&lt;211&gt; 86

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1634

```

Xaa Gly Thr Leu Ala Ile Asn Leu Val Gly Ala Phe Val Leu Ala Thr
 1                5                10                15
Leu Leu Glu Leu Leu Val His Ala Gly Pro Gly Pro Gly Val Arg Arg
                20                25                30
Ala Val Arg Leu Cys Ile Gly Thr Gly Leu Leu Gly Gly Phe Thr Thr
                35                40                45
Tyr Ser Ala Leu Thr Val Glu Thr Gly Gln Arg Val Met Ser Gly Gln
                50                55                60
Trp Leu Trp Gly Ile Ala Tyr Leu Leu Thr Ser Val Val Ala Gly Ala
65                70                75                80
Leu Leu Ala Trp Val Met
                85

```

&lt;210&gt; 1635

&lt;211&gt; 792

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1635

```

nngtcctttt ttatgaaccg gcggactcgg ttggcggtgt ggggcagggg gtggcggagc
60

```

aagatggcgg ctcatctgtc ctacggccga gtgaacctaa acgtgttgcg cgaggcgggtg  
 120  
 cgtcgcgagc tgcgcgagtt cctggacaag tgcgcaggaa gcaaggcaat agtttgggat  
 180  
 gaatacctaa ctggaccctt tggcctgatt gcacagtatt cactattgaa ggaacatgaa  
 240  
 gtggaaaaaa tgttcacact taaaggaaat cgtttgccgg cagctgatgt gaagaatata  
 300  
 attttttttg tcagaccag gctagagttg atggatataa tcgctgaaaa cgtgctcagt  
 360  
 gaagatagac gaggcccaac gagagatttt catattctgt ttgtgccacg ccgtagcctg  
 420  
 ttgtgcgaac agcggttgaa ggatctgggt gtcttgggat cctttattca caggaggag  
 480  
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 660  
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 720  
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 780  
 actcatgaat tc  
 792

&lt;210&gt; 1636

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1636

Met Ala Ala His Leu Ser Tyr Gly Arg Val Asn Leu Asn Val Leu Arg  
 1 5 10 15  
 Glu Ala Val Arg Arg Glu Leu Arg Glu Phe Leu Asp Lys Cys Ala Gly  
 20 25 30  
 Ser Lys Ala Ile Val Trp Asp Glu Tyr Leu Thr Gly Pro Phe Gly Leu  
 35 40 45  
 Ile Ala Gln Tyr Ser Leu Leu Lys Glu His Glu Val Glu Lys Met Phe  
 50 55 60  
 Thr Leu Lys Gly Asn Arg Leu Pro Ala Ala Asp Val Lys Asn Ile Ile  
 65 70 75 80  
 Phe Phe Val Arg Pro Arg Leu Glu Leu Met Asp Ile Ile Ala Glu Asn  
 85 90 95  
 Val Leu Ser Glu Asp Arg Arg Gly Pro Thr Arg Asp Phe His Ile Leu  
 100 105 110  
 Phe Val Pro Arg Arg Ser Leu Leu Cys Glu Gln Arg Leu Lys Asp Leu  
 115 120 125  
 Gly Val Leu Gly Ser Phe Ile His Arg Glu Glu Tyr Ser Leu Asp Leu  
 130 135 140  
 Ile Pro Phe Asp Gly Asp Leu Leu Ser Met Glu Ser Glu Gly Ala Phe  
 145 150 155 160  
 Lys Glu Cys Tyr Leu Glu Gly Asp Gln Thr Ser Leu Tyr His Ala Ala

```

          165          170          175
Lys Gly Leu Met Thr Leu Gln Ala Leu Tyr Gly Thr Ile Pro Gln Ile
          180          185          190
Phe Gly Lys Gly Glu Cys Ala Arg Val Arg Thr Gly Cys Phe Val Val
          195          200          205
Val Lys Glu Gly Pro Ser His Pro Lys Arg Glu Glu Arg Glu Ala
          210          215          220
Pro Tyr Lys Gln Ile Gln Leu Ile Leu Ile Ile Tyr Glu Tyr Cys Thr
          225          230          235          240
His Glu Phe

```

<210> 1637  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1637
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120
cgcggtgaca gctgcggcat cctcggcgcc tccgggtccg gcaagagcac cctgctcaat
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240
ttggcgetca ccccgacga actgtcggcg atccgcaact cagntnnaat ggttggttc
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cagagcttca acctgctgcc ggcctcagc gccctggaca acgtcgccct gccctg
357

```

<210> 1638  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1638
Xaa Met Met Thr Gln Thr Pro Ala His Pro Gly Leu Ile Ser Leu Gln
1      5      10      15
Gly Ile Gly Lys Arg Tyr Gln Leu Ala Gly Gln Lys Leu Ser Ile Leu
20     25     30
Asn Asp Val Cys Leu Ser Ile Ser Arg Gly Asp Ser Cys Gly Ile Leu
35     40     45
Gly Ala Ser Gly Ser Gly Lys Ser Thr Leu Leu Asn Ile Leu Gly Leu
50     55     60
Leu Asp Leu Pro Asn Ser Gly Gln Tyr His Phe Ala Gly His Asp Ile
65     70     75     80
Leu Ala Leu Thr Pro Asp Glu Leu Ser Ala Ile Arg Asn Ser Xaa Xaa
85     90     95
Met Val Val Phe Gln Ser Phe Asn Leu Leu Pro Arg Leu Ser Ala Leu
100    105    110
Asp Asn Val Ala Leu Pro Leu
115

```



<210> 1639  
 <211> 396  
 <212> DNA  
 <213> Homo sapiens

<400> 1639  
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 aaagttatcg ttatgggaca taagcgacca gatttagatg ctataggtgc agctatcgga  
 120  
 gtttcgcgct ttgcatcaat gaataattta gaggcattta tcgttcttaa tgattctgat  
 180  
 attgatccga cattacgtcg tggtatggat gagattgata agaaaccgga actaaaagaa  
 240  
 cgctttgtaa catcggtatga ggcttgggat atgatgactt ctaagacgac tgcgttgtt  
 300  
 gtagatacac ataaacctga aatggtctta gatgaaaatg tcttaaataa agcaaaccgc  
 360  
 aaagtagtca ttgatcatca tagacgtggc gaaact  
 396

<210> 1640  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 1640  
 Thr Arg Val Arg Ala Arg Val Ile Ser His Ala Leu Lys Asp Ile Leu  
 1 5 10 15  
 Thr Glu Gly Asp Lys Val Ile Val Met Gly His Lys Arg Pro Asp Leu  
 20 25 30  
 Asp Ala Ile Gly Ala Ala Ile Gly Val Ser Arg Phe Ala Ser Met Asn  
 35 40 45  
 Asn Leu Glu Ala Phe Ile Val Leu Asn Asp Ser Asp Ile Asp Pro Thr  
 50 55 60  
 Leu Arg Arg Val Met Asp Glu Ile Asp Lys Lys Pro Glu Leu Lys Glu  
 65 70 75 80  
 Arg Phe Val Thr Ser Asp Glu Ala Trp Asp Met Met Thr Ser Lys Thr  
 85 90 95  
 Thr Val Val Val Val Asp Thr His Lys Pro Glu Met Val Leu Asp Glu  
 100 105 110  
 Asn Val Leu Asn Lys Ala Asn Arg Lys Val Val Ile Asp His His Arg  
 115 120 125  
 Arg Gly Glu Thr  
 130

<210> 1641  
 <211> 376  
 <212> DNA  
 <213> Homo sapiens

<400> 1641  
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tggccaaacg aactgatgga tgggctcttg gagtgggaga gactgggcag aagctgtgtg  
 120  
 ggggtgggtga ctcccaacct aaagaaccca ctgagacata tgtggcttcc ctcttcacc  
 180  
 ttcattgcct ctttccgtct agatgctggc aaggggggac ttggtggaca aagagagcta  
 240  
 ctattcattc aggagctatg ttacaccagt cactttacat gtgccacttg ctctgggtta  
 300  
 aactgtgcct cccctcactc atatgttgaa gtcctaacc ctaactacctc agaatgggac  
 360  
 gttatttgga aaaaag  
 376

<210> 1642

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1642

Met	Asp	Gly	Leu	Leu	Glu	Trp	Glu	Arg	Leu	Gly	Arg	Ser	Cys	Val	Gly
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Trp	Val	Thr	Pro	Asn	Leu	Lys	Asn	Pro	Leu	Arg	His	Met	Trp	Leu	Pro
			20					25					30		
Ser	Ser	Thr	Phe	Ile	Ala	Ser	Phe	Arg	Leu	Asp	Ala	Gly	Lys	Gly	Gly
		35					40					45			
Leu	Gly	Gly	Gln	Arg	Glu	Leu	Leu	Phe	Ile	Gln	Glu	Leu	Cys	Tyr	Thr
		50				55					60				
Ser	His	Phe	Thr	Cys	Ala	Thr	Cys	Ser	Gly	Leu	Asn	Cys	Ala	Ser	Pro
65					70					75				80	
His	Ser	Tyr	Val	Glu	Val	Leu	Thr	Leu	Thr	Thr	Ser	Glu	Trp	Asp	Val
			85					90						95	
Ile	Trp	Lys	Lys												
			100												

<210> 1643

<211> 494

<212> DNA

<213> Homo sapiens

<400> 1643

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 120  
 ggccagaatc ccagatcta ggtccaagag ggggctccat gacctcccca tgctgctcct  
 180  
 ctgcttgat ccaggatata agaaaggagg ggcacacact gtgggggaac tctgggggtcc  
 240  
 cctgtgtgca tcagcgagtc ccgggtctgc cccaccagga tgcaaagggc ctggctgctc  
 300  
 cagcccatg ctcacagccc tataagtgca cgatggcacc ctatatcatc taagcggggc  
 360  
 tgtgctcct gaggttttag ggacaccaga atgagcccc ctcggcggag tctggctctg  
 420

gggtgtgtgga gatgccacct gggacgggaa ccccaggtgc atggagcccc actgcagaca  
 480  
 ccattccccg tgtg  
 494

<210> 1644  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 1644  
 Met Gly Leu Glu Gln Pro Gly Pro Leu His Pro Gly Gly Ala Asp Pro  
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 Gly Leu Ala Asp Ala His Arg Gly Pro Gln Ser Ser Pro Thr Val Cys  
 20 25 30  
 Ala Pro Pro Phe Leu Tyr Pro Gly Ser Lys Gln Arg Ser Ser Met Gly  
 35 40 45  
 Arg Ser Trp Ser Pro Leu Leu Asp Leu Asp Leu Gly Ile Leu Ala Pro  
 50 55 60  
 Gly Phe Arg Gly Pro Gly Gly Ala His Thr Phe Ser Cys Thr Cys Ser  
 65 70 75 80  
 Gln Thr Leu Gly Ser Thr Ser Leu Arg Tyr Gln Lys Gly Ser Trp Val  
 85 90 95  
 Pro Met Glu Phe Trp Lys Leu  
 100

<210> 1645  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 1645  
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 aggagccggg ctctgaaaca cgtggccctt ggaaggaact tcaacgttcg gtgcaaggag  
 120  
 accctggacg atgtcctgca tcggatagcc cagctaatagc aggatgacga ctgtcctttg  
 180  
 cagtcaactat ccgtggctga gtcgcggttg aagcaggggtg ccagcatcct gatccgggct  
 240  
 ttgggcacca atcctaaact gacagcgctg gatatcagtg gcaatgccat aggggatgct  
 300  
 ggggccaaga tgctagccaa ggctctacgc  
 330

<210> 1646  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 1646  
 Xaa Asp Leu Ser Asp Asn Gly Phe Gly Ser Asp Met Val Thr Leu Val  
 1 5 10 15  
 Leu Ala Ile Gly Arg Ser Arg Ser Leu Lys His Val Ala Leu Gly Arg

```

      20      25      30
Asn Phe Asn Val Arg Cys Lys Glu Thr Leu Asp Asp Val Leu His Arg
      35      40      45
Ile Ala Gln Leu Met Gln Asp Asp Asp Cys Pro Leu Gln Ser Leu Ser
      50      55      60
Val Ala Glu Ser Arg Leu Lys Gln Gly Ala Ser Ile Leu Ile Arg Ala
      65      70      75      80
Leu Gly Thr Asn Pro Lys Leu Thr Ala Leu Asp Ile Ser Gly Asn Ala
      85      90      95
Ile Gly Asp Ala Gly Ala Lys Met Leu Ala Lys Ala Leu Arg
      100      105      110

```

&lt;210&gt; 1647

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1647

```

aggccgctcg gtgatccgcg gcggcggcag cggcgcttcc tgctaggacc ggccggggcc
60
gtaccggagg ctggggctcc accgacctc ctccacccc ctccactca cctctgggg
120
cgcgactgcg cagggcgggg ccggccgaac catgggccgc ggtgtgggct aagctggtg
180
ccccggcttt agactggacc ccacaatgtt tgcagagatg ttcaggcacg cgggagctga
240
ttacacacaa tgaatggggg caatgagagc agtggagcag acagagctgg gggccctgtg
300
gccacatctg tccccatcgg ctggcagcgc tgtgtgcgag aggggtgctgt gctctacatc
360
agtccaagtg gcacagagct gtcttccttg gagcaaacc ggagctacct cctcagcgat
420
gggacctgca agtgcggtct ggagtgtcca cttaatgtcc ccaaggtttt caactttgac
480
cctttggccc cggtgacccc g
501

```

&lt;210&gt; 1648

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1648

```

Met Asn Gly Gly Asn Glu Ser Ser Gly Ala Asp Arg Ala Gly Gly Pro
1      5      10      15
Val Ala Thr Ser Val Pro Ile Gly Trp Gln Arg Cys Val Arg Glu Gly
      20      25      30
Ala Val Leu Tyr Ile Ser Pro Ser Gly Thr Glu Leu Ser Ser Leu Glu
      35      40      45
Gln Thr Arg Ser Tyr Leu Leu Ser Asp Gly Thr Cys Lys Cys Gly Leu
      50      55      60
Glu Cys Pro Leu Asn Val Pro Lys Val Phe Asn Phe Asp Pro Leu Ala
65      70      75      80
Pro Val Thr Pro

```

<210> 1649  
 <211> 441  
 <212> DNA  
 <213> Homo sapiens

<400> 1649  
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 60  
 accaactcac ggttgctcgc catcttctcc aacaaggatga tccggcgcta tccggccttt  
 120  
 gaagacttcc acgggatgga agaatgcata gatcagatcg tttcgtattt ccgccacgcc  
 180  
 gcccaaggcc tggaagagaa gaaacagatc ctttacctgc tgggccccgt cggcggcggt  
 240  
 aaatcgtoccc tggccgaaaa gctgaaacag ctgatcgaga aggtccccctt ctacgccatc  
 300  
 aagggtctgc cgggtcttca gtcgcccctg ggggtgttca acgccactga agacggcgcg  
 360  
 atcctcgagg aagacttcgg gattccacgg cgttacctga acaccatcat gtcgcccctg  
 420  
 gcgaccaagc gcctggccga a  
 441

<210> 1650  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<400> 1650  
 Ala Ser Ala Ala Glu Arg Val Leu Leu Ala Ile Gly Glu Pro Glu Leu  
 1 5 10 15  
 Leu Asp Thr Ser Thr Asn Ser Arg Leu Ser Arg Ile Phe Ser Asn Lys  
 20 25 30  
 Val Ile Arg Arg Tyr Pro Ala Phe Glu Asp Phe His Gly Met Glu Glu  
 35 40 45  
 Cys Ile Asp Gln Ile Val Ser Tyr Phe Arg His Ala Ala Gln Gly Leu  
 50 55 60  
 Glu Glu Lys Lys Gln Ile Leu Tyr Leu Leu Gly Pro Val Gly Gly Gly  
 65 70 75 80  
 Lys Ser Ser Leu Ala Glu Lys Leu Lys Gln Leu Ile Glu Lys Val Pro  
 85 90 95  
 Phe Tyr Ala Ile Lys Gly Ser Pro Val Phe Glu Ser Pro Leu Gly Leu  
 100 105 110  
 Phe Asn Ala Thr Glu Asp Gly Ala Ile Leu Glu Glu Asp Phe Gly Ile  
 115 120 125  
 Pro Arg Arg Tyr Leu Asn Thr Ile Met Ser Pro Trp Ala Thr Lys Arg  
 130 135 140  
 Leu Ala Glu  
 145

<210> 1651  
 <211> 408

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1651

ncccgccgcat cctccggcat cctgggtatc gctccctcga aggaatccgg agcccgactg  
60  
cgccgcgagc ttccgaacg cctcgaggat tacgccgcac aaacttccat ggtgcgttcc  
120  
gtacactccc tcgcattcgc gttgctgcgc acagcggccg aggaggagct gcgccttatt  
180  
accggtgcgg acnaagacgc cgttatccgc gagctgctca cgggccaagc agaagacgga  
240  
catggctcgt ggcccgcgga gatgcgcccc gcgtggaatn natgtgggct ttcgcggcag  
300  
ctgcgcgatt tccttttgcg ttccattgaa cgcggcctgg gaccgggtga cctagagagc  
360  
ctcggtgccg agcacggccg ccccatgtgg tctgcggcgg gtgaattc  
408

&lt;210&gt; 1652

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1652

Xaa	Ala	Asp	Pro	Ser	Gly	Ile	Leu	Val	Ile	Ala	Pro	Ser	Lys	Glu	Ser
1			5					10					15		
Gly	Ala	Arg	Leu	Arg	Arg	Glu	Leu	Ser	Glu	Arg	Leu	Glu	Asp	Tyr	Ala
			20				25					30			
Ala	Gln	Thr	Ser	Met	Val	Arg	Ser	Val	His	Ser	Leu	Ala	Phe	Ala	Leu
			35				40					45			
Leu	Arg	Thr	Ala	Ala	Glu	Glu	Glu	Leu	Arg	Leu	Ile	Thr	Gly	Ala	Asp
			50				55				60				
Xaa	Asp	Ala	Val	Ile	Arg	Glu	Leu	Leu	Thr	Gly	Gln	Ala	Glu	Asp	Gly
65					70				75					80	
His	Gly	Ser	Trp	Pro	Ala	Glu	Met	Arg	Pro	Ala	Trp	Asn	Xaa	Cys	Gly
				85					90					95	
Leu	Ser	Arg	Gln	Leu	Arg	Asp	Phe	Leu	Leu	Arg	Ser	Ile	Glu	Arg	Gly
			100						105				110		
Leu	Gly	Pro	Gly	Asp	Leu	Glu	Ser	Leu	Gly	Ala	Glu	His	Gly	Arg	Pro
			115				120						125		
Met	Trp	Ser	Ala	Ala	Gly	Glu	Phe								
			130				135								

&lt;210&gt; 1653

&lt;211&gt; 398

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1653

ccagcctctc tccgaccgcg tcctttcttcc ggccatacgg cacccaatgt cgcgtcacca  
60  
tcacccgcgc acatggccat cgctccaccg gacgagttga gtgacaagat ccggtgcatt  
120

ctgcgcaccc ttgaacctgg tgacagtgtg aaggagattc tcaacacgtc gcgtgtcgtc  
 180  
 ggcatcgacg tccagagcag cctgcttatt gctgggtgctc agcatctgta cttgttggac  
 240  
 gattacttcc agcgtccgaa cggtgaaatc gtcaatgtct gggaagctcc gccacacgag  
 300  
 cgcgatgcct tgatcgtggc ggccgggtgc gcacaggtgg cacaagcag cacacccgtg  
 360  
 cagatatggc gctgggaaca gctccgactt tgtctaga  
 398

<210> 1654

<211> 132

<212> PRT

<213> Homo sapiens

<400> 1654

Pro	Ala	Ser	Leu	Arg	Pro	Arg	Pro	Ser	Ser	Gly	His	Thr	Ala	Pro	Asn
1				5					10					15	
Val	Ala	Ser	Pro	Ser	Pro	Ala	His	Met	Ala	Ile	Ala	Pro	Pro	Asp	Glu
			20					25					30		
Leu	Ser	Asp	Lys	Ile	Arg	Cys	Ile	Leu	Arg	Thr	Leu	Glu	Pro	Gly	Asp
		35				40					45				
Ser	Val	Lys	Glu	Ile	Leu	Asn	Thr	Ser	Arg	Val	Val	Gly	Ile	Asp	Val
	50				55					60					
Gln	Ser	Ser	Leu	Leu	Ile	Ala	Gly	Ala	Gln	His	Leu	Tyr	Leu	Leu	Asp
65				70					75					80	
Asp	Tyr	Phe	Gln	Arg	Pro	Asn	Gly	Glu	Ile	Val	Asn	Val	Trp	Glu	Ala
			85					90					95		
Pro	Pro	His	Glu	Arg	Asp	Ala	Leu	Ile	Val	Ala	Ala	Gly	Val	Ala	Gln
		100				105						110			
Val	Ala	Gln	Ser	Ser	Thr	Pro	Val	Gln	Ile	Trp	Arg	Trp	Glu	Gln	Leu
	115					120						125			
Arg	Leu	Cys	Leu												
	130														

<210> 1655

<211> 1115

<212> DNA

<213> Homo sapiens

<400> 1655

nccctgacct gacctgtcct cgccatggcc gaggccgcct ccggcgccgg gggcacgtcc  
 60  
 ctggagggcg agcgtggcaa gagggccccc cgggagggcg agcctgcagc cccggcgctcc  
 120  
 ggagttcttg ataagctttt cggaagcgg ctctgcagg ctggtcgcta cctggtgtcc  
 180  
 cacaaggcgt ggatgaagac ggtgcctaca gagaactgcg acgtgctgat gaccttccca  
 240  
 gacacgaccg atgaccacac gctgctatgg ctgctgaacc acatccgcgt gggcattccc  
 300  
 gagctcatcg tgcaagtccg ccaccaccgc cacacgcgtg cctacgcctt ctttgtcacc  
 360

gccacgtatg agagcctact ccgagggggcc gacgagctgg gtctgcgcaa agcagtgaag  
 420  
 gccgagtttg gcggggggcac ccgcggtctc tcctgcgagg aggactttat ctatgagaat  
 480  
 gtggagagcg agctacgctt cttcacctcc caggaacgcc agagcatcat ccgcttctgg  
 540  
 ctgcagaatt tgcgtgccaa gcagggagaa gcactccaca acgtgcgctt cctggaggac  
 600  
 cagccaatca tcccggagct ggcagcacgt gggatcatcc agcaggtgtt ccctgtccac  
 660  
 gagcagcgta ttctgaaccg cctcatgaag tcatgggtgc aggccgtgtg tgaaaaccag  
 720  
 cctctagatg acatctgtga ttactttggt gtgaaaattg ccatgtactt cgcctggctg  
 780  
 ggcttctaca cgtcggctat ggtataccca gctgtcttcg ggtctgtcct gtacacattc  
 840  
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 900  
 atctggtcga cgctgttcct ataggaatgg aagcgtatag gggctgagct gggatataat  
 960  
 tgggggacgc tggactcatc ctgggaagcc gtggaggagc caccgccccca gttcaggtgc  
 1020  
 gtgcgacgta tcatcccat cactcggggc gaggagttct actacccgcc ctggaagcgg  
 1080  
 ctgctcttcc agctgcttgt tagcctccgc ctgtg  
 1115

&lt;210&gt; 1656

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1656

Met Ala Glu Ala Ala Ser Gly Ala Gly Gly Thr Ser Leu Glu Gly Glu  
 1 5 10 15  
 Arg Gly Lys Arg Pro Pro Pro Glu Gly Glu Pro Ala Ala Pro Ala Ser  
 20 25 30  
 Gly Val Leu Asp Lys Leu Phe Gly Lys Arg Leu Leu Gln Ala Gly Arg  
 35 40 45  
 Tyr Leu Val Ser His Lys Ala Trp Met Lys Thr Val Pro Thr Glu Asn  
 50 55 60  
 Cys Asp Val Leu Met Thr Phe Pro Asp Thr Thr Asp Asp His Thr Leu  
 65 70 75 80  
 Leu Trp Leu Leu Asn His Ile Arg Val Gly Ile Pro Glu Leu Ile Val  
 85 90 95  
 Gln Val Arg His His Arg His Thr Arg Ala Tyr Ala Phe Phe Val Thr  
 100 105 110  
 Ala Thr Tyr Glu Ser Leu Leu Arg Gly Ala Asp Glu Leu Gly Leu Arg  
 115 120 125  
 Lys Ala Val Lys Ala Glu Phe Gly Gly Gly Thr Arg Gly Phe Ser Cys  
 130 135 140  
 Glu Glu Asp Phe Ile Tyr Glu Asn Val Glu Ser Glu Leu Arg Phe Phe  
 145 150 155 160  
 Thr Ser Gln Glu Arg Gln Ser Ile Ile Arg Phe Trp Leu Gln Asn Leu



```

                165                170                175
Arg Ala Lys Gln Gly Glu Ala Leu His Asn Val Arg Phe Leu Glu Asp
                180                185                190
Gln Pro Ile Ile Pro Glu Leu Ala Ala Arg Gly Ile Ile Gln Gln Val
                195                200                205
Phe Pro Val His Glu Gln Arg Ile Leu Asn Arg Leu Met Lys Ser Trp
                210                215                220
Val Gln Ala Val Cys Glu Asn Gln Pro Leu Asp Asp Ile Cys Asp Tyr
225                230                235                240
Phe Gly Val Lys Ile Ala Met Tyr Phe Ala Trp Leu Gly Phe Tyr Thr
                245                250                255
Ser Ala Met Val Tyr Pro Ala Val Phe Gly Ser Val Leu Tyr Thr Phe
                260                265                270
Thr Glu Ala Asp Gln Thr Ser Arg Asp Val Ser Cys Val Val Phe Ala
                275                280                285
Leu Phe Asn Val Ile Trp Ser Thr Leu Phe Leu
                290                295

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&lt;210&gt; 1657

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1657

```

tgtagaggct cgaggtcatc cggaccatgt ggtccaggac gcccccgctcc tccggggcccc
60
gcacggagac gcggcgctcag cacggacagc acgcagtctg tgagcctctg caggcagttc
120
ttggagcccc cgggcttccc gcgcgcttc agggggcggg cggcagctcg ggccggtact
180
tctcccaaaa ctgctccggg caggggcgct ccagcagcct ctgcatgaga cggacggcat
240
ccacgcggcc cgtgtaagtg gccactcct gcggcgacat tccacggcgg gggtaccctc
300
gcgtggacat ccgccctgc tagcatcagg gct
333

```

&lt;210&gt; 1658

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1658

```

Met Leu Ala Gly Ala Asp Val His Ala Arg Val Pro Pro Pro Trp Asn
1      5      10      15
Val Ala Ala Gly Val Gly His Leu His Gly Pro Arg Gly Cys Arg Pro
20     25     30
Ser His Ala Glu Ala Ala Gly Ala Pro Leu Pro Gly Ala Val Leu Gly
35     40     45
Glu Val Pro Ala Arg Ala Ala Ala Arg Pro Leu Lys Arg Arg Gly Lys
50     55     60
Pro Ala Gly Ser Lys Asn Cys Leu Gln Arg Leu Thr Asp Cys Val Leu
65     70     75     80
Ser Val Leu Thr Pro Arg Leu Arg Ala Gly Pro Gly Gly Arg Gly Arg

```

<400> 1661

acgcgtcgat gatcatggag aagacgcggg ccggctcctt gcctgtgacc ttcttgtaca  
 60  
 gctgcgggta gtagagctcc aggtctctga ggaaggccac gtagcccttg tggccggtec  
 120  
 gctgcaggat gtccaggagc acaccactt tccgtttgcg gatgaccagg ttgggggtcg  
 180  
 tgagcacctg ctccatca tcagggttca ggaccttgca ctgccgcagg taagggtga  
 240  
 tgcgtgaggg gtcgatgacc gaggtgagcg tcaccggaa gccctccagg acgttccagc  
 300  
 actcgtcatc gttctcgtag tccgacatgg cctcagcagg caggctgggg agtgtggggc  
 360  
 agtgctgaga gcgatgccg ctcttgcccc caccggggcc cagctccac tccttctcag  
 420  
 acgctggggc agggctctcg tcagggcatc gagggggatc agcccaggcg catccaggag  
 480  
 aggtgcccag ctccgtgtcc catcccacgc ttgatcgtg catg  
 524

&lt;210&gt; 1662

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1662

Met	Gln	Arg	Ser	Ser	Val	Gly	Trp	Asp	Thr	Glu	Leu	Gly	Thr	Ser	Pro
1				5					10					15	
Gly	Cys	Ala	Trp	Ala	Asp	Pro	Pro	Arg	Cys	Pro	Asp	Glu	Ser	Pro	Gly
			20					25					30		
Pro	Ala	Ser	Glu	Lys	Glu	Trp	Glu	Leu	Gly	Pro	Gly	Gly	Gly	Arg	Ser
		35					40					45			
Arg	His	Arg	Ser	Gln	His	Cys	Pro	Thr	Leu	Pro	Ser	Leu	Pro	Ala	Glu
		50				55					60				
Ala	Met	Ser	Asp	Tyr	Glu	Asn	Asp	Asp	Glu	Cys	Trp	Asn	Val	Leu	Glu
65					70					75				80	
Gly	Phe	Arg	Val	Thr	Leu	Thr	Ser	Val	Ile	Asp	Pro	Ser	Arg	Ile	Thr
			85					90					95		
Pro	Tyr	Leu	Arg	Gln	Cys	Lys	Val	Leu	Asn	Pro	Asp	Asp	Glu	Glu	Gln
			100					105					110		
Val	Leu	Ser	Asp	Pro	Asn	Leu	Val	Ile	Arg	Lys	Arg	Lys	Val	Gly	Val
			115				120					125			
Leu	Leu	Asp	Ile	Leu	Gln	Arg	Thr	Gly	His	Lys	Gly	Tyr	Val	Ala	Phe
		130				135					140				
Leu	Glu	Ser	Leu	Glu	Leu	Tyr	Tyr	Pro	Gln	Leu	Tyr	Lys	Lys	Val	Thr
145					150					155				160	
Gly	Lys	Glu	Pro	Ala	Arg	Val	Phe	Ser	Met	Ile	Ile	Asp	Ala		
			165						170						

&lt;210&gt; 1663

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1663

nnagtacttg tcatgattac gcctagtttg ggtatctatt tctctcagcg ttctcagatc  
 60  
 tcccgaaccc aagacgacga ggctcggaca cgcgcttcta tctcgaccct tcaagacgag  
 120  
 gtcaagaggt ggacgatcc cgactacgtc cgtgctcagg cgcgctccca gctcggctgg  
 180  
 gtgatgccgg gcgaaactgg gtatcaggtc attggagaaa acggttaaggc cattggatcg  
 240  
 acgacttctt tggacgaaaa agatccggcg agtgaagcca gcgctgacgc tcggtggtgg  
 300  
 caagaggctt gcggatcagt c  
 321

<210> 1664

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1664

Xaa	Val	Leu	Val	Met	Ile	Thr	Pro	Ser	Leu	Gly	Ile	Tyr	Phe	Ser	Gln
1				5					10					15	
Arg	Ser	Gln	Ile	Ser	Arg	Thr	Gln	Asp	Asp	Glu	Ala	Arg	Thr	Arg	Ala
		20						25					30		
Ser	Ile	Ser	Thr	Leu	Gln	Asp	Glu	Val	Lys	Arg	Trp	His	Asp	Pro	Asp
		35				40						45			
Tyr	Val	Arg	Ala	Gln	Ala	Arg	Ser	Gln	Leu	Gly	Trp	Val	Met	Pro	Gly
	50					55					60				
Glu	Thr	Gly	Tyr	Gln	Val	Ile	Gly	Glu	Asn	Gly	Lys	Val	Ile	Gly	Ser
65				70					75					80	
Thr	Thr	Ser	Leu	Asp	Glu	Lys	Asp	Pro	Ala	Ser	Glu	Ala	Ser	Ala	Asp
			85					90						95	
Ala	Arg	Trp	Trp	Gln	Glu	Ala	Cys	Gly	Ser	Val					
			100					105							

<210> 1665

<211> 431

<212> DNA

<213> Homo sapiens

<400> 1665

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 ggcccgaacta tctccggtgg tgaagtactc atgcaacgcg cttttgcgtg gaacttgctc  
 120  
 atgagtgccta agtcgatggg cattcatacc tgtatcgata cctccggttt tttgggggct  
 180  
 gcggcaacag atgacttttt agagtctgtt gatttggtgt tgctcgacgt caaatcggga  
 240  
 gatgaagaaa tctaccgtgc cctcaccggc agagcgttgc aacctaccat cgattttggt  
 300  
 gatcgtctca ccgcgctcgg taaagaaatc tggattcggg tcgttggtgg ccccggtatc  
 360  
 accgactcgg tagagaacgt ggaaaagggt gccgatatcg tccgcagatg gcgcaccgct  
 420

gtttcacgcg t  
431

<210> 1666  
<211> 143  
<212> PRT  
<213> Homo sapiens

<400> 1666  
Ala Ser Glu Leu Ile Lys Lys Leu Lys Arg Tyr Lys Met Val Leu Arg  
1 5 10 15  
Ser Thr Gly Gly Gly Pro Thr Ile Ser Gly Gly Glu Val Leu Met Gln  
20 25 30  
Arg Ala Phe Ala Trp Asn Leu Leu Met Ser Ala Lys Ser Met Gly Ile  
35 40 45  
His Thr Cys Ile Asp Thr Ser Gly Phe Leu Gly Ala Ala Thr Asp  
50 55 60  
Asp Phe Leu Glu Ser Val Asp Leu Val Leu Leu Asp Val Lys Ser Gly  
65 70 75 80  
Asp Glu Glu Ile Tyr Arg Ala Leu Thr Gly Arg Ala Leu Gln Pro Thr  
85 90 95  
Ile Asp Phe Gly Asp Arg Leu Thr Ala Leu Gly Lys Glu Ile Trp Ile  
100 105 110  
Arg Phe Val Val Val Pro Gly Tyr Thr Asp Ser Val Glu Asn Val Glu  
115 120 125  
Lys Val Ala Asp Ile Val Arg Arg Trp Arg Thr Ala Val Ser Arg  
130 135 140

<210> 1667  
<211> 370  
<212> DNA  
<213> Homo sapiens

<400> 1667  
tccgctgaga ccagcgttgg tgacttccca ggtgagactg tccgcaccat ggccaagatc  
60  
gttgagtcta ctgaggcccg tggcttggac aagatcgcca agatcgactg ggatccgcac  
120  
accaccagtg gcatcatgtc gaaggcagct gctgagatcg ctgagcgcgc cgaggccaag  
180  
ttcatcgtgg cctttaccaa gtccggtgac accgcccgtc gtatcgctcg tctgcgtccg  
240  
agcaccgccg tcatcgtttt cacctctgat gagaccacga ccaagaccct cgcttgggtc  
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360  
gttaacgcgt  
370

<210> 1668  
<211> 123  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 1668

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Ser Ala Glu Thr Ser Val Gly Asp Phe Pro Gly Glu Thr Val Arg Thr
 1           5           10           15
Met Ala Lys Ile Val Glu Ser Thr Glu Ala Arg Gly Leu Asp Lys Ile
      20           25           30
Ala Lys Ile Asp Trp Asp Pro His Thr Thr Ser Gly Ile Met Ser Lys
      35           40           45
Ala Ala Ala Glu Ile Ala Glu Arg Ala Glu Ala Lys Phe Ile Val Ala
      50           55           60
Phe Thr Lys Ser Gly Asp Thr Ala Arg Arg Ile Ala Arg Leu Arg Pro
65           70           75           80
Ser Thr Pro Leu Ile Val Phe Thr Ser Asp Glu Thr Thr Thr Lys Thr
      85           90           95
Leu Ala Trp Val Trp Gly Ala His Ala Val Val Thr Pro Val Phe Lys
      100          105          110
Asn Ala Glu Leu Tyr Arg Trp Val Asn Ala
      115          120

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&lt;210&gt; 1669

&lt;211&gt; 1491

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1669

```

ggatcctgca gtggtgatct gtcacgtca cgtcacagaa ctgaacatgg aaatgaacaa
60
cgaaaactcc accccttct caaacgagtt attcctagct ccgccccag tccttgctc
120
tcccagcctt ggtggttaatt agcttgaaag tgggaacgag agtgcggtcc gcaaagaaag
180
gacttctggt tagacactga aatacaaaaca gactgccaac gagctctggg caaagctgcc
240
ccgtcttctt ttttcgaaag accctcaaaa actgcctttc cttctgctac caaaacttgg
300
gccctagaaa gtggctgcgg agtggagcag atggacatca ctgagaatgg tagaggaggg
360
gctgtgtttt ctgaggggga gtcattggcag cttgtgctgg gggccaggaa gggaaaaaac
420
caatctggca ttcaggttgt ggaaggcaaa gtgaaacaag aagtcatttg ggaaaatatt
480
atattataaa cacatagaat aatatgtaca cgctcatata catcccaaag agaagcctca
540
aggagtccg tttcttctca aaagaaactt cactatgata aagcattcct atagtgggaa
600
ttaactacaa tgaaataatt taacaatttc atttatgcta tatctgtgtc cactacagag
660
tctacggtga aggctgtgtg gagcgagtgt gtctagtgga ctggaacacc aacgcgttct
720
tcaaaaatag gcaatgacct gtttttttct attcacattt acaatagcta cacagtgtg
780
aaacgcagac tgaaaaatca aatggcagga cgatggaact gtcgtcaagg ttctcagact
840
tgtggcttct gcacctgtta tacttttgga tacgagttag ctccacttag cttcgttaag
900

```

attagaaatt tccatgaaac acttaccac atataaattc tgtgtaaagc tttatTTTTT  
 960  
 tccccaccta ctttaatttt ttttaaaaag tgaaataaga ggaaaaactc ttataaaata  
 1020  
 taaggtttaa catacgagag agcgaggaac accccggagg ctgccggtgc gtgtggcttc  
 1080  
 atgtttctgt gctacatgag tctagtgtcc tcatcttcca ttgtgacaac ctttctcccc  
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 1200  
 gctgtggttt ggttgactac atttgactac caccactgaa ggcgggcgac gtctgaagcg  
 1260  
 gctggatacc gcaacgatgg aaaatcaggc gaggtactag cgtggagggc cgggctgcca  
 1320  
 ggtcaaggtc gtctgggttc tcaggagcca gtctgtgcca cagaaccatc ggcagctgcc  
 1380  
 ttcgtaaggc acctcgtct ggcattcgga aaaccacccc atcttgccag agtccttgg  
 1440  
 tccttgggta gcaaaagccg tatgcatct aaatcaagct ttcaatcatg a  
 1491

<210> 1670

<211> 132

<212> PRT

<213> Homo sapiens

<400> 1670

Met	Pro	Asp	Trp	Phe	Phe	Pro	Phe	Leu	Ala	Pro	Ser	Thr	Ser	Cys	His
1				5				10						15	
Asp	Ser	Pro	Ser	Glu	Asn	Thr	Ala	Pro	Pro	Leu	Pro	Phe	Ser	Val	Met
			20					25					30		
Ser	Ile	Cys	Ser	Thr	Pro	Gln	Pro	Leu	Ser	Arg	Ala	Gln	Val	Leu	Val
		35					40					45			
Ala	Glu	Gly	Lys	Ala	Val	Phe	Glu	Gly	Leu	Ser	Lys	Lys	Glu	Asp	Gly
	50					55					60				
Ala	Ala	Leu	Pro	Arg	Ala	Arg	Trp	Gln	Ser	Val	Cys	Ile	Ser	Val	Ser
65					70					75				80	
Asn	Gln	Lys	Ser	Phe	Leu	Cys	Gly	Pro	His	Ser	Arg	Ser	His	Phe	Gln
				85					90					95	
Ala	Asn	Tyr	His	Gln	Gly	Trp	Glu	Arg	Gln	Gly	Leu	Gly	Ala	Glu	Leu
			100					105					110		
Gly	Ile	Thr	Arg	Leu	Arg	Arg	Gly	Trp	Ser	Phe	Arg	Cys	Ser	Phe	Pro
		115					120					125			
Cys	Ser	Val	Leu												
			130												

<210> 1671

<211> 432

<212> DNA

<213> Homo sapiens

<400> 1671

gcgcgccggg gcgggaggac gccagtcgtc ttcccgcgcc tcaccacgac acgaccatta  
 60

tcgcgacgaa ggaagcccat ggctgaaacc acatcgccgg cacagcggaa acccacggcg  
 120  
 gcatccccga tgaagccggt gtcgcggttc ggggacacga ttttcgctgg cgctctgctg  
 180  
 gttattgcc a tagccctggc cgtcatcgtc atcctgatgt tcgtcttcct catgaagacg  
 240  
 gcagccccga cgttgttggc taacaccgat aactttttca cgtccccggc ttggacaacg  
 300  
 gatcagaacc cgccggcctt tggatatccag gccctgctat ggacgacagt catctcatcc  
 360  
 ctgcttgccc tgctcatcgc agtgccgctc tcgggtgggca tcgctctgtt tatcaccacg  
 420  
 ctgcgacctt gg  
 432

<210> 1672  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 1672  
 Ala Arg Arg Gly Gly Arg Thr Pro Val Val Phe Pro Pro Leu Thr Thr  
 1 5 10 15  
 Thr Arg Pro Leu Ser Arg Arg Arg Lys Pro Met Ala Glu Thr Thr Ser  
 20 25 30  
 Pro Ala Gln Arg Lys Pro Thr Ala Ala Ser Arg Met Lys Pro Val Ser  
 35 40 45  
 Arg Val Gly Asp Thr Ile Phe Ala Gly Ala Ser Ser Val Ile Ala Ile  
 50 55 60  
 Ala Leu Ala Val Ile Val Ile Leu Met Phe Val Phe Leu Met Lys Thr  
 65 70 75 80  
 Ala Ala Pro Thr Leu Leu Ala Asn Thr Asp Asn Phe Phe Thr Ser Arg  
 85 90 95  
 Ala Trp Thr Thr Asp Gln Asn Pro Pro Ala Phe Gly Ile Gln Ala Leu  
 100 105 110  
 Leu Trp Thr Thr Val Ile Ser Ser Leu Leu Ala Leu Leu Ile Ala Val  
 115 120 125  
 Pro Leu Ser Val Gly Ile Ala Leu Phe Ile Thr Gln Leu Ala Pro Arg  
 130 135 140

<210> 1673  
 <211> 401  
 <212> DNA  
 <213> Homo sapiens

<400> 1673  
 tcgcgagcac actccagcct ctggggcgctc tgccagggcc tctgtgtttt gatatactct  
 60  
 gacctggcag tgaagctgct gatgaatgca cgacaaagac cagtttgctc cgtaacccca  
 120  
 ggctcccagc gtctttttcca tgagccaaag gcctggtcct ggaggggggt gccctgcagc  
 180  
 tctgctggcc ttcttccagg ggagttcatt gctgggggtg gccctgcagg gacctccact  
 240



gtgctgggga ggggaagaag aaggatgcaa cagggggagg ggagaatttg agaaaatagg  
 300  
 atgcaaattc tccacttggtg aataaagaaa tagagagcca ttgctaagaa ctatgtttac  
 360  
 gcagggttag tgctgggacc cagaaccagt caactggttt t  
 401

<210> 1674

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1674

Met	Ala	Leu	Tyr	Phe	Phe	Ile	His	Lys	Trp	Arg	Ile	Cys	Ile	Leu	Phe
1				5					10				15		
Ser	Gln	Ile	Leu	Pro	Ser	Pro	Cys	Cys	Ile	Leu	Leu	Leu	Pro	Leu	Pro
			20					25				30			
Ser	Thr	Val	Glu	Val	Pro	Ala	Gly	Pro	Pro	Pro	Ala	Met	Asn	Ser	Pro
		35					40				45				
Gly	Arg	Arg	Pro	Ala	Glu	Leu	Gln	Gly	Thr	Pro	Leu	Gln	Asp	Gln	Ala
	50				55				60						
Phe	Gly	Ser	Trp	Lys	Arg	Arg	Trp	Glu	Pro	Gly	Val	Thr	Glu	Gln	Thr
65				70				75				80			
Gly	Leu	Cys	Arg	Ala	Phe	Ile	Ser	Ser	Phe	Thr	Ala	Arg	Ser	Glu	Tyr
			85					90				95			
Ile	Lys	Thr	Gln	Arg	Pro	Trp	Gln	Thr	Pro	Gln	Arg	Leu	Glu	Cys	Ala
			100				105					110			

Arg

<210> 1675

<211> 500

<212> DNA

<213> Homo sapiens

<400> 1675

gccggcgcac ccacctggga cgtggtgaaa tcggcaaaac tcacctcttt agctacctgc  
 60  
 gcgccaaccg caggggcagc ctccacacag ccctctagag cgctgctgga cagaatggct  
 120  
 tgattgtttg gcatgctctc aggatacccg tttagccagg aaacaccggt aggcttgcta  
 180  
 ctatgcgagc agccgacgca cgggtagagg gaattccac cacagtcctt cgcactccac  
 240  
 ccgcacacgc cctgggaacc gtcaccgcg gtaccaccgg gtcaatcggc tccgcaaatg  
 300  
 cgaccgtggt atgtgccacc accccgcnc tccgcagtgc gctccgtaac gccgtctgca  
 360  
 acaccgtccc ctccgtatct gccgacacct gtgccaacac ttgtaccgat gcatgcaccg  
 420  
 atgcagcaac aggcgctccg ctccgtatcg atctgggata cggcgccgcc ccctggacca  
 480  
 ctgttgagat ggctacgcgt  
 500

<210> 1676  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 1676  
 Arg Glu Phe Pro Pro Gln Ser Leu Ala Leu His Pro His Thr Pro Trp  
 1 5 10 15  
 Glu Pro Ser Pro Ala Val Pro Pro Gly Gln Ser Ala Pro Gln Met Arg  
 20 25 30  
 Pro Leu Asp Val Pro Pro Pro Arg Xaa Ser Ala Val Arg Ser Val Thr  
 35 40 45  
 Pro Ser Ala Thr Pro Ser Pro Pro Tyr Leu Pro Thr Pro Val Pro Thr  
 50 55 60  
 Leu Val Pro Met His Ala Pro Met Gln Gln Gln Ala Leu Arg Ser Leu  
 65 70 75 80  
 Ser Ile Trp Asp Thr Ala Pro Pro Pro Gly Pro Leu Leu Arg Trp Leu  
 85 90 95  
 Arg

<210> 1677  
 <211> 631  
 <212> DNA  
 <213> Homo sapiens

<400> 1677  
 nntcatgatt tcctcaatga tgccaagggtg atggaggccg gctataacctg ggtgcagggtg  
 60  
 gatttgcgcg gtacgggtgc ttctactggg tgtttgngac tggaatgggtc cnnccggggag  
 120  
 cagcaggatg ttgtgaccgc cgtggaatgg gcggcggtac agccgtgggtc gaatgggtcgg  
 180  
 gtggggcctt tcggtaaatc ctacgatggg gggacgggggt cttattgctg caggtaatca  
 240  
 gccgcggggg ttggtgctg tggtggcgca ggagccagct atggagccct acacttacct  
 300  
 gtataacaat gaggtccttt actacaacgc tattggtacg agcctttctt atgatgagat  
 360  
 tgctgcctcc cccggccgtg tccttcacga cactcccgaa tatatgaaga acagtgtcta  
 420  
 cgaggtggcc caccgcatt gcctgtccga caatttgcgt aattcttttag accccatccg  
 480  
 tagccacaaa taatgggcgg gatcgggtctt tccctcacca agacgcataa tttcccccg  
 540  
 gcccttgctt atttccgctg gccttattga ggacaatacg gagcctgatg gtttgggtgga  
 600  
 attgttgaag gaccgtaagg ctccgacgcg t  
 631

<210> 1678  
 <211> 78  
 <212> PRT

<213> Homo sapiens

<400> 1678

```

Xaa His Asp Phe Leu Asn Asp Ala Lys Val Met Glu Ala Gly Tyr Thr
 1           5           10           15
Trp Val Gln Val Asp Leu Arg Gly Thr Gly Ala Ser Thr Gly Cys Leu
      20           25           30
Xaa Leu Glu Trp Ser Xaa Gly Glu Gln Gln Asp Val Val Thr Ala Val
      35           40           45
Glu Trp Ala Ala Val Gln Pro Trp Ser Asn Gly Arg Val Gly Leu Phe
      50           55           60
Gly Lys Ser Tyr Asp Gly Gly Thr Gly Ser Tyr Cys Cys Arg
65           70           75

```

<210> 1679

<211> 531

<212> DNA

<213> Homo sapiens

<400> 1679

```

nctacttaga gcaaaggtag gaaaagaagg cagctaggcg tggctctcat tccttccac
60
agaatggatt ataagtcgag cctgatccag gatgggaatc ccatggagaa cttggagaag
120
cagctgatct gccctatctg cctggagatg tttaccaagc cagtggatcat cttgccgtgc
180
cagcacaacc tgtgccggaa gtgtgccaat gacatcttcc aggctgcaaa tccctactgg
240
accagccggg gcagctcagt gtccatgtct ggaggccgtt tccgctgccc tacctgccgc
300
cacgaggtga tcatggatcg tcacggagtg tacggcctgc agaggaaacct gctggtggag
360
aacatcatcg acatctacaa acaggagtgc tccagtcggc cgctgcagaa gggcagtcac
420
cccatgtaca aggagcacga agatgagaaa atcaacatct actgtctcac gtgtgaggtg
480
cccacctgct ccatgtgcaa ggtgtttggg atccacaagg cctgcgaggt g
531

```

<210> 1680

<211> 143

<212> PRT

<213> Homo sapiens

<400> 1680

```

Met Glu Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
 1           5           10           15
Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
      20           25           30
Lys Cys Ala Asn Asp Ile Phe Gln Ala Ala Asn Pro Tyr Trp Thr Ser
      35           40           45
Arg Gly Ser Ser Val Ser Met Ser Gly Gly Arg Phe Arg Cys Pro Thr
      50           55           60
Cys Arg His Glu Val Ile Met Asp Arg His Gly Val Tyr Gly Leu Gln

```

```

65          70          75          80
Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Cys
          85          90          95
Ser Ser Arg Pro Leu Gln Lys Gly Ser His Pro Met Tyr Lys Glu His
          100          105          110
Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu Thr Cys Glu Val Pro Thr
          115          120          125
Cys Ser Met Cys Lys Val Phe Gly Ile His Lys Ala Cys Glu Val
          130          135          140

```

&lt;210&gt; 1681

&lt;211&gt; 396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1681

```

gagttccaca actgcaggac agatgacaag acgttccaat gtgagatgtg tttcagattc
60
ttttccacca acagcaacct ctccaagcac aagaagaagc acggcgacaa gaagtttgcc
120
tgtgaggtct gcagcaagat gttctaccgc aaggacgtca tgctggacca ccagcgccgg
180
cacnctggaa ggagtgcggc gagtgaagcg nnagaggacc tggaggccgg tggggagaac
240
ctgggtccggtt acaagaagga gccttcggg tgcccggtgt gtggcaaggt gttctcctgc
300
cggagcaata tgaacaagca cctgctcacc cacggcgaca agaagtacac ctgcgagatc
360
tgcgggcgca agttcttcgg cgtggatgtg ctcagg
396

```

&lt;210&gt; 1682

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1682

```

Glu Phe His Asn Cys Arg Thr Asp Asp Lys Thr Phe Gln Cys Glu Met
1      5      10      15
Cys Phe Arg Phe Phe Ser Thr Asn Ser Asn Leu Ser Lys His Lys Lys
20     25     30
Lys His Gly Asp Lys Lys Phe Ala Cys Glu Val Cys Ser Lys Met Phe
35     40     45
Tyr Arg Lys Asp Val Met Leu Asp His Gln Arg Arg His Xaa Gly Arg
50     55     60
Ser Ala Ala Ser Glu Ala Xaa Glu Asp Leu Glu Ala Gly Gly Glu Asn
65     70     75     80
Leu Val Arg Tyr Lys Lys Glu Pro Ser Gly Cys Pro Val Cys Gly Lys
85     90     95
Val Phe Ser Cys Arg Ser Asn Met Asn Lys His Leu Leu Thr His Gly
100    105    110
Asp Lys Lys Tyr Thr Cys Glu Ile Cys Gly Arg Lys Phe Phe Arg Val
115    120    125
Asp Val Leu Arg

```

130

&lt;210&gt; 1683

&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1683

```

nncggccgga cagggtcccga gcagccccgc ccaacatgga cccagacccc caggcgggcg
60
tgcaggtggg catgcgggtg gtgcgcggcg tggaccggaa gtggggccag caggacggcg
120
gcgaggggcg cgtgggcacg gtggtggagc ttggccgcca cggcagcccc tcgacacccg
180
accgcacagt ggtcgtgcag tgggaccagg gcacgcgcac caactaccgc gccggctacc
240
agggcgcgca cgacctgtg ctgtacgaca acgcccagat cggcgtcccg caccccaaca
300
tcattctgtga ctgtgcgaag aagcacgggc tgcgggggat gcgctggaag tgccgtgtgt
360
gcctggacta cgacctctgc acgcagtgtc acatgcacaa caagcatgag ctgcgccacg
420
ccttcgaccg ctacgagacc gtcactcgc gccctgtcac actgagtccc cgccagggcc
480
tcccaggat cccactaagg ggcattctcc agggagcgaa ggtggtgcga ggccccgact
540
gggagtgggg ctacacaggat ggtgagtgga ggcagagggg cggggtcagg gctgggctgt
600
ggctggctca tggctcagcc ttagcctgct gggggggcct ctttccccag gaggggaagg
660
aaaccggggc gccgga
676

```

&lt;210&gt; 1684

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1684

```

Xaa Gly Arg Thr Gly Pro Glu Gln Pro Arg Pro Thr Trp Thr Gln Thr
 1           5           10           15
Pro Arg Arg Ala Cys Arg Trp Ala Cys Gly Trp Cys Ala Ala Trp Thr
      20           25           30
Gly Ser Gly Ala Ser Arg Thr Ala Ala Arg Ala Ala Trp Ala Arg Trp
      35           40           45
Trp Ser Leu Ala Ala Thr Ala Ala Pro Arg His Pro Thr Ala Gln Trp
      50           55           60
Ser Cys Ser Gly Thr Arg Ala Arg Ala Pro Thr Thr Ala Pro Ala Thr
      65           70           75           80
Arg Ala Arg Thr Thr Cys Cys Cys Thr Thr Thr Pro Arg Ser Ala Ser
      85           90           95
Gly Thr Pro Thr Ser Ser Val Thr Ala Ala Arg Ser Thr Gly Cys Gly
      100          105          110
Gly Cys Ala Gly Ser Ala Val Cys Ala Trp Thr Thr Thr Ser Ala Arg

```

[illegible]

ctggtggagg aagaagccaa catcctgggc aggaaaatcg tcgaactgga ggtggagaac  
1320  
agaggcctga aggcggaact ggacgacctt aggggcgatg acnnttcaac ggctcggcca  
1380  
accgctcat gagggagca gagcgaatcc ctgtcggagc tgcggcagca cctgcagctg  
1440  
gtggaagacg agacggagct gctgcggagg aacgtggccg acctggagga gcagaacaag  
1500  
cgcacacggc cggagctcaa caagtacaag tacaagnntc cggcggccac gacagcgcgc  
1560  
ggcaccacga caacgccana gaccgaggcc ctgcaggagg agctgaaggc ggcgcgcctg  
1620  
cagatcaacg agctcagcgg caaggtcatg cagctgcagt acgagaaccg cgtgcttatg  
1680  
tccaacatgc agcgtacga cctggcctcg cacctgggca tccgcggcag cccccgcgac  
1740  
agcgacgccg agagcgacgc gggcaagaag gagagcgacg acgactcgcg gcctccgcac  
1800  
cgcaagcgcg aagggcccat cggcggcgag agcgactcgg aggaggtggn cgcaacatcc  
1860  
gctgcctcan cgcccactcg ctcttcttac ccggcgcccc ggccctggcc caagagcttc  
1920  
tccgatcggc agcagatgaa ggacatccgc tcggaggccg agcgccctgg caagaccatc  
1980  
gaccggctca tcgccgacac gagcaccatc atcaccgagg cgcgcacnt acgtggccaa  
2040  
cggggacctg ttncggact catggacgag gaggacgacg gcagccgcat ccgggagcac  
2100  
gagctgctct accgcatcaa cgctcagatg aaggccttcc gcaaggagct gcagaccttc  
2160  
atcgaccgcc tcgaggtgcc caagtctgcg gacgaccgcg gcgccgagga gccatttcc  
2220  
gtgagtcaga tggtccagcc tatcatttta cttatttctca ttcttgattt attttcatca  
2280  
ctttcttaca caacaatatt taaacttgtc ttcttttta cactgttttt tgtactgtaa  
2340  
atctttcatc atttaccatt cattgtagta ttttcagttt gtttattttg ttcacccttc  
2400  
aagacaagaa gtaaaagaag tataatttct gtagtaacca atgctataaa aacactgaag  
2460  
actgcttatt tctttacaaa gatacaactc atcttaccaa gaccaaattc aataagaagc  
2520  
ccaaacacta aaatatttca ggtaagaaag tgtgacattt ttctgtatga attgttttaa  
2580  
tttttacttc ttttttcat cctgtttgtc tcctcttgat aaataattgg catactgaat  
2640  
ataaaaatgg actacatgtc tcataattat ttctcagtag ttcactatta ttattcaaaa  
2700  
gctggacgga cattcacaat ttggtcacat ttccaaaaag  
2740

&lt;210&gt; 1686

&lt;211&gt; 463

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1686

Xaa Gly Gly Ala Gly Gly Gly Ser Gly Glu Arg Glu Gly Gly Ala Pro  
 1 5 10 15  
 Gln Pro Pro Pro Arg Gly Trp Arg Gly Lys Gly Val Arg Ala Gln  
 20 25 30  
 Gln Arg Gly Gly Ser Gly Gly Glu Gly Ala Ser Pro Ser Pro Ser Ser  
 35 40 45  
 Ser Ser Ala Gly Lys Thr Pro Gly Thr Gly Ser Arg Asn Ser Gly Ser  
 50 55 60  
 Gly Val Ala Gly Gly Gly Ser Gly Gly Gly Gly Ser Tyr Trp Lys Glu  
 65 70 75 80  
 Gly Cys Leu Gln Ser Glu Leu Ile Gln Phe His Leu Lys Lys Glu Arg  
 85 90 95  
 Ala Ala Ala Ala Ala Ala Ala Gln Met His Ala Lys Asn Gly Gly  
 100 105 110  
 Gly Ser Ser Ser Arg Ser Ser Pro Val Ser Gly Pro Pro Ala Val Cys  
 115 120 125  
 Glu Thr Leu Ala Val Ala Ser Ala Ser Pro Met Ala Ala Ala Ala Glu  
 130 135 140  
 Gly Pro Gln Gln Ser Ala Glu Gly Ser Ala Ser Gly Gly Gly Met Gln  
 145 150 155 160  
 Ala Ala Ala Pro Pro Ser Ser Gln Pro His Pro Gln Gln Leu Gln Glu  
 165 170 175  
 Gln Glu Glu Met Gln Glu Glu Met Glu Lys Leu Arg Glu Glu Asn Glu  
 180 185 190  
 Thr Leu Lys Asn Glu Ile Asp Glu Leu Arg Thr Glu Met Asp Glu Met  
 195 200 205  
 Arg Asp Thr Phe Phe Glu Glu Asp Ala Cys Gln Leu Gln Glu Met Arg  
 210 215 220  
 His Glu Leu Glu Arg Ala Asn Lys Asn Cys Arg Ile Leu Gln Tyr Arg  
 225 230 235 240  
 Leu Arg Lys Ala Glu Arg Lys Arg Leu Arg Tyr Ala Gln Thr Gly Glu  
 245 250 255  
 Ile Asp Gly Glu Leu Leu Arg Ser Leu Glu Gln Asp Leu Lys Val Ala  
 260 265 270  
 Lys Asp Val Ser Val Arg Leu His His Glu Leu Glu Asn Val Glu Glu  
 275 280 285  
 Lys Arg Thr Thr Thr Glu Asp Glu Asn Glu Lys Leu Arg Gln Gln Leu  
 290 295 300  
 Ile Glu Val Glu Ile Ala Lys Gln Ala Leu Gln Asn Glu Leu Glu Lys  
 305 310 315 320  
 Met Lys Glu Leu Ser Leu Lys Arg Arg Gly Ser Lys Asp Leu Pro Lys  
 325 330 335  
 Ser Glu Lys Lys Ala Gln Gln Thr Pro Thr Glu Glu Asp Asn Glu Asp  
 340 345 350  
 Leu Lys Cys Gln Leu Gln Phe Val Lys Glu Glu Ala Ala Leu Met Arg  
 355 360 365  
 Lys Lys Met Ala Lys Ile Asp Lys Glu Lys Asp Arg Phe Glu His Glu  
 370 375 380  
 Leu Gln Lys Tyr Arg Ser Phe Tyr Gly Asp Leu Asp Ser Pro Leu Pro  
 385 390 395 400  
 Lys Gly Glu Ala Gly Gly Pro Pro Ser Thr Arg Glu Ala Glu Leu Lys



405 410 415  
 Leu Arg Leu Arg Leu Val Glu Glu Glu Ala Asn Ile Leu Gly Arg Lys  
 420 425 430  
 Ile Val Glu Leu Glu Val Glu Asn Arg Gly Leu Lys Ala Glu Leu Asp  
 435 440 445  
 Asp Leu Arg Gly Asp Asp Xaa Ser Thr Ala Arg Pro Thr Arg Ser  
 450 455 460

<210> 1687  
 <211> 326  
 <212> DNA  
 <213> Homo sapiens

<400> 1687  
 gtgcacacag gtgagcgtcc ctacaagtgt ccacactgcg actatgcagg taccagtcg  
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 ggctcgctca agtatcacct tcagcgtcac caccgagagc agaagaacag tgcgggttcc  
 120  
 tgggcctccc ccagaacccc cgccaccttc ccagcggggc tactgcagc cgcagtcagg  
 180  
 agccaagcca actcaggcct cagccacctg ggtagagggc actgcaagta cccggcctcc  
 240  
 ttcgagcagc accggaccag ggtcccgtag gaagcctgct agccctggga ggaccctgcg  
 300  
 aaacggcgat gtggtgaagc cgaact  
 326

<210> 1688  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 1688  
 Val His Thr Gly Glu Arg Pro Tyr Lys Cys Pro His Cys Asp Tyr Ala  
 1 5 10 15  
 Gly Thr Gln Ser Gly Ser Leu Lys Tyr His Leu Gln Arg His His Arg  
 20 25 30  
 Glu Gln Lys Asn Ser Ala Gly Ser Trp Ala Ser Pro Arg Thr Pro Ala  
 35 40 45  
 Thr Phe Pro Ala Gly Leu Thr Ala Ala Val Arg Ser Gln Ala Asn  
 50 55 60  
 Ser Gly Leu Ser His Leu Gly Arg Gly His Cys Lys Tyr Pro Ala Ser  
 65 70 75 80  
 Phe Glu Gln His Arg Thr Arg Val Pro  
 85

<210> 1689  
 <211> 301  
 <212> DNA  
 <213> Homo sapiens

<400> 1689  
 nggggaagcc atggctgctt aaggacaatg cactgtcagc tcggtgatgt cttgatttgg  
 60

tctgggattc tgcacttagt aattgcagat aatactcatg tggcgccaag gaaaaaaaaa  
 120  
 ttggcctttt cccagtccat taagcctaaa caaaccacat cactttacat caggcagatc  
 180  
 atgtggtacc agaattttcc agtttggcgg actatcttga tcaaataaac taaattattg  
 240  
 ccactgtggc tatctgtgaa agaacacaat gaagaaaatc tggagcctta tctcatactc  
 300  
 a  
 301

<210> 1690  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 1690  
 Met His Cys Gln Leu Gly Asp Val Leu Ile Trp Ser Gly Ile Leu His  
 1 5 10 15  
 Leu Val Ile Ala Asp Asn Thr His Val Ala Pro Arg Lys Lys Lys Leu  
 20 25 30  
 Ala Phe Ser Gln Ser Ile Lys Pro Lys Gln Thr Thr Ser Leu Tyr Ile  
 35 40 45  
 Arg Gln Ile Met Trp Tyr Gln Asn Phe Pro Val Trp Arg Thr Ile Leu  
 50 55 60  
 Ile Lys Ser Thr Lys Leu Leu Pro Leu Trp Leu Ser Val Lys Glu His  
 65 70 75 80  
 Asn Glu Glu Asn Leu Glu Pro Tyr Leu Ile Leu  
 85 90

<210> 1691  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<400> 1691  
 nacgcgttcc ggtatgccga tgggcgggtg ctgctgggcg tccgccggcg gcgcggtgag  
 60  
 ttgtgccttg aagtgtggga ccgcgggccc ggcattcctc aagacaaaca aaagtcattc  
 120  
 ttcgaagaat tcaaacgcct ggacagtcac cagaccgcg cagagaaagg cctgggcctg  
 180  
 ggccctggcga ttgccgacgg cttgtgccgc gtgctcgggc atcgcttgag cgtgcgttcg  
 240  
 tggccgggca agggcagcgt gttcagcgtg cgcgtgccgt tggcgcgcac ccaggtcagc  
 300  
 gcgcctgccca agccggcgca ggaaagcggc cagccgttga gtggcgcgca ggtgctgtgt  
 360  
 gtgaataaca aagaaagcat cctgatcggc atgcgcagct tgctcccgcg ctggggctgc  
 420  
 gaagtctggc ccgcgcgcga ccaggcgcaa tgtgccgcgc tgttggtgta ggggtgtgcg  
 480  
 ccg  
 483

<210> 1692  
 <211> 161  
 <212> PRT  
 <213> Homo sapiens

<400> 1692  
 Xaa Ala Phe Arg Tyr Ala Asp Gly Pro Val Leu Leu Gly Val Arg Arg  
 1 5 10 15  
 Arg Arg Gly Glu Leu Cys Leu Glu Val Trp Asp Arg Gly Pro Gly Ile  
 20 25 30  
 Pro Gln Asp Lys Gln Lys Ser Phe Phe Glu Glu Phe Lys Arg Leu Asp  
 35 40 45  
 Ser His Gln Thr Arg Ala Glu Lys Gly Leu Gly Leu Gly Leu Ala Ile  
 50 55 60  
 Ala Asp Gly Leu Cys Arg Val Leu Gly His Arg Leu Ser Val Arg Ser  
 65 70 75 80  
 Trp Pro Gly Lys Gly Ser Val Phe Ser Val Arg Val Pro Leu Ala Arg  
 85 90 95  
 Thr Gln Val Ser Ala Pro Ala Lys Pro Ala Gln Glu Ser Gly Gln Pro  
 100 105 110  
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 115 120 125  
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<210> 1693  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 1693  
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<210> 1694  
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 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 1694

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Met Leu Ala Phe Arg Glu Val Cys Arg Ser Thr Gln Pro Pro Glu Val
             20             25             30
Ala Ser Phe Ser Val Leu Val Ala Cys Ile Ser Arg Leu Thr Leu Thr
             35             40             45
Lys Lys Arg Ile Leu Ser Pro Asp Thr Met Glu Glu Leu Ala Val Ser
             50             55             60
Lys Ala Ser Ser Pro Pro Val Ser Pro Leu Gly Leu Arg Arg Cys His
65             70             75             80
Leu Cys His Thr Cys Ser Ser Leu Asn Pro Arg Ser Ile Gln Ser Ala
             85             90             95
Thr Trp Trp Glu Ser Phe Arg Thr Ala Ala Asp Gly Thr Arg
             100             105             110

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&lt;210&gt; 1695

&lt;211&gt; 485

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1695

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485

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&lt;210&gt; 1696

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1696

```

Met Leu Asn Pro Ser Lys Arg Gln Glu Phe Glu Asp Tyr Leu His Gln
 1             5             10             15
Glu Met Gln Asn Ser Lys Glu Asn Phe Thr Thr Ala His Asn Thr Ser
             20             25             30
Gly Arg Ser Ala Pro Pro Ser Thr Asn Val Arg Ser Ala Asp Gln Glu
             35             40             45
Asn Gly Glu Ile Thr Leu Val Lys Arg Arg Ile Phe Gly His Arg Ile

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Ile Thr Val Asn Phe Ala Ile Asn Asp Leu Tyr Phe Phe Ser Glu Met
65              70              75              80
Glu Lys Phe Asn Asp Leu Val Ser Ser Ala His Met Leu Gln Val Asn
      85              90              95
Arg Ala Tyr Asn Glu Asn Asp Val Ile Leu Met Arg Ser Lys Met Asn
      100             105             110
Ile Ile Gln Lys Leu Phe Leu Asn Ser Asp Ile Pro Pro Lys Leu Arg
      115             120             125
Val Asn Val Pro Glu Phe Gln Lys Asp Ala Ile Leu Ala Ala Ile Thr
      130             135             140
Glu Gly Tyr Leu
145

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&lt;210&gt; 1697

&lt;211&gt; 337

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1697

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337

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&lt;210&gt; 1698

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1698

```

Met Ala Gly Ala Leu Pro Ile Ala Ser Pro Leu Arg Ala Gln Thr Ala
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Thr Ala Gly Leu Arg Val Lys Gly Trp Met Asn Ser Gln Ala Gly Arg
      20      25      30
Val Leu Ser Glu Pro Ala Gly Gln Arg Arg Gln Pro Leu Arg Pro Leu
      35      40      45
Leu Lys Pro Cys Ala Ile Thr Ala Ala Ala Pro Val Val Pro Arg Arg
      50      55      60
Gln Leu Leu Ala Phe Pro Leu Gly Val Glu Phe Ala Gly Ser Pro Ile
65      70      75      80
His Arg Pro Leu Gly Gly Gly Lys Thr Ser Arg Ser Pro Lys Pro Val
      85      90      95
Thr Cys Asp Ser Pro Glu Asp Gly Gly Asn Leu
      100      105

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 <212> DNA  
 <213> Homo sapiens

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 Ser Leu His Lys Val Tyr Glu Lys Gly Ile Asn Leu Pro Ala Ser Leu  
 35 40 45  
 Phe Ala Leu Asp Ile Asn Gly Ser Thr Val Glu Ser Thr Gly Leu Gly  
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 Thr Met His Glu Leu Glu Gly Glu Pro Phe Phe Ala Asp Pro Arg Glu  
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 Val Leu Arg Gln Val Val Ser Lys Phe Asp Asp Leu Gly Leu Thr Ile  
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<212> PRT

<213> Homo sapiens

<400> 1702

Met	Val	Ala	Leu	Ser	Leu	Lys	Ile	Ser	Ile	Gly	Asn	Val	Val	Lys	Thr
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Met	Gln	Phe	Glu	Pro	Ser	Thr	Met	Val	Tyr	Asp	Ala	Cys	Arg	Ile	Ile
			20					25					30		
Arg	Glu	Arg	Ile	Pro	Glu	Ala	Pro	Ala	Gly	Pro	Pro	Ser	Asp	Phe	Gly
			35				40					45			
Leu	Phe	Leu	Ser	Asp	Asp	Asp	Pro	Lys	Lys	Gly	Ile	Trp	Leu	Glu	Ala
			50			55					60				
Gly	Lys	Ala	Leu	Asp	Tyr	Tyr	Met	Leu	Arg	Asn	Gly	Asp	Thr	Met	Glu
65					70					75				80	
Tyr	Arg	Lys	Lys	Gln	Arg	Pro	Leu	Lys	Ile	Arg	Met	Leu	Asp	Gly	Thr
				85					90					95	
Val	Lys	Thr	Ile	Met	Val	Asp	Asp	Ser	Lys	Thr	Val	Thr	Asp	Met	Leu
			100					105					110		
Met	Thr	Ile	Cys	Ala	Arg	Ile	Gly	Ile	Thr	Asn	His	Asp	Glu	Tyr	Ser
			115				120					125			
Leu	Val	Arg	Glu	Leu	Met	Glu	Glu	Lys	Lys	Glu	Glu	Gly	Thr	Gly	Thr
			130				135					140			
Leu	Lys	Lys	Asp	Lys	Thr	Leu	Leu	Arg	Asp	Glu	Lys	Lys	Met	Glu	Lys
145					150					155				160	
Leu	Lys	Gln	Lys	Leu	His	Thr	Asp	Asp	Glu	Leu	Asn	Trp	Leu	Asp	His
				165					170					175	
Gly	Arg	Thr	Leu	Arg	Glu	Gln	Gly	Val	Glu	Glu	His	Glu	Thr	Leu	Leu
			180					185					190		
Leu	Arg	Arg	Lys	Phe	Phe	Tyr	Ser	Asp	Gln	Asn	Val	Asp	Ser	Arg	Asp
			195				200					205			
Pro	Val	Gln	Leu	Asn	Leu	Leu	Tyr	Val	Gln	Ala	Arg	Asp	Asp	Ile	Leu
			210				215					220			
Asn	Gly	Ser	His	Pro	Val	Ser	Phe	Asp	Lys	Ala	Cys	Glu	Phe	Ala	Gly
225					230					235				240	
Phe	Gln	Cys	Gln	Ile	Gln	Phe	Gly	Pro	His	Asn	Glu	Gln	Lys	His	Lys
				245					250					255	
Ala	Gly	Phe	Leu	Asp	Leu	Lys	Asp	Phe	Leu	Pro	Lys	Glu	Tyr	Val	Lys
			260					265					270		
Gln	Lys	Gly	Glu	Arg	Lys	Ile	Phe	Gln	Ala	His	Lys	Asn	Cys	Gly	Gln
			275				280					285			
Met	Ser	Glu	Ile	Glu	Ala	Lys	Val	Arg	Tyr	Val	Lys	Leu	Ala	Arg	Ser
			290				295					300			
Leu	Lys	Thr	Tyr	Gly	Val	Ser	Phe	Phe	Leu	Val	Lys	Glu	Lys	Met	Lys

1350

1351

1170	1175	1180
Leu Ala Gln Val Ala Lys Ala Val Thr Gln Ala Leu Asn Arg Cys Val		
1185	1190	1195
Ser Cys Leu Pro Gly Gln Arg Asp Val Asp Asn Ala Leu Arg Ala Val		1200
	1205	1210
Gly Asp Ala Ser Lys Arg Leu Leu Ser Asp Ser Leu Pro Pro Ser Thr		1215
	1220	1225
Gly Thr Phe Gln Glu Ala Gln Ser Arg Leu Asn Glu Ala Ala Ala Gly		1230
	1235	1240
Leu Asn Gln Ala Ala Thr Glu Leu Val Gln Ala Ser Arg Gly Thr Pro		1245
	1250	1255
Gln Asp Leu Ala Arg Ala Ser Gly Arg Phe Gly Gln Asp Phe Ser Thr		1260
1265	1270	1275
Phe Leu Glu Ala Gly Val Glu Met Ala Gly Gln Ala Pro Ser Gln Glu		1280
	1285	1290
Asp Arg Ala Gln Val Val Ser Asn Leu Lys Gly Ile Ser Met Ser Ser		1295
	1300	1305
Ser Lys Leu Leu Leu Ala Ala Lys Ala Leu Ser Thr Asp Pro Ala Ala		1310
	1315	1320
Pro Asn Leu Lys Ser Gln Leu Ala Ala Ala Arg Ala Val Thr Asp		1325
	1330	1335
Ser Ile Asn Gln Leu Ile Thr Met Cys Thr Gln Gln Ala Pro Gly Gln		1340
1345	1350	1355
Lys Glu Cys Asp Asn Ala Leu Arg Glu Leu Glu Thr Val Arg Glu Leu		1360
	1365	1370
Leu Glu Asn Pro Val Gln Pro Ile Asn Asp Met Ser Tyr Phe Gly Cys		1375
	1380	1385
Leu Asp Ser Val Met Glu Asn Ser Lys Val Leu Gly Glu Ala Met Thr		1390
	1395	1400
Gly Ile Ser Gln Asn Ala Lys Asn Gly Asn Leu Pro Glu Phe Gly Asp		1405
	1410	1415
Ala Ile Ser Thr Ala Ser Lys Ala Leu Cys Gly Phe Thr Glu Ala Ala		1420
1425	1430	1435
Ala Gln Ala Ala Tyr Leu Val Gly Val Ser Asp Pro Asn Ser Gln Ala		1440
	1445	1450
Gly Gln Gln Gly Leu Val Glu Pro Thr Gln Phe Ala Arg Ala Asn Gln		1455
	1460	1465
Ala Ile Gln Met Ala Cys Gln Ser Leu Gly Glu Pro Gly Cys Thr Gln		1470
	1475	1480
Ala Gln Val Leu Ser Ala Ala Thr Ile Val Ala Lys His Thr Ser Ala		1485
	1490	1495
Leu Cys Asn Ser Cys Arg Leu Ala Ser Ala Arg Thr Thr Asn Pro Thr		1500
1505	1510	1515
Ala Lys Arg Gln Phe Val Gln Ser Ala Lys Glu Val Ala Asn Ser Thr		1520
	1525	1530
Ala Asn Leu Val Lys Thr Ile Lys Ala Leu Asp Gly Ala Phe Thr Glu		1535
	1540	1545
Glu Asn Arg Ala Gln Cys Arg Ala Ala Thr Ala Pro Leu Leu Glu Ala		1550
	1555	1560
Val Asp Asn Leu Ser Ala Phe Ala Ser Asn Pro Glu Phe Ser Ser Ile		1565
	1570	1575
Pro Ala Gln Ile Ser Pro Glu Gly Arg Ala Ala Met Glu Pro Ile Val		1580
1585	1590	1595
Ile Ser Ala Lys Thr Met Leu Glu Ser Ala Gly Gly Leu Ile Gln Thr		1600

										1605				1610				1615			
Ala	Arg	Ala	Leu	Ala	Val	Asn	Pro	Arg	Asp	Pro	Pro	Ser	Trp	Ser	Val						
										1620				1625				1630			
Leu	Ala	Gly	His	Ser	Arg	Thr	Val	Ser	Asp	Ser	Ile	Lys	Lys	Leu	Ile						
										1635				1640				1645			
Thr	Ser	Met	Arg	Asp	Lys	Ala	Pro	Gly	Gln	Leu	Glu	Cys	Glu	Thr	Ala						
										1650				1655				1660			
Ile	Ala	Ala	Leu	Asn	Ser	Cys	Leu	Arg	Asp	Leu	Asp	Gln	Ala	Ser	Leu						
										1665				1670				1675			
Ala	Ala	Val	Ser	Gln	Gln	Leu	Ala	Pro	Arg	Glu	Gly	Ile	Ser	Gln	Glu						
										1685				1690				1695			
Ala	Leu	His	Thr	Gln	Met	Leu	Thr	Ala	Val	Gln	Glu	Ile	Ser	His	Leu						
										1700				1705				1710			
Ile	Glu	Pro	Leu	Ala	Asn	Ala	Ala	Arg	Ala	Glu	Ala	Ser	Gln	Leu	Gly						
										1715				1720				1725			
His	Lys	Val	Ser	Gln	Met	Ala	Gln	Tyr	Phe	Glu	Pro	Leu	Thr	Leu	Ala						
										1730				1735				1740			
Ala	Val	Gly	Ala	Ala	Ser	Lys	Thr	Leu	Ser	His	Pro	Gln	Gln	Met	Ala						
										1745				1750				1755			
Leu	Leu	Asp	Gln	Thr	Lys	Thr	Leu	Ala	Glu	Ser	Ala	Leu	Gln	Leu	Leu						
										1765				1770				1775			
Tyr	Thr	Ala	Lys	Glu	Ala	Gly	Gly	Asn	Pro	Lys	Gln	Ala	Ala	His	Thr						
										1780				1785				1790			
Gln	Glu	Ala	Leu	Glu	Glu	Ala	Val	Gln	Met	Met	Thr	Glu	Ala	Val	Glu						
										1795				1800				1805			
Asp	Leu	Thr	Thr	Thr	Leu	Asn	Glu	Ala	Ala	Ser	Ala	Ala	Gly	Val	Val						
										1810				1815				1820			
Gly	Gly	Met	Val	Asp	Ser	Ile	Thr	Gln	Ala	Ile	Asn	Gln	Leu	Asp	Glu						
										1825				1830				1835			
Gly	Pro	Met	Gly	Glu	Pro	Glu	Gly	Ser	Phe	Val	Asp	Tyr	Gln	Thr	Thr						
										1845				1850				1855			
Met	Val	Arg	Thr	Ala	Lys	Ala	Ile	Ala	Val	Thr	Val	Gln	Glu	Met	Val						
										1860				1865				1870			
Thr	Lys	Ser	Asn	Thr	Ser	Pro	Glu	Glu	Leu	Gly	Pro	Leu	Ala	Asn	Gln						
										1875				1880				1885			
Leu	Thr	Ser	Asp	Tyr	Gly	Arg	Leu	Ala	Ser	Glu	Ala	Lys	Pro	Ala	Ala						
										1890				1895				1900			
Val	Ala	Ala	Glu	Asn	Glu	Glu	Ile	Gly	Ser	His	Ile	Lys	His	Arg	Val						
										1905				1910				1915			
Gln	Glu	Leu	Gly	His	Gly	Cys	Ala	Ala	Leu	Val	Thr	Lys	Ala	Gly	Ala						
										1925				1930				1935			
Leu	Gln	Cys	Ser	Pro	Ser	Asp	Ala	Tyr	Thr	Lys	Lys	Glu	Leu	Ile	Glu						
										1940				1945				1950			
Cys	Ala	Arg	Arg	Val	Ser	Glu	Lys	Val	Ser	His	Val	Leu	Ala	Ala	Leu						
										1955				1960				1965			
Gln	Ala	Gly	Asn	Arg	Gly	Thr	Gln	Ala	Cys	Ile	Thr	Ala	Ala	Ser	Ala						
										1970				1975				1980			
Val	Ser	Gly	Ile	Ile	Ala	Asp	Leu	Asp	Thr	Thr											



2035	2040	2045
Gln Ser Ser Val Ala Thr Ile Thr Arg Leu Ala Asp Val Val Lys Leu		
2050	2055	2060
Gly Ala Ala Ser Leu Gly Ala Glu Asp Pro Glu Thr Gln Val Val Leu		
2065	2070	2075
Ile Asn Ala Val Lys Asp Val Ala Lys Ala Leu Gly Asp Leu Ile Ser		2080
2085	2090	2095
Ala Thr Lys Ala Ala Ala Gly Lys Val Gly Asp Asp Pro Ala Val Trp		
2100	2105	2110
Gln Leu Lys Asn Ser Ala Lys Val Met Val Thr Asn Val Thr Ser Leu		
2115	2120	2125
Leu Lys Thr Val Lys Ala Val Glu Asp Glu Ala Thr Lys Gly Thr Arg		
2130	2135	2140
Ala Leu Glu Ala Thr Thr Glu His Ile Arg Gln Glu Leu Ala Val Phe		
2145	2150	2155
Cys Ser Pro Glu Pro Pro Ala Lys Thr Ser Thr Pro Glu Asp Phe Ile		2160
2165	2170	2175
Arg Met Thr Lys Gly Ile Thr Met Ala Thr Ala Lys Ala Val Ala Ala		
2180	2185	2190
Gly Asn Ser Cys Arg Gln Glu Asp Val Ile Ala Thr Ala Asn Leu Ser		
2195	2200	2205
Arg Arg Ala Ile Ala Asp Met Leu Arg Ala Cys Lys Glu Ala Ala Tyr		
2210	2215	2220
His Pro Glu Val Ala Pro Asp Val Arg Leu Arg Ala Leu His Tyr Gly		
2225	2230	2235
Arg Glu Cys Ala Asn Gly Tyr Leu Glu Leu Asp His Val Leu Leu		2240
2245	2250	2255
Thr Leu Gln Lys Pro Ser Pro Glu Leu Lys Gln Gln Leu Thr Gly His		
2260	2265	2270
Ser Lys Arg Val Ala Gly Ser Val Thr Glu Leu Ile Gln Ala Ala Glu		
2275	2280	2285
Ala Met Lys Gly Thr Glu Trp Val Asp Pro Glu Asp Pro Thr Val Ile		
2290	2295	2300
Ala Glu Asn Glu Leu Leu Gly Ala Ala Ala Ala Ile Glu Ala Ala Ala		
2305	2310	2315
Lys Lys Leu Glu Gln Leu Lys Pro Arg Ala Lys Pro Lys Glu Ala Asp		2320
2325	2330	2335
Glu Ser Leu Asn Phe Glu Glu Gln Ile Leu Glu Ala Ala Lys Ser Ile		
2340	2345	2350
Ala Ala Ala Thr Ser Ala Leu Val Lys Ala Ala Ser Ala Ala Gln Arg		
2355	2360	2365
Glu Leu Val Ala Gln Gly Lys Val Gly Ala Ile Pro Ala Asn Ala Leu		
2370	2375	2380
Asp Asp Gly Gln Trp Ser Gln Gly Leu Ile Ser Ala Ala Arg Met Val		
2385	2390	2395
Ala Ala Ala Thr Asn Asn Leu Cys Glu Ala Ala Asn Ala Ala Val Gln		2400
2405	2410	2415
Gly His Ala Ser Gln Glu Lys Leu Ile Ser Ser Ala Lys Gln Val Ala		
2420	2425	2430
Ala Ser Thr Ala Gln Leu Leu Val Ala Cys Lys Val Lys Ala Asp Gln		
2435	2440	2445
Asp Ser Glu Ala Met Lys Arg Leu Gln Ala Ala Gly Asn Ala Val Lys		
2450	2455	2460
Arg Ala Ser Asp Asn Leu Val Lys Ala Ala Gln Lys Ala Ala Phe		

2465	2470	2475	2480
Glu Glu Gln Glu Asn Glu Thr Val Val Val Lys Glu Lys Met Val Gly			
	2485	2490	2495
Gly Ile Ala Gln Ile Ile Ala Ala Gln Glu Glu Met Leu Arg Lys Glu			
	2500	2505	2510
Arg Glu Leu Glu Glu Ala Arg Lys Lys Leu Ala Gln Ile Arg Gln Gln			
	2515	2520	2525
Gln Tyr Lys Phe Leu Pro Ser Glu Leu Arg Asp Glu His			
2530	2535	2540	

<210> 1703  
 <211> 346  
 <212> DNA  
 <213> Homo sapiens

<400> 1703  
 ggatccccgag gagaaaaatc ctctgttact tcatgggtca tgtgactgag aatcttttta  
 60  
 ggaatctgtg atggagaaga atgactcctc ttcttctctg agtcctgtag taatgcattc  
 120  
 tctgctctac cttcttccat gactgctgcc tggctctgcc tagccttgct ctgatccaca  
 180  
 ctgagctggc cttgagcagg gtcgcacctg tacatgaaga caatggctgg tttctcactg  
 240  
 gactctcctt tcgcctctgt gaaccagtga tggcgctgaa ctggaggaag aggcagcatg  
 300  
 tgaatgactg tgccatccat ggccaccaag ttccctttct ctcgct  
 346

<210> 1704.  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 1704
Met Asp Gly Thr Val Ile His Met Leu Pro Leu Pro Pro Val Gln Arg
1 5 10 15
His His Trp Phe Thr Glu Ala Lys Gly Glu Ser Ser Glu Lys Pro Ala
20 25 30
Ile Val Phe Met Tyr Arg Cys Asp Pro Ala Gln Gly Gln Leu Ser Val
35 40 45
Asp Gln Ser Lys Ala Arg Thr Asp Gln Ala Ala Val Met Glu Lys Gly
50 55 60
Arg Ala Glu Asn Ala Leu Leu Gln Asp Ser Glu Lys Lys Arg Ser His
65 70 75 80
Ser Ser Pro Ser Gln Ile Pro Lys Lys Ile Leu Ser His Met Thr His
85 90 95
Glu Val Thr Glu Asp Phe Ser Pro Arg Asp
100 105

<210> 1705  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 1705

gtgcaccttt tctcaggact cgctcagaag gtccttctgg gaggacaatg gacaagacta  
60  
aaccatcaaa tccattctca atgggtcaaa ttccaaatct tctgaaggg ctggcttcta  
120  
ctgggtgctcc aatcgagttg cagaaaggta tacagggtgg agcaagttta tttaatcctg  
180  
gttttggtg gaacaaaaat ccacaagttc aaaccttgaa gaattctcaa ggttctatc  
240  
ataatttagt gaggtctgga gttactgttg aaaggaaagt taatgtaggg gcacaaggag  
300  
cttttaactc tgcccctgca ccacagatgg aatttcccac agttctctca tacaaccct  
360  
cttccttcgg agctagc  
377

&lt;210&gt; 1706

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1706

Met	Asp	Lys	Thr	Lys	Pro	Ser	Asn	Pro	Phe	Ser	Met	Gly	Gln	Ile	Pro
1				5					10					15	
Asn	Phe	Pro	Glu	Gly	Leu	Ala	Ser	Thr	Gly	Ala	Pro	Ile	Glu	Leu	Gln
		20						25					30		
Lys	Gly	Ile	Gln	Gly	Gly	Ala	Ser	Leu	Phe	Asn	Pro	Gly	Phe	Gly	Trp
		35					40				45				
Asn	Gln	Asn	Pro	Gln	Val	Gln	Thr	Leu	Lys	Asn	Ser	Gln	Gly	Ser	Ile
	50				55					60					
His	Asn	Leu	Val	Arg	Ser	Gly	Val	Thr	Val	Glu	Arg	Lys	Val	Asn	Val
65				70						75				80	
Gly	Ala	Gln	Gly	Ala	Phe	Asn	Ser	Ala	Pro	Ala	Pro	Gln	Met	Glu	Phe
		85						90					95		
Pro	Thr	Val	Pro	Pro	Tyr	Asn	Pro	Ser	Ser	Phe	Gly	Ala	Ser		
		100					105						110		

&lt;210&gt; 1707

&lt;211&gt; 427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1707

nnctcggtga acccgaagcc cggacgcagc gccgataccc atgtgcgccc agtactacgc  
60  
catcacgcca agcgagtgtc catcatcggg gccgggctag ccggcatgga ggctgcgcga  
120  
gttctcagcg aacgcgcaca cgaacctctc atcgtcgagg ccagcgacca cattggcgga  
180  
gtcatccttg cgggtgggtca accttcttcc aaggaggacg acctagctct gctggagtgg  
240  
taccgcacca ccttgaggga gttgggcgtg gagattcgac tcaacaccac cgtaacggct  
300

gatcttatcg cttccttcgg ggccgatcac gtggtcctgg cgaccggatc gaggccgcgt  
 360  
 cgactcgacc taggtgatga tgccaaggtc attgacgcca ccgacgctct gctcaaccgc  
 420  
 gacgcgt  
 427

<210> 1708  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 1708  
 Xaa Ser Val Asn Pro Lys Pro Gly Arg Ser Ala Asp Thr His Val Arg  
 1 5 10 15  
 Pro Val Leu Arg His His Ala Lys Arg Val Leu Ile Ile Gly Ala Gly  
 20 25 30  
 Leu Ala Gly Met Glu Ala Ala Arg Val Leu Ser Glu Arg Ala His Glu  
 35 40 45  
 Pro Leu Ile Val Glu Ala Ser Asp His Ile Gly Gly Val Ile Leu Ala  
 50 55 60  
 Gly Gly Gln Pro Ser Phe Lys Glu Asp Asp Leu Ala Leu Leu Glu Trp  
 65 70 75 80  
 Tyr Arg Thr Thr Leu Glu Glu Leu Gly Val Glu Ile Arg Leu Asn Thr  
 85 90 95  
 Thr Val Thr Ala Asp Leu Ile Ala Ser Phe Gly Ala Asp His Val Val  
 100 105 110  
 Leu Ala Thr Gly Ser Arg Pro Arg Arg Leu Asp Leu Gly Asp Asp Ala  
 115 120 125  
 Lys Val Ile Asp Ala Thr Asp Ala Leu Leu Asn Arg Asp Ala  
 130 135 140

<210> 1709  
 <211> 446  
 <212> DNA  
 <213> Homo sapiens

<400> 1709  
 acgcgtgaag gggaccagga gggtggacac agaccattgc aatggaaatg atgatttaga  
 60  
 ctgttctttt ctgactgatg actgggagtc agggaagatg aatgcagagt ctgtgatcac  
 120  
 ctctctttcc agccacatca tatctcagcc tcttgaggga aactcccata gcttgtctct  
 180  
 tcagtccag ttgacagctt ctgaacgttt ccaagagaat agttcggatc attcagaaac  
 240  
 cagggtgttg caagaggtct tctttcaggc aatcctgctt gctgtgtgct taatcatttc  
 300  
 tgcattgtga agatgggtta tgggagaaat attagccagt gtcttcacat gctcattgat  
 360  
 gataactgta gcttatgtga aatcattgtt tctcagcctt gccagctatt tcaaaaccac  
 420  
 tgcctgtgct cggtttgtca aaattt  
 446

<210> 1710  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 1710  
 Met Asn Ala Glu Ser Val Ile Thr Ser Ser Ser Ser His Ile Ile Ser  
 1 5 10 15  
 Gln Pro Pro Gly Gly Asn Ser His Ser Leu Ser Leu Gln Ser Gln Leu  
 20 25 30  
 Thr Ala Ser Glu Arg Phe Gln Glu Asn Ser Ser Asp His Ser Glu Thr  
 35 40 45  
 Arg Leu Leu Gln Glu Val Phe Gln Ala Ile Leu Leu Ala Val Cys  
 50 55 60  
 Leu Ile Ile Ser Ala Cys Ala Arg Trp Val Met Gly Glu Ile Leu Ala  
 65 70 75 80  
 Ser Val Phe Thr Cys Ser Leu Met Ile Thr Val Ala Tyr Val Lys Ser  
 85 90 95  
 Leu Phe Leu Ser Leu Ala Ser Tyr Phe Lys Thr Thr Ala Cys Ala Arg  
 100 105 110  
 Phe Val Lys Ile  
 115

<210> 1711  
 <211> 426  
 <212> DNA  
 <213> Homo sapiens

<400> 1711  
 nggggggattc atgttagtat ttgtcagaaa aggcttttga aagagccaaa ttaaaaagag  
 60  
 cactagaaca tgaacaggga aagcagagga aatacttgta gaaagtattt ttacagctc  
 120  
 cctcaataca attcagtaat gttcattcct ggtgagaagt ctgtccgcac acacagcatc  
 180  
 agccaagcag cagaagcagt ggtgtctggg gggctgggaa gtttttcccc caaataccca  
 240  
 ccccatgcac tgcccagtc ccagacccca aagactttgt cctcgccctca cgcacctttt  
 300  
 gcaggctcac actgtctgtg tgcgcaagag gtagcgacag gagacaatgg ggaaagagct  
 360  
 gaaggaggca aacaaggcca gggggaaagc ctacctcgag gcacagaggg gccccaagat  
 420  
 ggatat  
 426

<210> 1712  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 1712  
 Met Asn Arg Glu Ser Arg Gly Asn Thr Cys Arg Lys Tyr Phe Leu Gln

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      1             5             10             15
Leu Pro Gln Tyr Asn Ser Val Met Phe Ile Pro Gly Glu Lys Ser Val
      20             25             30
Arg Thr His Ser Ile Ser Gln Ala Ala Glu Ala Val Val Ser Gly Gly
      35             40             45
Leu Gly Ser Phe Ser Pro Lys Tyr Pro Pro His Ala Leu Pro Ser Pro
      50             55             60
Gln Thr Pro Lys Thr Leu Ser Ser Pro His Ala Pro Phe Ala Gly Ser
      65             70             75             80
His Cys Leu Cys Ala Gln Glu Val Ala Thr Gly Asp Asn Gly Glu Arg
      85             90             95
Ala Glu Gly Gly Lys Gln Gly Gln Gly Glu Ser Leu Pro Arg Gly Thr
      100            105            110
Glu Gly Pro Gln Asp Gly Tyr
      115

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&lt;210&gt; 1713

&lt;211&gt; 328

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1713

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tctagaagg tttatttcat gggccaaggc ttgtgtttcc aaagccagga agggctgaag
60
ccagaattgg ccctggctgc ttgccacaga gtctggccgg gggaccctgg acctcagcag
120
ggtcgatgatg aggtcagctt tggaggagca gggccagcgt gtcttgcttt ctgctcctgg
180
aatgagcctc actccctccc tgetcaaggc agcccttcac ccagccgccc ggacaggtgc
240
cctgtgccac ctgccatccc tgggattctc catctcagtg agtgctccct ggggcctggg
300
aacgcactctg gctggtgact cctggggg
328

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&lt;210&gt; 1714

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1714

```

Met Gly Gln Gly Leu Cys Phe Gln Ser Gln Glu Gly Leu Lys Pro Glu
      1             5             10             15
Leu Ala Leu Ala Ala Cys His Arg Val Trp Pro Gly Asp Pro Gly Pro
      20             25             30
Gln Gln Gly His Asp Glu Val Ser Phe Gly Gly Ala Gly Pro Ala Cys
      35             40             45
Pro Ala Phe Cys Ser Trp Asn Glu Pro His Ser Leu Pro Ala Gln Gly
      50             55             60
Ser Pro Ser Pro Ser Arg Arg Asp Arg Cys Pro Val Pro Pro Ala Ile
      65             70             75             80
Pro Gly Ile Leu His Leu Ser Glu Cys Ser Leu Gly Pro Gly Asn Ala
      85             90             95
Ser Gly Trp

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<210> 1715  
 <211> 489  
 <212> DNA  
 <213> Homo sapiens

<400> 1715  
 gttgccagcg atgggccgca tttgtacatc ccggtatttc gtgttcggtg tgggtgtaaaa  
 60  
 gatgccccat gtgtgacatt ctgtggatag ttattgtag cattatttga caagttctag  
 120  
 aaatcgatcc acccaggcgt gtagctgcgg tatttcatca gagttgatcg ttgcgatgag  
 180  
 ttgatcatgg cctgtcatgg cgtagtcttc tacgtcgtaa agtatgagac aatccacggt  
 240  
 aatatggtgt tttttggcca actcggaagc cggggtgtcg gggaagtcgg tccctgtaag  
 300  
 gtatgggcct gtcccaatga cgacgtgtgc tgggtccatg aggagttcgt ccaaggttcg  
 360  
 aactcattac cgtcgaatac gacgctgtcg ccatcggcgg tgcgaatcg aatcctcaa  
 420  
 gtgtatccgt actcgggtgc gcgcaacagg tgcctaacct cagcgctagt gggctgtgca  
 480  
 ctgacgcgt  
 489

<210> 1716  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 1716  
 Met Ala Cys His Gly Val Val Phe Tyr Val Val Lys Tyr Glu Thr Ile  
 1 5 10 15  
 His Gly Asn Met Val Phe Phe Gly Gln Leu Gly Ser Arg Gly Val Gly  
 20 25 30  
 Glu Val Gly Pro Cys Lys Val Trp Ala Cys Pro Asn Asp Asp Val Cys  
 35 40 45  
 Trp Val His Glu Glu Phe Val Gln Gly Ser Asn Ser Leu Pro Ser Asn  
 50 55 60  
 Thr Thr Leu Ser Pro Ser Ala Val Ser Asn Arg Ile Leu Lys Val Tyr  
 65 70 75 80  
 Pro Tyr Ser Val Ser Arg Asn Arg Cys Leu Thr Ser Ala Leu Val Gly  
 85 90 95  
 Cys Ala Leu Thr Arg  
 100

<210> 1717  
 <211> 312  
 <212> DNA  
 <213> Homo sapiens

<400> 1717

nggcatacaa cggagtaaaa accacatcaa cagaagtga aacaggccca gagagcgtga  
 60  
 gaggtttctg gtttcaagaa ggcacactga gtccctgcac ccgatgcctc tccttcccca  
 120  
 aatcccactg gaatacacag agagacataa aaacaaggag tgtcctgtag cagagcagcc  
 180  
 aggctggctc atgagacaga gggagcagtc ttctgggaga catggctctt gctgctgcgg  
 240  
 atcagccaac agatccatgg aaagcaaagg gcccttctcc ggaggcttcc tggggcctgc  
 300  
 catgaatgtg tc  
 312

<210> 1718

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1718

Met	Ala	Gly	Pro	Arg	Lys	Pro	Pro	Glu	Lys	Gly	Pro	Leu	Leu	Ser	Met
1				5				10						15	
Asp	Leu	Leu	Ala	Asp	Pro	Gln	Gln	Gln	Glu	Pro	Cys	Leu	Pro	Glu	Asp
			20					25					30		
Cys	Ser	Leu	Cys	Leu	Met	Ser	Gln	Pro	Gly	Cys	Ser	Ala	Thr	Gly	His
		35					40					45			
Ser	Leu	Phe	Leu	Cys	Leu	Ser	Val	Tyr	Ser	Ser	Gly	Ile	Trp	Gly	Arg
	50					55					60				
Arg	Gly	Ile	Gly	Cys	Arg	Asp	Ser	Val	Cys	Leu	Leu	Glu	Thr	Arg	Asn
65					70					75				80	
Leu	Ser	Arg	Ser	Leu	Gly	Leu	Phe	Pro	Leu	Leu	Leu	Met	Trp	Phe	Leu
				85					90					95	
Leu	Arg	Cys	Met	Pro											
				100											

<210> 1719

<211> 404

<212> DNA

<213> Homo sapiens

<400> 1719

tgatcaccac ggccctgccca ttttttgtcg ggaccgcaga ccgatgctg cccctcgaag  
 60  
 tcagagacaa tccaaccggc ctgcaaaact gcggctctgc ccggggcaac gtcgtaggg  
 120  
 ccaacagttt ctccaacctc ataggtagaa gaagtgtat agctgctgga aatggagatg  
 180  
 tggatcacat cgagcagtgg gaagtcaatg cctgccgaaa ccgaccagtt cttcgtctta  
 240  
 gtttctgtga tggatgcgct gaccggctgc ggagtgtcgt tgagttggaa atcgtcacgt  
 300  
 cccagcagag ccacgaagt agctgcgcac cacatgaacg ggctgtccgt gtcacccgga  
 360  
 ttcgagcagg gagcaccat tggtgngtgg tgtccccggg gggt  
 404



<210> 1720  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 1720  
 Met Gly Ala Pro Cys Ser Asn Pro Gly Asp Thr Asp Ser Pro Phe Met  
 1 5 10 15  
 Trp Cys Ala Ala Thr Ser Met Ala Leu Leu Gly Arg Asp Asp Phe Gln  
 20 25 30  
 Leu Asn Asp Thr Pro Gln Pro Val Thr Arg Ser Ile Thr Glu Thr Lys  
 35 40 45  
 Thr Lys Asn Trp Ser Val Ser Ala Gly Ile Asp Phe Pro Leu Leu Asp  
 50 55 60  
 Val Ile His Ile Ser Ile Ser Ser Ser Tyr Ser Thr Ser Ser Thr Tyr  
 65 70 75 80  
 Glu Val Gly Glu Thr Val Gly Pro Tyr Asp Val Ala Pro Gly Lys Thr  
 85 90 95  
 Ala Val Leu Gln Ala Gly Trp Ile Val Ser Asp Phe Glu Gly Gln His  
 100 105 110  
 Thr Val Cys Gly Pro Asp Lys Lys Trp Gln Gly Arg Gly Asp  
 115 120 125

<210> 1721  
 <211> 529  
 <212> DNA  
 <213> Homo sapiens

<400> 1721  
 ccattggccac cctttcagga cagagctgcc cttcccatgc tggaggagcc acagggcctg  
 60  
 gtcgctgtgg cttcagcctc ccagctcctc ctgtcctctg ctgggcactt gtaatgtcca  
 120  
 ggcactccct gcttgatca ggggatctgg gtttcatctt ccagctcct cctgtcctct  
 180  
 gctgggcacc tgtgatgtcc aggcactccc tgcttgatt ggggatctg gggttcatct  
 240  
 tccagctcc tctgtcctc cgctgggcac ctgtgatgtc caggcactcc ctgcttgat  
 300  
 cgggggggtct gggttttgtg ctatacttgg tgctccctt cactcaggcc ccttcttgac  
 360  
 tctgcagagc taccctcgc catctctttc acgcgggcct cctgcagtct ctgtgtcac  
 420  
 cctgtgactc tgcttccggt gttgtcaaat gggggtcac ccaggaccg caccactggg  
 480  
 tcgtgtgcag gtttctgggg tggcagagtg cggatgagtg ggcacgcgt  
 529

<210> 1722  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 1722

```

Met Ala Thr Leu Ser Gly Gln Ser Cys Pro Ser His Ala Gly Gly Ala
 1           5           10           15
Thr Gly Pro Gly Arg Cys Gly Phe Ser Leu Pro Ala Pro Val Leu
          20           25           30
Cys Trp Ala Leu Val Met Ser Arg His Ser Leu Leu Gly Ser Gly Asp
          35           40           45
Leu Gly Phe Ile Phe Pro Ala Pro Pro Val Leu Cys Trp Ala Pro Val
          50           55           60
Met Ser Arg His Ser Leu Leu Gly Leu Gly Asp Leu Gly Phe Ile Phe
65           70           75           80
Pro Ala Pro Pro Val Leu Arg Trp Ala Pro Val Met Ser Arg His Ser
          85           90           95
Leu Leu Gly Ser Gly Gly Leu Gly Phe Val Leu Tyr Leu Val Leu Pro
          100          105          110
Phe Thr Gln Ala Pro Ser
          115

```

&lt;210&gt; 1723

&lt;211&gt; 371

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1723

```

acgcgtttga agctggatgc atggatatcc agcgcgcgcca tcgggtcaaa tgggttgacg
60
ctgcccttga tggtcaccgg ggcgtagcga tctaccttac cgttgatgtc gacgctcgcc
120
ggtttggcct ggcggctgtc aatgggtgcc atcttcccg ttagttgttg aatggcagtg
180
gcaaagttgg gcgtgaggct gaagtcggcg aagttggccg agccatcatt gatcgcaacc
240
tgccaatgt gaatgcccag tggcttctct ttgctggccg ccggtgtct tgttgccagt
300
gtcggccggg tgcgggatca gcaagtcatc gatgttggtg gggcggatc cggtgatcgc
360
tgcatccaat a
371

```

&lt;210&gt; 1724

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1724

```

Met Asp Ile Gln Arg Arg His Arg Val Lys Trp Val Asp Ala Ala Leu
 1           5           10           15
Asp Gly His Arg Gly Val Ala Ile Tyr Leu Thr Val Asp Val Asp Ala
          20           25           30
Arg Arg Phe Gly Leu Ala Ala Val Asn Gly Ala Asn Leu Pro Val Glu
          35           40           45
Leu Leu Asn Gly Ser Gly Lys Val Gly Arg Glu Ala Glu Val Gly Glu
          50           55           60
Val Gly Arg Ala Ile Ile Asp Arg Asn Leu Pro Asn Val Asn Ala Gln

```

```

<400> 1726
Asp His Ala Val Leu Glu Ala Glu Arg Gln Lys Met Ser Ala Leu Val
 1          5          10          15
Arg Gly Leu Gln Arg Glu Leu Glu Glu Thr Ser Glu Glu Thr Gly His
 20          25          30
Trp Gln Ser Met Phe Gln Lys Asn Lys Glu Asp Leu Arg Ala Thr Lys
 35          40          45
Gln Glu Leu Leu Gln Leu Arg Met Glu Lys Glu Glu Met Glu Glu Glu

```

```

      50      55      60
Leu Gly Glu Lys Ile Glu Val Leu Gln Arg Glu Leu Glu Gln Ala Arg
65      70      75      80
Ala Ser Ala Gly Asp Thr Arg Gln Val Glu Val Leu Lys Lys Glu Leu
      85      90      95
Leu Arg Thr Gln Glu Glu Leu Lys Glu Leu Gln Ala Glu Arg Gln Ser
      100      105      110
Gln Glu Val Ala Gly Arg His Arg Asp Arg Glu Leu Glu Lys Gln Leu
      115      120      125
Ala Val Leu Arg Val Glu Ala Asp Arg Gly Arg Glu Leu Glu Glu Gln
      130      135      140
Asn Leu Gln Leu Gln Lys Thr Leu Gln Gln Leu Arg Gln Asp Cys Glu
145      150      155      160
Glu Ala Ser Lys Ala Lys Met Val Ala Glu Ala Glu Ala Thr Val Leu
      165      170      175
Gly Gln Arg Arg Ala Ala Val Glu Thr Thr Leu Arg Glu Thr Gln Glu
      180      185      190
Glu Asn Asp Glu Phe Arg Arg Arg Ile Leu Gly Leu Glu Gln Gln Leu
      195      200      205
Lys Glu Thr Arg Gly Leu Val Asp Gly Gly Glu Ala Val Glu Ala Arg
      210      215      220
Leu Arg Asp Lys Leu Gln
225      230

```

&lt;210&gt; 1727

&lt;211&gt; 474

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1727

```

aaccaactct ccacaacatc gccagaaaca gtcgctgcc aagggtcca ccatgtttta
60
gcagcttcag aagacaaaga taagatgaaa aaggaagttt tacaaagctc aaggacatt
120
atgcaatcca aatcagcttg cgaaattaaa caaagtcacc aagaatgtag tacccaacaa
180
acacaacaga agaagtattt ggagcagttg cacttgcccc aaagcaaacc aatttcccca
240
aatttcaaag ttaaaaccat caaacttcca actctagatc atacattaaa tgaaacagac
300
cacagctatg aaagtcataa acagcaatct gagattgatg ttcaaacctt taccaaaaaa
360
caatatctga aaaccaagaa aactgaagca agcactgaat gtagtcataa gcaatctctg
420
gctgaaagac attatcagtt acctaagaag gagaaaagag tgacagtaca attg
474

```

&lt;210&gt; 1728

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1728

Met Lys Lys Glu Val Leu Gln Ser Ser Arg Asp Ile Met Gln Ser Lys

```

      1           5           10           15
Ser Ala Cys Glu Ile Lys Gln Ser His Gln Glu Cys Ser Thr Gln Gln
      20           25           30
Thr Gln Gln Lys Lys Tyr Leu Glu Gln Leu His Leu Pro Gln Ser Lys
      35           40           45
Pro Ile Ser Pro Asn Phe Lys Val Lys Thr Ile Lys Leu Pro Thr Leu
      50           55           60
Asp His Thr Leu Asn Glu Thr Asp His Ser Tyr Glu Ser His Lys Gln
      65           70           75           80
Gln Ser Glu Ile Asp Val Gln Thr Phe Thr Lys Lys Gln Tyr Leu Lys
      85           90           95
Thr Lys Lys Thr Glu Ala Ser Thr Glu Cys Ser His Lys Gln Ser Leu
      100          105          110
Ala Glu Arg His Tyr Gln Leu Pro Lys Lys Glu Lys Arg Val Thr Val
      115          120          125
Gln Leu
      130

```

&lt;210&gt; 1729

&lt;211&gt; 470

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1729

```

acgcgtgact cgccataaca ttgctgacac gttttccacg gcaagggagg catcatgacg
60
aggatcgacg tgtggctgtg gtcggtgcgc gtctataagt cccggtcggt ggctaccgcc
120
gccgtcaagg gcggccacat tcgcctcaat ggagaccggt ttaaaccctc ccacgacgtg
180
aaaccggcgc ataccgtcac catccacacc cccggatggg accgggtcct caaggctcatc
240
aaccgatca cgaaaagagt cggcgccaaa ctgcggtcgc aggcttacga agatctgtca
300
nngccccccg accgcctac ctctctgnet cccctcgccc gccgcgaccg tggggctgga
360
cgaccaccca agaaggatcg tcgcgagatc gatcggtccc gaggcgggga ctctcgctat
420
tgaggactct tcgcccggcc caacacacca cggctcgcgg ccgaattggc
470

```

&lt;210&gt; 1730

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1730

```

His Val Phe His Gly Lys Gly Gly Ile Met Thr Arg Ile Asp Val Trp
      1           5           10           15
Leu Trp Ser Val Arg Val Tyr Lys Ser Arg Ser Leu Ala Thr Ala Ala
      20           25           30
Val Lys Gly Gly His Ile Arg Leu Asn Gly Asp Pro Val Lys Pro Ser
      35           40           45
His Asp Val Lys Pro Gly Asp Thr Val Thr Ile His Thr Pro Gly Trp

```

```

      50              55              60
Asp Arg Val Leu Lys Val Ile Asn Pro Ile Thr Lys Arg Val Gly Ala
65              70              75              80
Lys Leu Ala Val Glu Ala Tyr Glu Asp Leu Ser Xaa Pro Pro Asp Pro
      85              90              95
Pro Thr Ser Leu Xaa Pro Leu Ala Arg Arg Asp Arg Gly Ala Gly Arg
      100              105              110
Pro Thr Lys Lys Asp Arg Arg Glu Ile Asp Arg Leu Arg Gly Arg Asp
      115              120              125
Ser Arg Tyr
      130

```

```

<210> 1731
<211> 534
<212> DNA
<213> Homo sapiens

```

```

<400> 1731
agcgctccct gcctgctgct gggcggaggg aaggcggcaa gagctgcgga gcccttgaa
60
gagcttccag gaacctgcg ctgtgggata aaggaatgag gttcagaaag gggcagggag
120
ttgcccgcag ccgcaccgca cgtcttcagc ccgaccgttg tcttgacctc tctgtcccg
180
ccctgcccc gtctcaccat ggccttcttg acacagctga tgctgctgct ctggaagaat
240
ttcatgtatc gccggagaca gccggtccag ctcttggtcg aattgctgtg gcctctcttc
300
ctctttctta tcttggtggc tgttcgccac tcccaccgc cctggagca ccatgaatgc
360
cacttcccaa acaagccact gccatcggcg ggcaccgtgc cctgggtcca gggctctatc
420
tgtaatgtga acaacacctg ctttccgcag ctgacaccgg gcgaggagcc cgggcgcctg
480
agcaacttca acgactccct ggtctcccgg ctgctacgtc ggagagaggc tgga
534

```

```

<210> 1732
<211> 112
<212> PRT
<213> Homo sapiens

```

```

<400> 1732
Met Ala Phe Trp Thr Gln Leu Met Leu Leu Trp Lys Asn Phe Met
1      5      10      15
Tyr Arg Arg Arg Gln Pro Val Gln Leu Val Glu Leu Leu Trp Pro
      20      25      30
Leu Phe Leu Phe Phe Ile Leu Val Ala Val Arg His Ser His Pro Pro
      35      40      45
Leu Glu His His Glu Cys His Phe Pro Asn Lys Pro Leu Pro Ser Ala
      50      55      60
Gly Thr Val Pro Trp Leu Gln Gly Leu Ile Cys Asn Val Asn Asn Thr
65      70      75      80
Cys Phe Pro Gln Leu Thr Pro Gly Glu Glu Pro Gly Arg Leu Ser Asn

```

	85		90		95										
Phe	Asn	Asp	Ser	Leu	Val	Ser	Arg	Leu	Leu	Arg	Arg	Arg	Glu	Ala	Gly
	100			105									110		

&lt;210&gt; 1733

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1733

```

acgcgtgatg gccgatccga ctgtgcccgg tcacgaccgg cggcgtccga gtccctgaccc
60
ggacatgccg tggetgatcc ggcacatcac cctcggcaac aacgtgatcg cgggcagcac
120
gggcaactgc accctctgcg tcgaggacta ctgcgcagg tacgcggcga ggatcctcaa
180
catcgtctcc gacggcaacg tcctgcagcg cgcacgggcc gcacagccag cgtggctggt
240
tggtgtggtc gcggggatca gcgaactccg atccgtacgt attctccagc ctgcacgctt
300
accggggcag cactggtttt taggaccttc gtcgggtctc gatcgatggc gtgctgtcac
360
cgcgcccgga gcgctgctcc cgggcattga tctcaaggcg gtcacgagg
409

```

&lt;210&gt; 1734

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1734

Met	Ala	Asp	Pro	Thr	Val	Pro	Gly	His	Asp	Pro	Arg	Arg	Pro	Ser	Pro
1				5					10					15	
Asp	Pro	Asp	Met	Pro	Trp	Leu	Ile	Arg	Asp	Ile	Thr	Leu	Gly	Asn	Asn
			20					25					30		
Val	Ile	Ala	Gly	Ser	Thr	Gly	Asn	Cys	Thr	Leu	Cys	Val	Glu	Asp	Tyr
		35				40						45			
Ser	Arg	Arg	Tyr	Ala	Ala	Arg	Ile	Leu	Asn	Ile	Val	Ser	Asp	Gly	Asn
		50				55					60				
Val	Leu	Gln	Arg	Ala	Ser	Ala	Ala	Gln	Pro	Ala	Trp	Leu	Val	Gly	Val
65				70					75					80	
Val	Ala	Gly	Ile	Ser	Glu	Leu	Arg	Ser	Val	Arg	Ile	Leu	Gln	Pro	Arg
			85					90					95		
Arg	Leu	Pro	Gly	Asp	His	Trp	Phe	Leu	Gly	Pro	Ser	Leu	Gly	Leu	Asp
		100					105					110			
Arg	Trp	Arg	Ala	Val	Thr	Ala	Ala	Gly	Ala	Leu	Leu	Pro	Gly	Ile	Asp
		115				120						125			
Leu	Lys	Ala	Val	Thr	Arg										
															130

&lt;210&gt; 1735

&lt;211&gt; 342

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1735

ggcgccatgg tcatcagcat catgtgttcg gcgcccgtg cacgaatgtt cgtgcgatca  
 60  
 agcgcgcctt ttagttcgac gcacggtaaa gcccggtgcg atcgatgtag gccaggaccg  
 120  
 cgtcaggcac caggaaacgt accgacttcc cgctggccgg cagttgacgg atctgggtgg  
 180  
 cggacaccgc aagcgggggc tgccagacga atgcaatatt cccgttcggc ccggtcaggg  
 240  
 ccaaggggtc acttaccgac cgcgcgccca gcaggttgcg caaggcatcc ggcggttcgc  
 300  
 tggcggcatc cgggcgttgc aaaaccagga tgtggcaatg ct  
 342

&lt;210&gt; 1736

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1736

Met	Val	Ile	Ser	Ile	Met	Cys	Ser	Ala	Pro	Ala	Ala	Arg	Met	Phe	Val
1				5					10					15	
Arg	Ser	Ser	Ala	Pro	Phe	Ser	Ser	Thr	His	Gly	Lys	Ala	Arg	Ala	His
			20					25					30		
Arg	Cys	Arg	Pro	Gly	Pro	Arg	Gln	Ala	Pro	Gly	Asn	Val	Pro	Thr	Ser
		35					40					45			
Arg	Trp	Pro	Ala	Val	Asp	Gly	Ser	Gly	Trp	Arg	Thr	Pro	Gln	Ala	Gly
	50					55					60				
Ser	Ala	Arg	Arg	Met	Gln	Tyr	Ser	Arg	Ser	Ala	Arg	Ser	Gly	Pro	Arg
65					70					75				80	
Gly	His	Leu	Pro	Thr	Ala	Arg	Pro	Ala	Gly	Cys	Ala	Arg	His	Pro	Ala
				85					90					95	
Val	Arg	Trp	Arg	His	Pro	Gly	Val	Ala	Lys	Pro	Gly	Cys	Gly	Asn	Ala
				100				105						110	

&lt;210&gt; 1737

&lt;211&gt; 506

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1737

acgcgtgttc accatgacct ggaccgcccc gcggcccgac gggtcgagcg cggaggagtc  
 60  
 ggacgagacg actgtggtgg tccctgccat ctacgcgcc cacgggtacg acgtgcaggc  
 120  
 gtccggcgcc cacgtcacct cccaccaggg cgaccgggtg gcgcggttgc acctcaacca  
 180  
 aggcagtacc acggcgaagg tcacgatcac cctgcgctaa cccttcaagc gtcttcagca  
 240  
 ccgacctata agtctcccag acacttttac gaccggccct ccccttggg gtgggccccg  
 300  
 tccttttcgt gtcgtgggat gcacctggca gcaccacctc cgcccccat ggagaacagt  
 360



aggtatcctc gcaggggtact acggccaagg catatttgac gttccacgct tgccactgcc  
 420  
 gtcttagggc catactgccg ccacgcagct gagacggtga ccaatcgggt aaggtgactg  
 480  
 gttgccgtag tccatgcgag gccggc  
 506

<210> 1738  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 1738  
 Met Ala Leu Arg Arg Gln Trp Gln Ala Trp Asn Val Lys Tyr Ala Leu  
 1 5 10 15  
 Ala Val Val Pro Cys Glu Asp Thr Tyr Cys Ser Pro Trp Gly Pro Glu  
 20 25 30  
 Val Val Leu Pro Gly Ala Ser His Asp Thr Lys Arg Thr Gly Pro Thr  
 35 40 45  
 Pro Arg Gly Arg Ala Gly Arg Lys Ser Val Trp Glu Thr Tyr Arg Ser  
 50 55 60  
 Val Leu Lys Thr Leu Glu Gly Leu Ala Gln Gly Asp Arg Asp Leu Arg  
 65 70 75 80  
 Arg Gly Thr Ala Leu Val Glu Val Gln Pro Arg His Pro Val Ala Trp  
 85 90 95  
 Val Gly Gly Asp Val Gly Ala Gly Arg Leu His Val Val Pro Val Gly  
 100 105 110  
 Arg

<210> 1739  
 <211> 420  
 <212> DNA  
 <213> Homo sapiens

<400> 1739  
 cgcgttattg aaaatgctgc tttttttact aaattaggac agcgtttaat cggcgcatta  
 60  
 catcaagtga cggttgatgg atttggttac cgtgttgata tgcggttacg cccttttgga  
 120  
 gagtctgggc cattgggttag cacgtttaat tcaatagagg actattatca aaccatgggt  
 180  
 cgagagtggg agtggttatgc catgggttaa gcccggtgta ttggtgttga ggacgagtat  
 240  
 aaacaagcgt tagaaaggat gttaaggcct ttcgtattta gacgttacat tgatttttagc  
 300  
 gctattgatt ctttgcgaaa aatgaaaacg atgatcagtg ctgaagtgcg tcgcaagggg  
 360  
 ttaaaagaca atattaagtt gggaatggga gggatccgtg aaattgaatt tgtggctcaa  
 420

<210> 1740  
 <211> 140  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1740

```

Arg Val Ile Glu Asn Ala Ala Phe Phe Thr Lys Leu Gly Gln Arg Leu
 1           5           10           15
Ile Gly Ala Leu His Gln Val Thr Val Asp Gly Phe Val Tyr Arg Val
      20           25           30
Asp Met Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Ser Thr
      35           40           45
Phe Asn Ser Ile Glu Asp Tyr Tyr Gln Thr His Gly Arg Glu Trp Glu
      50           55           60
Cys Tyr Ala Met Val Lys Ala Arg Val Ile Gly Val Glu Asp Glu Tyr
      65           70           75           80
Lys Gln Ala Leu Glu Arg Met Leu Arg Pro Phe Val Phe Arg Arg Tyr
      85           90           95-
Ile Asp Phe Ser Ala Ile Asp Ser Leu Arg Lys Met Lys Thr Met Ile
      100          105          110
Ser Ala Glu Val Arg Arg Lys Gly Leu Lys Asp Asn Ile Lys Leu Gly
      115          120          125
Met Gly Gly Ile Arg Glu Ile Glu Phe Val Ala Gln
      130          135          140

```

&lt;210&gt; 1741

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1741

```

nnacgcgctcg aggtgattca ggccgacgcc actgaccgcg tggtccttca cagtctcaat
60
gggcaggtcg acgtcgctcg ctccaacccg ccctacgtgc cagccggcgc cgtggaggac
120
accgagacgg cccagcacga gcccacggtg gcgctctatg gcggggggccc ggacgggtga
180
gagattccga ttgacgtcct gngtgcgctc agtcgcgctg ctgccaccgg cggagtgtc
240
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&lt;210&gt; 1742

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1742

```

Xaa Arg Val Glu Val Ile Gln Ala Asp Ala Thr Asp Pro Leu Val Leu
 1           5           10           15
His Ser Leu Asn Gly Gln Val Asp Val Val Val Ser Asn Pro Pro Tyr
      20           25           30
Val Pro Ala Gly Ala Val Glu Asp Thr Glu Thr Ala Gln His Glu Pro

```

35                      40                      45  
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 50                      55

<210> 1743

<211> 4121

<212> DNA

<213> Homo sapiens

<400> 1743

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 4121

&lt;210&gt; 1744

&lt;211&gt; 796

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1744

Ile	Thr	Tyr	Asn	Cys	Lys	Glu	Glu	Phe	Gln	Ile	His	Asp	Glu	Leu	Leu
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Lys	Ala	His	Tyr	Thr	Leu	Gly	Arg	Leu	Ser	Asp	Asn	Thr	Pro	Glu	His
		20					25					30			
Tyr	Leu	Val	Gln	Gly	Arg	Tyr	Phe	Leu	Val	Arg	Asp	Val	Thr	Glu	Lys
	35					40					45				
Met	Asp	Val	Leu	Gly	Thr	Val	Gly	Ser	Cys	Gly	Ala	Pro	Asn	Phe	Arg

50		55		60	
Gln Val Gln Gly Gly	Leu Thr Val Phe Gly Met Gly Gln Pro Ser Leu				
65	70	75	80		
Ser Gly Phe Arg Arg	Val Leu Gln Lys Leu Gln Lys Asp Gly His Arg				
	85	90	95		
Glu Cys Val Ile Phe Cys Val Arg Glu Glu Pro Val Leu Phe Leu Arg					
	100	105	110		
Ala Asp Glu Asp Phe Val Ser Tyr Thr Pro Arg Asp Lys Gln Asn Leu					
	115	120	125		
His Glu Asn Leu Gln Gly Leu Gly Pro Gly Val Arg Val Glu Ser Leu					
	130	135	140		
Glu Leu Ala Ile Arg Lys Glu Ile His Asp Phe Ala Gln Leu Ser Glu					
	145	150	155		160
Asn Thr Tyr His Val Tyr His Asn Thr Glu Asp Leu Trp Gly Glu Pro					
	165	170	175		
His Ala Val Ala Ile His Gly Glu Asp Asp Leu His Val Thr Glu Glu					
	180	185	190		
Val Tyr Lys Arg Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His Arg					
	195	200	205		
Leu Pro Leu Pro Glu Gln Gly Ser Pro Leu Glu Ala Gln Leu Asp Ala					
	210	215	220		
Phe Val Ser Val Leu Arg Glu Thr Pro Ser Leu Leu Gln Leu Arg Asp					
	225	230	235		240
Ala His Gly Pro Pro Pro Ala Leu Val Phe Ser Cys Gln Met Gly Val					
	245	250	255		
Gly Arg Thr Asn Leu Gly Met Val Leu Gly Thr Leu Ile Leu Leu His					
	260	265	270		
Arg Ser Gly Thr Thr Ser Gln Pro Glu Ala Ala Pro Thr Gln Ala Lys					
	275	280	285		
Pro Leu Pro Met Glu Gln Phe Gln Val Ile Gln Ser Phe Leu Arg Met					
	290	295	300		
Val Pro Gln Gly Arg Arg Met Val Glu Glu Val Asp Arg Ala Ile Thr					
	305	310	315		320
Ala Cys Ala Glu Leu His Asp Leu Lys Glu Val Val Leu Glu Asn Gln					
	325	330	335		
Lys Lys Leu Glu Gly Ile Arg Pro Glu Ser Pro Ala Gln Gly Ser Gly					
	340	345	350		
Ser Arg His Ser Val Trp Gln Arg Ala Leu Trp Ser Leu Glu Arg Tyr					
	355	360	365		
Phe Tyr Leu Ile Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro Leu					
	370	375	380		
Ala Phe Ala Leu Ser Phe Ser Arg Trp Leu Cys Ala His Pro Glu Leu					
	385	390	395		400
Tyr Arg Leu Pro Val Thr Leu Ser Ser Ala Gly Pro Val Ala Pro Arg					
	405	410	415		
Asp Leu Ile Ala Arg Gly Ser Leu Arg Glu Asp Asp Leu Val Ser Pro					
	420	425	430		
Asp Ala Leu Ser Thr Val Arg Glu Met Asp Val Ala Asn Phe Arg Arg					
	435	440	445		
Val Pro Arg Met Pro Ile Tyr Gly Thr Ala Gln Pro Ser Ala Lys Ala					
	450	455	460		
Leu Gly Ser Ile Leu Ala Tyr Leu Thr Asp Ala Lys Arg Arg Leu Arg					
	465	470	475		480
Lys Val Val Trp Val Ser Leu Arg Glu Glu Ala Val Leu Glu Cys Asp					

485 490 495  
 Gly His Thr Tyr Ser Leu Arg Trp Pro Gly Pro Pro Val Ala Pro Asp  
 500 505 510  
 Gln Leu Glu Thr Leu Glu Ala Gln Leu Lys Ala His Leu Ser Glu Pro  
 515 520 525  
 Pro Pro Gly Lys Glu Gly Pro Leu Thr Tyr Arg Phe Gln Thr Cys Leu  
 530 535 540  
 Thr Met Gln Glu Val Phe Ser Gln His Arg Arg Ala Cys Pro Gly Leu  
 545 550 555 560  
 Thr Tyr His Arg Ile Pro Met Pro Asp Phe Cys Ala Pro Arg Glu Glu  
 565 570 575  
 Asp Phe Asp Gln Leu Leu Glu Ala Leu Arg Ala Ala Leu Ser Lys Asp  
 580 585 590  
 Pro Gly Thr Gly Phe Val Phe Ser Cys Leu Ser Gly Gln Gly Arg Thr  
 595 600 605  
 Thr Thr Ala Met Val Val Ala Val Leu Ala Phe Trp His Ile Gln Gly  
 610 615 620  
 Phe Pro Glu Val Gly Glu Glu Glu Leu Val Ser Val Pro Asp Ala Lys  
 625 630 635 640  
 Phe Thr Lys Gly Glu Phe Gln Val Val Met Lys Val Val Gln Leu Leu  
 645 650 655  
 Pro Asp Gly His Arg Val Lys Lys Glu Val Asp Ala Ala Leu Asp Thr  
 660 665 670  
 Val Ser Glu Thr Met Thr Pro Met His Tyr His Leu Arg Glu Ile Ile  
 675 680 685  
 Ile Cys Thr Tyr Arg Gln Ala Lys Ala Ala Lys Glu Ala Gln Glu Met  
 690 695 700  
 Arg Arg Leu Gln Leu Arg Ser Leu Gln Tyr Leu Glu Arg Tyr Val Cys  
 705 710 715 720  
 Leu Ile Leu Phe Asn Ala Tyr Leu His Leu Glu Lys Ala Asp Ser Trp  
 725 730 735  
 Gln Arg Pro Phe Ser Thr Trp Met Gln Glu Val Ala Ser Lys Ala Gly  
 740 745 750  
 Ile Tyr Glu Ile Leu Asn Glu Leu Gly Phe Pro Glu Leu Glu Ser Gly  
 755 760 765  
 Glu Asp Gln Pro Phe Ser Arg Leu Arg Tyr Arg Trp Gln Glu Gln Ser  
 770 775 780  
 Cys Ser Leu Glu Pro Ser Ala Pro Glu Asp Leu Leu  
 785 790 795

&lt;210&gt; 1745

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1745

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 120  
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 180  
 aaagacggta tcactttgga atttacggag ttcacaggct actcacaacc aaacaaggca  
 240

actgctgatg gcgaagtaga tttgaacgct ttccaacact ataacttctt gaacaactgg  
 300  
 aacaaagaaa acgggaaaga ccttgtagcg attgcagata cttacatctc tccaatccgt  
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 420  
 tcgcga  
 426

<210> 1746

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1746

Xaa	Met	Lys	Ile	Lys	Lys	Trp	Leu	Gly	Val	Ala	Ala	Leu	Ala	Thr	Val
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Ala	Gly	Leu	Ala	Leu	Ala	Ala	Cys	Gly	Asn	Ser	Glu	Lys	Lys	Ala	Asp
		20						25				30			
Asn	Ala	Thr	Thr	Ile	Lys	Ile	Ala	Thr	Val	Asn	Arg	Ser	Gly	Ser	Glu
		35					40					45			
Glu	Lys	Arg	Trp	Asp	Lys	Ile	Gln	Glu	Leu	Val	Lys	Lys	Asp	Gly	Ile
	50					55				60					
Thr	Leu	Glu	Phe	Thr	Glu	Phe	Thr	Gly	Tyr	Ser	Gln	Pro	Asn	Lys	Ala
65					70					75				80	
Thr	Ala	Asp	Gly	Glu	Val	Asp	Leu	Asn	Ala	Phe	Gln	His	Tyr	Asn	Phe
			85					90						95	
Leu	Asn	Asn	Trp	Asn	Lys	Glu	Asn	Gly	Lys	Asp	Leu	Val	Ala	Ile	Ala
		100						105					110		
Asp	Thr	Tyr	Ile	Ser	Pro	Ile	Arg	Leu	Tyr	Ser	Gly	Leu	Asn	Gly	Ser
		115					120					125			
Asp	Asn	Lys	Tyr	Thr	Lys	Val	Glu	Ala	Gly	Val	Cys	Ser	Arg		
	130					135					140				

<210> 1747

<211> 373

<212> DNA

<213> Homo sapiens

<400> 1747

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 120  
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 240  
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 373



<210> 1748  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 1748  
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 Leu Glu Ala Pro Ala Gly Ser Leu Leu Lys Asp Gly Thr Trp His Ile  
 20 25 30  
 Met Tyr Gln Tyr Glu Pro His Ala Asp Gly His Gly Leu Trp Gly His  
 35 40 45  
 Val Thr Ser Pro Asn Phe Ser Pro Phe Asn Trp Thr Asp Gly Glu Asp  
 50 55 60  
 Ile Leu Val Pro Glu Gly Glu Glu Thr Asp Leu Trp Ala Gly Ser Val  
 65 70 75 80  
 Ile Ser Asn Ala Gly Lys Val Thr Leu Phe Phe Thr Ser Val Lys Gly  
 85 90 95  
 Asp Xaa Asp Gly Asn Pro Ser Gly Arg Cys Arg Arg Arg Gln Ser Tyr  
 100 105 110  
 Ala

<210> 1749  
 <211> 853  
 <212> DNA  
 <213> Homo sapiens

<400> 1749  
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 aaggggagga gagtgagggc caagaacgag ccttaaggga gcagtcccaa gctggagcca  
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 aggacactga gga  
 853

<210> 1750  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<400> 1750  
 Glu Lys Pro Arg Thr His Cys Val Leu Ala Pro Leu Arg Pro Ala Trp  
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 His Thr Val Ala Cys Trp Arg Leu Ser Trp Gly Ser Ala Trp Ala Leu  
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 Gly Ile Ala Cys Gly Pro Leu Asn Ser Trp Gly Ser Gly Arg Asn Pro  
 35 40 45  
 Ser Leu Pro Glu Ala Leu Met Ser Pro Tyr Val Pro Gly Thr Gly Ala  
 50 55 60

<210> 1751  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 1751  
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 420  
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 531

<210> 1752  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 1752  
 Gly Arg Ile Pro His Leu Gly Arg Trp Arg Met Gly Asn Phe Ser Arg

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Arg Gln Gly His Asp Asp Ala Val Val Glu Lys Ala Met Ala Thr Thr			
	20	25	30
Gly Val Ser Glu Leu Thr Asp Arg Ala Trp Ser Ser Leu Ser Gly Gly			
	35	40	45
Glu Arg Gln Arg Val Gln Leu Ala Arg Ala Leu Ala Gln Glu Pro Glu			
	50	55	60
Ile Leu Phe Leu Asp Glu Pro Thr Asn His Leu Asp Leu Pro His Gln			
65	70	75	80
Ile Asp Leu Leu Glu Arg Val Arg Gly Leu Gly Leu Thr Thr Val Thr			
	85	90	95
Val Ile His Asp Leu Asp Leu Ala Ala Ala Tyr Ala Asp Asp Leu Ile			
	100	105	110
Val Leu Asp Ser Gly Arg Met Val Ala Gly Gly Pro Ala Ser Thr Val			
	115	120	125
Leu Thr Pro Gly Leu Val Arg Asp His Phe Gly Val Asp Gly Glu Val			
	130	135	140
Trp Ser Ser Ser Arg Arg Gly Phe Thr Trp Asn Gly Leu Gln Thr			
145	150	155	

&lt;210&gt; 1753

&lt;211&gt; 920

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1753

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120  
acacagacca ggatcagcca aaagggccgc cgtctgcagc ccccggggac tccctcggcc  
180  
ccaccccgga gaaggcccg gaaacagctg aaccctgcc ggggcaccga gagagtggac  
240  
cctgggttcg agggggtgac tctgaagttt cagataaagc cggactccag cctgcagatc  
300  
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360  
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420  
gagccccggc gctgtgcttc ctgtcggacc cagaggaccc cgctctggag agacgtgaa  
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ggagtgtccc tggaccccat tcaggaaggt taaaccagc ttcaccctgc tgagctgctg  
660  
cttctgcctc cgtttcacca gtgggagaat gggcagaagc agctctccta ggaggattgg  
720  
ggaaagagcc ggctgcctc ctctctgcca tctccagatt caaggatccc gggggaagac  
780  
ccaggcctca ggtggcagag cctgctaggg gtcaccagcc cttctccag tcagccttgg  
840

ccgaggcccc ctcaggagac gctctcagga aggatgagca ttgttacagc agggacaata  
 900  
 aagtacagag atatgccgag  
 920

<210> 1754  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens

<400> 1754  
 Glu Thr Val Glu Arg Leu Gly Gln Ser Pro Ala Gln Asp Thr Pro Val  
 1 5 10 15  
 Leu Gly Pro Cys Trp Asp Pro Met Ala Leu Gly Thr Gln Gly Arg Leu  
 20 25 30  
 Leu Leu Asp Arg Asp Ser Lys Asp Thr Gln Thr Arg Ile Ser Gln Lys  
 35 40 45  
 Gly Arg Arg Leu Gln Pro Pro Gly Thr Pro Ser Ala Pro Pro Gln Arg  
 50 55 60  
 Arg Pro Arg Lys Gln Leu Asn Pro Cys Arg Gly Thr Glu Arg Val Asp  
 65 70 75 80  
 Pro Gly Phe Glu Gly Val Thr Leu Lys Phe Gln Ile Lys Pro Asp Ser  
 85 90 95  
 Ser Leu Gln Ile Ile Pro Thr Tyr Ser Leu Pro Cys Ser Ser Arg Ser  
 100 105 110  
 Gln Glu Ser Pro Ala Asp Ala Val Gly Gly Xaa Ala Ala Ile Pro Glu  
 115 120 125  
 Gly Thr Glu Gly His Ser Ala Gly Ser Glu Ala Leu Glu Pro Arg Arg  
 130 135 140  
 Cys Ala Ser Cys Arg Thr Gln Arg Thr Pro Leu Trp Arg Asp Ala Glu  
 145 150 155 160  
 Asp Gly Thr Leu Leu Cys Asn Ala Cys Gly Ile Arg Tyr Lys Lys Tyr  
 165 170 175  
 Gly Thr Arg Cys Ser Ser Cys Trp Leu Val Pro Arg Lys Asn Val Gln  
 180 185 190  
 Pro Lys Arg Leu Cys Gly Arg Cys Gly Val Ser Leu Asp Pro Ile Gln  
 195 200 205  
 Glu Gly  
 210

<210> 1755  
 <211> 437  
 <212> DNA  
 <213> Homo sapiens

<400> 1755  
 nnttctgcag agtagggaga cagtcttggg cctggatggc cattagtgc tggagtcag  
 60  
 ggagcaatca gaaatgatca aggagaatcc ttgatacgaa ctgcattcca gtgtcttcag  
 120  
 ttggttgatga cagatcttct accaacaatg ccttgactt gcctgcaa atgttgtagat  
 180  
 gttgcaggta gctttggcct ccataaccaa gaactcaata ttagtttaac ttcaatagg  
 240

ttattgtgga atatttcaga ttattttttc caaagagggg aaactattga aaaagaacta  
 300  
 aataaggaag aggcagcaca gcaaaagcag gcagaagaga aaggagttgt tttaaactcg  
 360  
 ccattccacc ctgcaccgcc atttgattgc ttgtgggttat gtctttatgc aaaattgggt  
 420  
 gaactatgtg tggatcc  
 437

<210> 1756

<211> 126

<212> PRT

<213> Homo sapiens

<400> 1756

Met	Gly	Ala	Ile	Arg	Asn	Asp	Gln	Gly	Glu	Ser	Leu	Ile	Arg	Thr	Ala
1				5					10					15	
Phe	Gln	Cys	Leu	Gln	Leu	Val	Val	Thr	Asp	Phe	Leu	Pro	Thr	Met	Pro
			20					25					30		
Cys	Thr	Cys	Leu	Gln	Ile	Val	Val	Asp	Val	Ala	Gly	Ser	Phe	Gly	Leu
			35					40				45			
His	Asn	Gln	Glu	Leu	Asn	Ile	Ser	Leu	Thr	Ser	Ile	Gly	Leu	Leu	Trp
	50					55				60					
Asn	Ile	Ser	Asp	Tyr	Phe	Gln	Arg	Gly	Glu	Thr	Ile	Glu	Lys	Glu	
65					70				75				80		
Leu	Asn	Lys	Glu	Glu	Ala	Ala	Gln	Gln	Lys	Gln	Ala	Glu	Glu	Lys	Gly
			85					90					95		
Val	Val	Leu	Asn	Arg	Pro	Phe	His	Pro	Ala	Pro	Pro	Phe	Asp	Cys	Leu
			100					105					110		
Trp	Leu	Cys	Leu	Tyr	Ala	Lys	Leu	Gly	Glu	Leu	Cys	Val	Asp		
		115					120					125			

<210> 1757

<211> 1297

<212> DNA

<213> Homo sapiens

<400> 1757

nggatccgac ggaaatagaa ttgaaggcat tctaaaatgg ctaaccgtac agtgaaggat  
 60  
 gcgcacagca tccatggcac caaccctcaa tatctggtgg agaagatcat tcgaacgcga  
 120  
 atctatgagt ccaagtactg gaaagaggag tgctttggac ttacagctga acttgtagtc  
 180  
 gataaagcca tggagttaag gtttgtgggt ggcgtctatg gtggcaacat aaaaccaaca  
 240  
 ccctttctgt gtttaacctt gaagatgctt caaattcaac ccgagaagga tatcattgta  
 300  
 gagtttatca aaaatgaaga ttcaagtat gtccgcatgc tgggggcact ttacatgagg  
 360  
 ctgacaggca ctgcaattga ttgtacaag tacttggaac ctttgtacaa tgactatcga  
 420  
 aaaatcaaga gccagaaccg aaatggggag tttgaattga tgcattgtga tgagtttatt  
 480

gatgaactat tgcacagtga gagagtctgt gatatcattc tgccccgact acagaaacgc  
 540  
 tatgtattag aggaagctga gcaactggag cctcgagtta gtgctctgga agaggacatg  
 600  
 gatgatgtgg agtccagtga agaggaagaa gaggaggatg agaagttgga aagagtgcc  
 660  
 tcacctgac accgccggag aagctaccga gacttggaca agccccgtcg ctctcccaca  
 720  
 ctgcgctaca ggaggagtag gagccggtct cccagaaggc ggagtcgac tcccaaaagg  
 780  
 agaagcccct cccctcgccg agaaaggcat cggagcaaga gtccaagacg tcaccgcagc  
 840  
 aggtcccag atcgccggca cagatcccgt tccaagtccc caggatcatca ccgtagtcac  
 900  
 agacacagga gccactcaaa gtctcccgaa aggtctaaga agagccacaa gaagagccgg  
 960  
 agagggaaatg agtaatggac tcagtttggg tttagtccac atggcctcct gtggatataa  
 1020  
 ggatatctgt atgtggaagg attaagatct ccccaggca gctataagaa tatttttagtt  
 1080  
 tttttcttat caagtttctc aacctttatt tttaatgaag gaggtgctga gttttgtatc  
 1140  
 tttttaatca taatcaacat cagtttttga cccaactaac cttgactgta ttcaaaacta  
 1200  
 tgagagtata aaggatctgg aggttgggga tatgactgac aaggaaaggc tgtggccacc  
 1260  
 tgatgacctt ttcctttttt attaaaccgg acacacc  
 1297

&lt;210&gt; 1758

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1758

Met	Ala	Asn	Arg	Thr	Val	Lys	Asp	Ala	His	Ser	Ile	His	Gly	Thr	Asn
1				5				10					15		
Pro	Gln	Tyr	Leu	Val	Glu	Lys	Ile	Ile	Arg	Thr	Arg	Ile	Tyr	Glu	Ser
		20					25					30			
Lys	Tyr	Trp	Lys	Glu	Glu	Cys	Phe	Gly	Leu	Thr	Ala	Glu	Leu	Val	Val
	35						40					45			
Asp	Lys	Ala	Met	Glu	Leu	Arg	Phe	Val	Gly	Gly	Val	Tyr	Gly	Gly	Asn
	50					55					60				
Ile	Lys	Pro	Thr	Pro	Phe	Leu	Cys	Leu	Thr	Leu	Lys	Met	Leu	Gln	Ile
65				70					75					80	
Gln	Pro	Glu	Lys	Asp	Ile	Ile	Val	Glu	Phe	Ile	Lys	Asn	Glu	Asp	Phe
			85					90					95		
Lys	Tyr	Val	Arg	Met	Leu	Gly	Ala	Leu	Tyr	Met	Arg	Leu	Thr	Gly	Thr
		100					105					110			
Ala	Ile	Asp	Cys	Tyr	Lys	Tyr	Leu	Glu	Pro	Leu	Tyr	Asn	Asp	Tyr	Arg
		115					120					125			
Lys	Ile	Lys	Ser	Gln	Asn	Arg	Asn	Gly	Glu	Phe	Glu	Leu	Met	His	Val
	130				135					140					
Asp	Glu	Phe	Ile	Asp	Glu	Leu	Leu	His	Ser	Glu	Arg	Val	Cys	Asp	Ile

```

145          150          155          160
Ile Leu Pro Arg Leu Gln Lys Arg Tyr Val Leu Glu Glu Ala Glu Gln
          165          170          175
Leu Glu Pro Arg Val Ser Ala Leu Glu Glu Asp Met Asp Asp Val Glu
          180          185          190
Ser Ser Glu Glu Glu Glu Glu Glu Asp Glu Lys Leu Glu Arg Val Pro
          195          200          205
Ser Pro Asp His Arg Arg Arg Ser Tyr Arg Asp Leu Asp Lys Pro Arg
          210          215          220
Arg Ser Pro Thr Leu Arg Tyr Arg Arg Ser Arg Ser Arg Ser Pro Arg
225          230          235          240
Arg Arg Ser Arg Ser Pro Lys Arg Arg Ser Pro Ser Pro Arg Arg Glu
          245          250          255
Arg His Arg Ser Lys Ser Pro Arg Arg His Arg Ser Arg Ser Arg Asp
          260          265          270
Arg Arg His Arg Ser Arg Ser Lys Ser Pro Gly His His Arg Ser His
          275          280          285
Arg His Arg Ser His Ser Lys Ser Pro Glu Arg Ser Lys Lys Ser His
          290          295          300
Lys Lys Ser Arg Arg Gly Asn Glu
305          310

```

&lt;210&gt; 1759

&lt;211&gt; 324

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1759

```

aattccatag tctcatggg caagagttac acagcgtgga ggaccaactc ccaggcactc
60
ggcctgggca gacacaatta ttgtcggaat ccagatggtg atgccagacc ttggtgccat
120
gtgatgaagg accgaaagct gacgtgggaa tactgtgaca tgtcccatg ctccacctgt
180
ggcctgaggc agtgcaaacy gcctcagttt agaactaaag gaggactcta cacagacatc
240
acctcacacc cttggcaggc tgccatcttt gtcagcaaca agaggtctcc tggagagaga
300
ttcctttgtg gaggggtgct gatc
324

```

&lt;210&gt; 1760

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1760

```

Asn Ser Ile Val Leu Met Gly Lys Ser Tyr Thr Ala Trp Arg Thr Asn
1          5          10          15
Ser Gln Ala Leu Gly Leu Gly Arg His Asn Tyr Cys Arg Asn Pro Asp
          20          25          30
Gly Asp Ala Arg Pro Trp Cys His Val Met Lys Asp Arg Lys Leu Thr
          35          40          45
Trp Glu Tyr Cys Asp Met Ser Pro Cys Ser Thr Cys Gly Leu Arg Gln

```

```

      50              55              60
Cys Lys Arg Pro Gln Phe Arg Thr Lys Gly Gly Leu Tyr Thr Asp Ile
65              70              75              80
Thr Ser His Pro Trp Gln Ala Ala Ile Phe Val Ser Asn Lys Arg Ser
      85              90              95
Pro Gly Glu Arg Phe Leu Cys Gly Gly Val Leu Ile
      100              105

```

<210> 1761  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1761
ngcgatctcg gctcactaca acctcgggtga cagagcgaga ctctatccca aaaaaataaa
60
aataaaaaatc aactggagaa ggaaatgggg ttggggagca tcctctgaat atataaaggc
120
agccattcat tgtaggagag gaggtagaag gaaatgctgt ttgtcgatgg ttcttttcca
180
gagaggaaga gaggagaaag gaagagcggg gagcaggtgg ggagcccgca gtaagacccc
240
acagtggggc caggtgggtct tgcacctgt attcccactt tggctggggc agcccagagt
300
ccaggccagc aggtaatgcc ccagccatgc ccactcggtc ctattggatc c
351

```

<210> 1762  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1762
Met Ala Gly Ala Leu Pro Ala Gly Leu Asp Ser Gly Leu Pro Gln Pro
1              5              10              15
Lys Trp Glu Tyr Arg Val Gln Asp His Leu Ala Pro Leu Trp Gly Leu
      20              25              30
Thr Ala Gly Ser Pro Pro Ala Pro Arg Ser Ser Phe Leu Leu Ser Ser
      35              40              45
Ser Leu Glu Lys Asn His Arg Gln Thr Ala Phe Pro Ser Thr Ser Ser
      50              55              60
Pro Thr Met Asn Gly Cys Leu Tyr Ile Phe Arg Gly Cys Ser Pro Thr
65              70              75              80
Pro Phe Pro Ser Pro Val Asp Phe Tyr Phe Tyr Phe Phe Gly Ile Glu
      85              90              95
Ser Arg Ser Val Thr Glu Val Val Val Ser Arg Asp Arg
      100              105

```

<210> 1763  
 <211> 356  
 <212> DNA  
 <213> Homo sapiens

<400> 1763



gcgcgccggg ggcgcgatgt ggagcgggca cttacccggt tcatggccaa gacaggcgag  
 60  
 actcagagtc ttttcaaaga tgacgtcagc acatttccat tgattgctgc cagacctttc  
 120  
 accatcccct acctgacagc tcttcttcg tctgaactgg agatgcaaca aatggaagag  
 180  
 acagattcct cggagcagga tgaacagaca gacacagaga accttgctct tcatatcagc  
 240  
 atggaggatt ctggagccga gaaagagaac acctctgtcc tgcagcagaa cccctccttg  
 300  
 tcgggtagcc ggaatgggga ggagaacatc atcgataacc cttatctgcg accggt  
 356

<210> 1764

<211> 118

<212> PRT

<213> Homo sapiens

<400> 1764

Ala	Arg	Arg	Gly	Arg	Asp	Val	Glu	Arg	Ala	Leu	Thr	Arg	Phe	Met	Ala
1			5						10					15	
Lys	Thr	Gly	Glu	Thr	Gln	Ser	Leu	Phe	Lys	Asp	Asp	Val	Ser	Thr	Phe
		20						25					30		
Pro	Leu	Ile	Ala	Ala	Arg	Pro	Phe	Thr	Ile	Pro	Tyr	Leu	Thr	Ala	Leu
	35						40					45			
Leu	Pro	Ser	Glu	Leu	Glu	Met	Gln	Gln	Met	Glu	Glu	Thr	Asp	Ser	Ser
	50					55					60				
Glu	Gln	Asp	Glu	Gln	Thr	Asp	Thr	Glu	Asn	Leu	Ala	Leu	His	Ile	Ser
65					70					75				80	
Met	Glu	Asp	Ser	Gly	Ala	Glu	Lys	Glu	Asn	Thr	Ser	Val	Leu	Gln	Gln
			85						90					95	
Asn	Pro	Ser	Leu	Ser	Gly	Ser	Arg	Asn	Gly	Glu	Glu	Asn	Ile	Ile	Asp
			100					105					110		
Asn	Pro	Tyr	Leu	Arg	Pro										
			115												

<210> 1765

<211> 357

<212> DNA

<213> Homo sapiens

<400> 1765

cggccgcatt cttcgtgact ggcgccccgc cgccggtgca aaagtgtcag gaaataccag  
 60  
 tcatgactat gtttagccgc acctctctgc agtatgcat cgttctggca gcgctgggag  
 120  
 gtgccggtct ggcgctctgg gccatgtcga gtgcgacgga ggccaatcag gcggaaattg  
 180  
 cccaggccag gccaggcatt attgcggcgg cgcgcggtgt cgtggatgtc gagggcgggc  
 240  
 tgctgcggct ctccaccag cgcgacgggg tgattcagga tgtgccggtg aaggaaggac  
 300  
 agcgggtcaa agccggcgat atctctgccg cgctcgacaa tcgcgcgaa ctgatcg  
 357

<210> 1766  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 1766  
 Met Thr Met Phe Ser Arg Thr Ser Leu Gln Tyr Ala Ile Val Leu Ala  
 1 5 10 15  
 Ala Leu Gly Gly Ala Gly Leu Ala Leu Trp Ala Met Ser Ser Ala Thr  
 20 25 30  
 Glu Ala Asn Gln Ala Glu Ile Ala Gln Ala Arg Pro Gly Ile Ile Ala  
 35 40 45  
 Ala Ala Arg Gly Val Val Asp Val Glu Gly Gly Leu Leu Arg Leu Ser  
 50 55 60  
 Thr Gln Arg Asp Gly Val Ile Gln Asp Val Pro Val Lys Glu Gly Gln  
 65 70 75 80  
 Arg Val Lys Ala Gly Asp Ile Leu Ala Ala Leu Asp Asn Arg Arg Glu  
 85 90 95  
 Leu Ile

<210> 1767  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

<400> 1767  
 nnnccgacgac ggccgcatg acgcaccgca ttgacgtgaa ccaggcgac gatgccaacc  
 60  
 ccggccaaca cgccaggctg cttgacgccg ccagccaacc cgacgaacgc cccaccaaga  
 120  
 acgagcccga gccatccccg gccaatcaac gccagacgta tggccacaac gagtgcgacg  
 180  
 agggacaaac ccacctggag tccgtcggtg tgcattgccc ccaccacgct caacgtcgtc  
 240  
 aatggacagc acaccgccag ccagagggca tgatccggat cggttccggc gtagcgn  
 297

<210> 1768  
 <211> 73  
 <212> PRT  
 <213> Homo sapiens

<400> 1768  
 Met Pro Thr Pro Ala Asn Thr Pro Gly Cys Leu Thr Pro Pro Ala Asn  
 1 5 10 15  
 Pro Thr Asn Ala Pro Pro Arg Thr Ser Pro Ser His Pro Arg Pro Ile  
 20 25 30  
 Asn Ala Arg Arg Met Ala Thr Thr Ser Ala Thr Arg Asp Lys Pro Thr  
 35 40 45  
 Trp Ser Pro Ser Leu Cys Met Pro Pro Thr Thr Leu Asn Val Val Asn  
 50 55 60  
 Gly Gln His Thr Ala Ser Gln Arg Ala

65

70

<210> 1769  
 <211> 474  
 <212> DNA  
 <213> Homo sapiens

<400> 1769  
 caccatgctg gctcgggttcg acgcattcgg gtgggtgagt ctgttctcgt caccgacggg  
 60  
 caggggtcatg ccgttcgtgg ccctgccatt gaggtgacga aagggtcagt tagcgtcgag  
 120  
 accgttgaga tcctccatac tcccgcgacc acgcattcgt gggtcgccgt ccaggcattg  
 180  
 ccgaagtccg atagagctga gctggcggtg gcgaccctca ccgagatggg agttcacgaa  
 240  
 atcctcgctt ggcaggctga tcggagcatc gtgcgatgga agggcgacaa gcaagccaag  
 300  
 ggcgtcgcca ggtggcaagc ggctgcccgt gaggccacca aacagtctcg acgttttctt  
 360  
 gtgccacagg tagaactagc gcaaaccctg gaagttgtta agcggatttg caatgccacg  
 420  
 gccgcctacg ttttgacga gtcggccagt gaaccgctgg tgcacagga gctc  
 474

<210> 1770  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<400> 1770  
 His His Ala Gly Ser Val Arg Arg Ile Arg Val Gly Glu Ser Val Leu  
 1 5 10 15  
 Val Thr Asp Gly Gln Gly His Ala Val Arg Gly Pro Ala Ile Glu Val  
 20 25 30  
 Thr Lys Gly Ser Val Ser Val Glu Thr Val Glu Ile Leu His Thr Pro  
 35 40 45  
 Ala Thr Thr His Arg Trp Val Ala Val Gln Ala Leu Pro Lys Ser Asp  
 50 55 60  
 Arg Ala Glu Leu Ala Val Ala Thr Leu Thr Glu Met Gly Val His Glu  
 65 70 75 80  
 Ile Leu Ala Trp Gln Ala Asp Arg Ser Ile Val Arg Trp Lys Gly Asp  
 85 90 95  
 Lys Gln Ala Lys Gly Val Ala Arg Trp Gln Ala Ala Arg Glu Ala  
 100 105 110  
 Thr Lys Gln Ser Arg Arg Phe Leu Val Pro Gln Val Glu Leu Ala Gln  
 115 120 125  
 Thr Arg Glu Val Val Lys Arg Ile Cys Asn Ala Gln Ala Tyr Val  
 130 135 140  
 Leu His Glu Ser Ala Ser Glu Pro Leu Val His Gln Glu Leu  
 145 150 155

<210> 1771  
 <211> 287

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1771

acgcgtgatg ggtaattcta atacatgcaa agaattatct ctgcaagtat actcagatat  
60  
taataacagc ggggtgctgca gaggaagaag cctgggagaa tggaagtcag ggaaggagag  
120  
caacaggctt ctactctgt gccatgagca tgtgctagcc atggagacac tctgcatgtt  
180  
acctagaact gctgattcat tgctctggaa ttattcagct attcaagacc cagtgaata  
240  
cagcaagcag ctttcattca tacacacaca tgtgcatcca tgtgcac  
287

&lt;210&gt; 1772

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1772

Met	Gly	Asn	Ser	Asn	Thr	Cys	Lys	Glu	Leu	Ser	Leu	Gln	Val	Tyr	Ser
1				5				10					15		
Asp	Ile	Asn	Asn	Ser	Gly	Cys	Arg	Arg	Gly	Arg	Ser	Leu	Gly	Glu	Trp
		20					25					30			
Lys	Ser	Gly	Lys	Glu	Ser	Asn	Arg	Leu	Leu	Thr	Leu	Cys	His	Glu	His
		35				40					45				
Val	Leu	Ala	Met	Glu	Thr	Leu	Cys	Met	Leu	Pro	Arg	Thr	Ala	Asp	Ser
	50					55				60					
Leu	Leu	Trp	Asn	Tyr	Ser	Ala	Ile	Gln	Asp	Pro	Val	Lys	Tyr	Ser	Lys
65			70					75					80		
Gln	Leu	Ser	Phe	Ile	His	Thr	His	Val	His	Pro	Cys	Ala			
			85					90							

&lt;210&gt; 1773

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1773

accggtgagt tctacgtccc ggtaaccac ctcggaggtg aacaggcgca cctcgacgtc  
60  
ttcgattctc cgcttaacga gtacgcagcg atgggatttg agtacggcta ctctgttgcc  
120  
cgtccggatt ctctggtatt gtgggaagcc caattcggcg atttcaccaa cgggtgccag  
180  
acgatcatcg atgagttcat cgcctcggct ggctccaagt ggggtcagaa gtcgggagtc  
240  
gtgctgctgc tgccgcacgg ttacgaaggt caggggcctg atcactcgtc ggcccgctcg  
300  
gagcgcttcc tcaatctatg cagtgaagac gctttggccg tctgccagcc ctcgaccccg  
360  
gcaagctaca gccatttatt gcgtcagcac gcg  
393

<210> 1774  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<400> 1774  
 Thr Gly Glu Phe Tyr Val Pro Val Asn His Leu Gly Gly Glu Gln Ala  
 1 5 10 15  
 His Leu Asp Val Phe Asp Ser Pro Leu Asn Glu Tyr Ala Ala Met Gly  
 20 25 30  
 Phe Glu Tyr Gly Tyr Ser Val Ala Arg Pro Asp Ser Leu Val Leu Trp  
 35 40 45  
 Glu Ala Gln Phe Gly Asp Phe Thr Asn Gly Ala Gln Thr Ile Ile Asp  
 50 55 60  
 Glu Phe Ile Ala Ser Ala Gly Ser Lys Trp Gly Gln Lys Ser Gly Val  
 65 70 75 80  
 Val Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His Ser  
 85 90 95  
 Ser Ala Arg Leu Glu Arg Phe Leu Asn Leu Cys Ser Glu Asp Ala Leu  
 100 105 110  
 Ala Val Cys Gln Pro Ser Thr Pro Ala Ser Tyr Ser His Leu Leu Arg  
 115 120 125  
 Gln His Ala  
 130

<210> 1775  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

<400> 1775  
 nncctccgag cagctctccg gggcagaccc cagctgcaag ccacagcccg gccctggtaa  
 60  
 cgggagggca tcgctagga ggggtgggc ggcccggctt cgatgcagcc atgtgggagg  
 120  
 gccactctca gagaccccc gccttccttg ccacccccac cccagagggg aagctggagc  
 180  
 tgggaggctg cagaccagg ccaagggtg gccagggtg gctttcttg gaggtttga  
 240  
 gcatectgct tctggccac ccagctctgg ggctgctgtc aactcttgat ttgtagacat  
 300  
 cactccagcc tctggcctgt caccctgaac ctcccccatg tctgtgtctt ttctcactgg  
 360  
 aacaccggt  
 369

<210> 1776  
 <211> 59  
 <212> PRT  
 <213> Homo sapiens

<400> 1776  
 Arg Glu Gly Ile Ala Arg Glu Gly Trp Gly Gly Pro Ala Ser Met Gln

```

      1             5             10             15
Pro Cys Gly Arg Ala Thr Leu Arg Asp Pro Pro Pro Ser Leu Pro Pro
      20             25             30
Pro Pro Gln Arg Gly Ser Trp Ser Trp Glu Ala Ala Asp Pro Gly Gln
      35             40             45
Gly Val Ala Arg Ala Gly Phe Leu Gly Arg Leu
      50             55

```

&lt;210&gt; 1777

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1777

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agcttcttat cactatcctt tagtgctttt tggctacct tagcggtaat gctccatcaa
60
gaatatgggtt ttggtagtgc aactgcggga ttttttggcc tcgctgggtgc cgccggagct
120
ttagcagcac cactgtccgg taaactaaca gataaacaag gaccgacacg ggtcacgcag
180
ctgggtgctg ccttagttgt cgtctctttc gcatctatgt tgttattgcc ttacttcagt
240
atcagtaccc aagttataat gattattggt gctaccatag tgtttgactt tgggtgttcag
300
gcggcactta ttgctcatca aaccttagtg tataacattg actctaccgc tcgtggacgc
360
cttaacgcgt
370

```

&lt;210&gt; 1778

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1778

```

Ser Phe Leu Ser Leu Ser Phe Ser Ala Phe Trp Ser Thr Leu Ala Val
      1             5             10             15
Met Leu His Gln Glu Tyr Gly Phe Gly Ser Ala Thr Ala Gly Phe Phe
      20             25             30
Gly Leu Ala Gly Ala Ala Gly Ala Leu Ala Ala Pro Leu Ser Gly Lys
      35             40             45
Leu Thr Asp Lys Gln Gly Pro Thr Arg Val Thr Gln Leu Gly Ala Ala
      50             55             60
Leu Val Val Val Ser Phe Ala Ser Met Leu Leu Pro Tyr Phe Ser
      65             70             75             80
Ile Ser Thr Gln Val Ile Met Ile Ile Val Ala Thr Ile Val Phe Asp
      85             90             95
Phe Gly Val Gln Ala Ala Leu Ile Ala His Gln Thr Leu Val Tyr Asn
      100            105            110
Ile Asp Ser Thr Ala Arg Gly Arg Leu Asn Ala
      115            120

```

&lt;210&gt; 1779

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1779

```

ccatgtgtgt gtatatgtctc gtgtgtgatg gtatgcatac gtgtatatgt gnntatatgt
60
atacacgtgt gttatgggtgt gtatatatgt atatacgtgt gtgtatatat atgtatatgg
120
gtatgtgtgt gcatgtgctg atgggtgtgt atatgtgtat atatgtaggt gtgtatatct
180
gggaatatat ggggtgtgtat atgtgtgtat aggtttttat atgtggggaa atatttaaac
240
ctgtgtatat tggaatgtgt gtgtatatgt gtgtatatat ggnggtgtgt atgtacatgt
300
atgtgtgtat atatgtgtgt atatacgtag gtgtgcatat gtgtg
345

```

&lt;210&gt; 1780

&lt;211&gt; 55

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1780

```

Pro Cys Val Cys Ile Cys Ser Cys Val Met Val Cys Ile Cys Val Tyr
1      5      10     15
Val Xaa Ile Cys Ile His Val Cys Tyr Gly Val Tyr Ile Cys Ile Tyr
20     25     30
Val Cys Val Tyr Ile Cys Ile Trp Val Cys Val Cys Met Cys Val Trp
35     40     45
Val Cys Ile Cys Val Tyr Met
50     55

```

&lt;210&gt; 1781

&lt;211&gt; 349

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1781

```

nacgcgtcat gctaaatddd gccctttatg gcaacatddd cgtcagaaca agcgggaagag
60
aagctactat ccaagtttca tacgccggtt aaaagaaaac atgatgatac gagatcatct
120
gatgtgaaca caacgcaaac tggttcaagc gccacgcca ttacacctgt acccttactg
180
cccagtgcac aagagcccag ttatctttgc cagtgggtgc ctccccagac acgaaagcac
240
aagacatggg aggggtgatgc tattcttata ttgcatggaa ataaaactac ttgttcgcta
300
cgatccgcac atgatggcag catgctagtg acgaatgctg ccttccgga
349

```

&lt;210&gt; 1782

&lt;211&gt; 107

&lt;212&gt; PRT

<213> Homo sapiens

<400> 1782

```

Met Ala Thr Phe Ser Ser Glu Gln Ala Glu Glu Lys Leu Leu Ser Lys
 1           5           10           15
Phe His Thr Pro Val Lys Arg Lys His Asp Asp Thr Arg Ser Ser Asp
      20           25           30
Val Asn Thr Thr Gln Thr Gly Ser Ser Ala Thr Pro Ile Thr Pro Val
      35           40           45
Pro Leu Leu Pro Ser Ala Gln Glu Pro Ser Tyr Leu Cys Gln Trp Cys
      50           55           60
Ala Pro Gln Thr Arg Lys His Lys Thr Trp Glu Gly Asp Ala Ile Leu
65           70           75           80
Ile Leu His Gly Asn Lys Thr Thr Cys Ser Leu Arg Ser Ala His Asp
      85           90           95
Gly Ser Met Leu Val Thr Asn Ala Ala Phe Arg
      100           105

```

<210> 1783

<211> 1829

<212> DNA

<213> Homo sapiens

<400> 1783

```

gtgcacgact tcgacgccag cctctcgggc atcgggcagg aactgggcgc cggcgcttac
60
agcatgagtg atgtcttggc attgcccatt ttcaagcagg aagattccag ccttccattg
120
gatggtgaaa cagagcacc accctttcag tatgtgatgt gtgctgcaac gtcaccagca
180
gtaaaactgc atgatgaaac gcttacttat ttgaaccaag gtcagtcata tgaaattcgg
240
atgctggata atcgaaaaat gggatgatat cctgagatca atggaaaatt agtaaagagc
300
atcataaggg ttgtattcca tgacagacgg ctacaatata cagagcatca gcaacttgaa
360
ggatggaagt ggaatcgccc aggagacaga cttcttgatt tagatattcc aatgtctgtg
420
ggaataattg acacaaggac gaatccaggc cagttaaatt cggttgaatt tctgtgggac
480
ccagcaaaac gcacctctgc tttcattcag gtacactgca tcagcacaga atttactcca
540
cggaagcacg gaggtgaaaa gggagtggcc tttaggatcc aggttgacac ctttaagcag
600
aatgaaaatg gagaatacac agatcatcta cactcagcta gctgccaaat caaagttttt
660
aagcctaaag gtgcagacag gaaacaaaaa actgaccgag agaagatgga gaagagaaca
720
gctcatgaaa aagaaaagta tcagccgtcc tatgatacca caatcctcac agagatgagg
780
cttgagccta taattgaaga tgcagttgaa catgagcaga aanaagtcca gcaagcggac
840
tttgccgcag actacggtga ttctctggca aagcgaggca gttgttctcc gtggcccgat
900

```



gccccacag cctatgtgaa taacagccct tccccagcgc ccactttcac ctccccacag  
 960  
 cagagcactt gcagtgtccc agacagcaat tcttcttccc caaatcatca gggagatgga  
 1020  
 gcttcacaga cctctggtga acaaattcag ccttcagcta cgatccagga aacacagcaa  
 1080  
 tggctgctca aaaacagatt ctcttcttac acaagactgt tctctaattt ttcaggtgcc  
 1140  
 gacttattaa aactgacaaa ggaggattta gttcaaattt gtggtgcagc cgatggaatt  
 1200  
 cggctctata attcactgaa gtcaaggctg gttagacccc gtttaaccat ctatgtctgc  
 1260  
 cgggagcagc caagcagcac agtgctgcaa gggcagcagc aagctgcaag cagtgcgaagc  
 1320  
 gagaatggca gtggggcacc ctatgtttat catgcaatct acttggaaga aatgattgcc  
 1380  
 tcagaagttg ctgaaaaact tgcgctggtg tttaatatcc ctctccacca aattaatcag  
 1440  
 gtttacagac agggctccac cggtattcac attcttgta gtgatcaggt aaatcaaac  
 1500  
 atttgttttt ccttttcaga ctggtattta cttttataca tgtaattgta gaactgtaga  
 1560  
 aaaattctgt gacctctttt gaaaatactt atgagaatca ttttcagaga gttgggaatc  
 1620  
 actttggaag aacttataac caagagtttc aggcaccta gtgataatat ggaatacaag  
 1680  
 ccaaggaaaa ctggcttagc ctccccccag cccttttaga tgcagccaat cactggggca  
 1740  
 ctctagggat agtggcaggc tttggccctt tttatgaggt gagtcactgg atgtgttttc  
 1800  
 cttttgtcta ttatttgatg actaattta  
 1829

&lt;210&gt; 1784

&lt;211&gt; 514

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1784

Val	His	Asp	Phe	Asp	Ala	Ser	Leu	Ser	Gly	Ile	Gly	Gln	Glu	Leu	Gly
1				5					10					15	
Ala	Gly	Ala	Tyr	Ser	Met	Ser	Asp	Val	Leu	Ala	Leu	Pro	Ile	Phe	Lys
			20					25					30		
Gln	Glu	Asp	Ser	Ser	Leu	Pro	Leu	Asp	Gly	Glu	Thr	Glu	His	Pro	Pro
		35				40						45			
Phe	Gln	Tyr	Val	Met	Cys	Ala	Ala	Thr	Ser	Pro	Ala	Val	Lys	Leu	His
	50					55				60					
Asp	Glu	Thr	Leu	Thr	Tyr	Leu	Asn	Gln	Gly	Gln	Ser	Tyr	Glu	Ile	Arg
65					70				75					80	
Met	Leu	Asp	Asn	Arg	Lys	Met	Gly	Asp	Met	Pro	Glu	Ile	Asn	Gly	Lys
			85				90						95		
Leu	Val	Lys	Ser	Ile	Ile	Arg	Val	Val	Phe	His	Asp	Arg	Arg	Leu	Gln
		100					105						110		
Tyr	Thr	Glu	His	Gln	Gln	Leu	Glu	Gly	Trp	Lys	Trp	Asn	Arg	Pro	Gly

115	120	125
Asp Arg Leu Leu Asp Leu Asp Ile Pro Met Ser Val Gly Ile Ile Asp		
130	135	140
Thr Arg Thr Asn Pro Gly Gln Leu Asn Ala Val Glu Phe Leu Trp Asp		
145	150	155
Pro Ala Lys Arg Thr Ser Ala Phe Ile Gln Val His Cys Ile Ser Thr		160
165	170	175
Glu Phe Thr Pro Arg Lys His Gly Gly Glu Lys Gly Val Pro Phe Arg		
180	185	190
Ile Gln Val Asp Thr Phe Lys Gln Asn Glu Asn Gly Glu Tyr Thr Asp		
195	200	205
His Leu His Ser Ala Ser Cys Gln Ile Lys Val Phe Lys Pro Lys Gly		
210	215	220
Ala Asp Arg Lys Gln Lys Thr Asp Arg Glu Lys Met Glu Lys Arg Thr		
225	230	235
Ala His Glu Lys Glu Lys Tyr Gln Pro Ser Tyr Asp Thr Thr Ile Leu		240
245	250	255
Thr Glu Met Arg Leu Glu Pro Ile Ile Glu Asp Ala Val Glu His Glu		
260	265	270
Gln Lys Xaa Val Gln Gln Ala Asp Phe Ala Ala Asp Tyr Gly Asp Ser		
275	280	285
Leu Ala Lys Arg Gly Ser Cys Ser Pro Trp Pro Asp Ala Pro Thr Ala		
290	295	300
Tyr Val Asn Asn Ser Pro Ser Pro Ala Pro Thr Phe Thr Ser Pro Gln		
305	310	315
Gln Ser Thr Cys Ser Val Pro Asp Ser Asn Ser Ser Ser Pro Asn His		
325	330	335
Gln Gly Asp Gly Ala Ser Gln Thr Ser Gly Glu Gln Ile Gln Pro Ser		
340	345	350
Ala Thr Ile Gln Glu Thr Gln Gln Trp Leu Leu Lys Asn Arg Phe Ser		
355	360	365
Ser Tyr Thr Arg Leu Phe Ser Asn Phe Ser Gly Ala Asp Leu Leu Lys		
370	375	380
Leu Thr Lys Glu Asp Leu Val Gln Ile Cys Gly Ala Ala Asp Gly Ile		
385	390	395
Arg Leu Tyr Asn Ser Leu Lys Ser Arg Ser Val Arg Pro Arg Leu Thr		
405	410	415
Ile Tyr Val Cys Arg Glu Gln Pro Ser Ser Thr Val Leu Gln Gly Gln		
420	425	430
Gln Gln Ala Ala Ser Ser Ala Ser Glu Asn Gly Ser Gly Ala Pro Tyr		
435	440	445
Val Tyr His Ala Ile Tyr Leu Glu Glu Met Ile Ala Ser Glu Val Ala		
450	455	460
Arg Lys Leu Ala Leu Val Phe Asn Ile Pro Leu His Gln Ile Asn Gln		
465	470	475
Val Tyr Arg Gln Gly Pro Thr Gly Ile His Ile Leu Val Ser Asp Gln		
485	490	495
Val Asn Gln Ile Ile Cys Phe Ser Phe Ser Asp Trp Tyr Leu Leu Leu		
500	505	510
Tyr Met		

&lt;210&gt; 1785

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1785

atcacggacg cagaggagaa agggctgatt actccaggcg tgagtgttct gattgaacca  
60  
actagcggca acacaggcat tggactggcc tttatggctg ctgccaaggg ctacaaactt  
120  
acactcacia tgccctgcctc catgagcatg gagaggagga tcatattgaa ggcttttggt  
180  
gctgaacttg tccttactga ccactcttg ggaatgaaag gagctgtcaa gaaagcggaa  
240  
gagatacaag caaagacacc caactcgtac atccttcaac aatttgaaaa tccagctaac  
300  
ccaagattc actatgagac tactgggcct gaaatctgga aagctacagc aggaaaaatt  
360  
gatggccttg tatctggtat c  
381

&lt;210&gt; 1786

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1786

Ile	Thr	Asp	Ala	Glu	Glu	Lys	Gly	Leu	Ile	Thr	Pro	Gly	Val	Ser	Val
1				5				10					15		
Leu	Ile	Glu	Pro	Thr	Ser	Gly	Asn	Thr	Gly	Ile	Gly	Leu	Ala	Phe	Met
			20				25					30			
Ala	Ala	Ala	Lys	Gly	Tyr	Lys	Leu	Thr	Leu	Thr	Met	Pro	Ala	Ser	Met
		35				40					45				
Ser	Met	Glu	Arg	Arg	Ile	Ile	Leu	Lys	Ala	Phe	Gly	Ala	Glu	Leu	Val
	50				55					60					
Leu	Thr	Asp	Pro	Leu	Leu	Gly	Met	Lys	Gly	Ala	Val	Lys	Lys	Ala	Glu
65				70				75						80	
Glu	Ile	Gln	Ala	Lys	Thr	Pro	Asn	Ser	Tyr	Ile	Leu	Gln	Gln	Phe	Glu
			85				90							95	
Asn	Pro	Ala	Asn	Pro	Lys	Ile	His	Tyr	Glu	Thr	Thr	Gly	Pro	Glu	Ile
		100				105							110		
Trp	Lys	Ala	Thr	Ala	Gly	Lys	Ile	Asp	Gly	Leu	Val	Ser	Gly	Ile	
		115				120						125			

&lt;210&gt; 1787

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1787

gtgcacacag caattcaata tgccaagaca ccagggttgca gcagagaaag atttaattgt  
60  
agggtcacct aacaaggaga tgagaacaaa ctttaaactct atctctctaa ggaatttgga  
120  
cttcggggttt ttaagggttta gaatgggcca aaacatggac attattgatt ggtcaaagag  
180

tacaggggtca tggaacctgg agatgaaaaa gccatattct catgctgac ctgttctct  
 240  
 gtggaaggtc ttcaaattgg ttgccggaat aaaagatctg tcaaaccatct tagg  
 294

<210> 1788  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 1788  
 Met Pro Arg His Gln Val Ala Ala Glu Lys Asp Leu Ile Val Gly Ser  
 1 5 10 15  
 Pro Asn Lys Glu Met Arg Thr Asn Phe Lys Ser Ile Ser Leu Arg Asn  
 20 25 30  
 Leu Asp Phe Gly Phe Leu Arg Phe Arg Met Gly Gln Asn Met Asp Ile  
 35 40 45  
 Ile Asp Trp Ser Lys Ser Thr Gly Ser Trp Asn Leu Glu Met Lys Lys  
 50 55 60  
 Pro Tyr Ser His Ala Asp Pro Val Pro Leu Trp Lys Val Phe Lys Leu  
 65 70 75 80  
 Val Ala Gly Ile Lys Asp Leu Ser Asn Ile Leu  
 85 90

<210> 1789  
 <211> 353  
 <212> DNA  
 <213> Homo sapiens

<400> 1789  
 ttccacata cacccacgcg gcatgtctcg acagagatgc acaccctag cacatattca  
 60  
 cacacacaga catgccacac cccgccatcc cccacactc gtacacgccc accaccctc  
 120  
 gcaggcacac atgcacacac gcgcgcgcac acgcacacac acccccagcc cggaccggcc  
 180  
 gacctgtctc cgggggtctc tcccgaggc aggtctctc gccgagtctc cgaaaagggg  
 240  
 cggtcgtggc ggccctggcg ccagctggg caacgcttcg tggtatctca ccgtttctct  
 300  
 ctgttggtgcc cagcgccccg actgaagatc cggatcttca gtccctggcg cgc  
 353

<210> 1790  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 1790  
 Met His Thr Pro Ser Thr Tyr Ser His Thr Gln Thr Cys His Thr Pro  
 1 5 10 15  
 Pro Ser Pro His Thr Arg Thr Arg Pro Pro Pro Leu Ala Gly Thr His  
 20 25 30  
 Ala His Thr Arg Ala His Thr His Thr His Pro Gln Pro Gly Pro Ala

```

      35              40              45
Asp Leu Leu Pro Gly Val Ser Pro Ala Gly Arg Ser Pro Arg Arg Val
      50              55              60
Ser Glu Lys Gly Arg Ser Trp Arg Pro Trp Arg Pro Ala Gly Gln Arg
65              70              75              80
Phe Val Val Ser His Arg Phe Ser Leu Leu Cys Pro Ala Pro Arg Leu
      85              90              95
Lys Ile Arg Ile Phe Ser Pro Trp Arg
      100              105

```

<210> 1791  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1791
aaatttcagt tagagattag ggaaaataaa gatgttattt ttcccatcc tagtttacag
60
acccccccaga aaccactca tggattctcc cgagtctttg gacctggctc agacaccctt
120
gctttggatc aagccaatgc atgtatcccc taacacaccc atgctttatg tggtcctgc
180
ccctccctgc tcaggggact gcttggttaac ttcattgggt tggggacata tatattatag
240
gagagagaca gagaaaaaga aagagaggaa atgttattct ccttgtctgt atctgtatct
300
ccactccgat tccattccc tctgtctc tcctctctct cctcccttca cgcgt
355

```

<210> 1792  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1792
Met Leu Phe Phe Pro Ile Leu Val Tyr Arg Pro Pro Arg Asn Pro Leu
1      5      10      15
Met Asp Ser Pro Glu Ser Leu Asp Leu Ala Gln Thr Pro Leu Leu Trp
      20      25      30
Ile Lys Pro Met His Val Ser Pro Asn Thr Pro Met Leu Tyr Val Val
      35      40      45
Pro Ala Pro Pro Cys Ser Gly Asp Cys Leu Leu Thr Ser Leu Gly Trp
      50      55      60
Gly His Ile Tyr Tyr Arg Arg Glu Thr Glu Lys Lys Lys Glu Arg Lys
65      70      75      80
Cys Tyr Ser Pro Cys Leu Tyr Leu Tyr Leu His Ser Asp Ser His Ser
      85      90      95
Leu Cys Cys Ser Pro Leu Ser Pro Pro Phe Thr Arg
      100      105

```

<210> 1793  
 <211> 510  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 1793

tgggttccag cccgtagatg accttggcct gggaggcctt ccgaaggcca cacccatata  
 60  
 caccctctcg gagctcctcg cttaccagtc gcccaaagag cttgtcccc cagcagccag  
 120  
 agtcagccag acccttagca aacaccatag gggcatctc aatctcttct ccaacttcac  
 180  
 cttcttctct ggagatgaat cctgacaaca cctcagggct gaggcagaag tcggtggagg  
 240  
 ccgagccgtg ctcattgtgg atgggtgcacc gatacacacc gcagtctacg ggggaggcct  
 300  
 gcacgatggc caaggccgcc ggcccctcat cccctgcgct cctgcccacc tcgcccactg  
 360  
 ggcgctgatc cttggcccat gtcaagactg agtcactaag aatgttgaaa aactggcacc  
 420  
 acagcttcag gctaccggag gcacaggaa actgctccac ccgaatcttc cggatcacct  
 480  
 gtggggcttt cagcaggtct ttggctttcc  
 510

&lt;210&gt; 1794

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1794

Met	Thr	Leu	Ala	Trp	Glu	Ala	Phe	Arg	Arg	Pro	His	Pro	Tyr	Pro	Pro
1				5					10					15	
Pro	Arg	Ser	Ser	Ser	Leu	Thr	Ser	Arg	Pro	Lys	Ser	Leu	Ser	Pro	Gln
			20					25				30			
Gln	Pro	Glu	Ser	Ala	Arg	Pro	Leu	Ala	Asn	Thr	Ile	Gly	Val	Ile	Ser
		35				40					45				
Ile	Ser	Ser	Pro	Thr	Ser	Pro	Ser	Ser	Leu	Glu	Met	Asn	Pro	Asp	Asn
	50				55					60					
Thr	Ser	Gly	Leu	Arg	Gln	Lys	Ser	Val	Glu	Ala	Glu	Pro	Cys	Ser	Leu
65				70					75					80	
Trp	Met	Val	His	Arg	Tyr	Thr	Pro	Gln	Ser	Thr	Gly	Glu	Ala	Cys	Thr
			85					90						95	
Met	Ala	Lys	Ala	Ala	Gly	Pro	Ser	Ser	Pro	Ala	Leu	Leu	Pro	Thr	Ser
			100				105						110		
Pro	Thr	Gly	Arg												
			115												

&lt;210&gt; 1795

&lt;211&gt; 386

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1795

ctatgctctg agtcacttct ccaagcattc ctttctgttc ttccttccct gggctgatca  
 60  
 tttcaagaag tcctacattc cagaaaactt gagaggtgct tcttctctgg aagccccctt  
 120

tcttttctgt gagctcaggg agcattctac atacctcagc tgtgtctgct atcttttctg  
 180  
 taattatcaa tctttccata taaacagtaa aggaccacag tttattcatc agattcccca  
 240  
 tccaaacctg cacctgcata cataaacgca ctggataaat gtaccgcagt agacagaggg  
 300  
 tctccagggt gagagctcca tgagggcacc aatttttctg tgtttagctg tgtcctcaaa  
 360  
 gcaaggaagg gttgatccgg tctaga  
 386

<210> 1796

<211> 86

<212> PRT

<213> Homo sapiens

<400> 1796

Met	Gln	Val	Gln	Val	Trp	Met	Gly	Asn	Leu	Met	Asn	Lys	Leu	Trp	Ser
1				5					10					15	
Phe	Thr	Val	Tyr	Met	Glu	Arg	Leu	Ile	Ile	Lys	Gln	Lys	Ile	Ala	Asp
			20					25					30		
Thr	Ala	Glu	Val	Cys	Arg	Met	Leu	Pro	Glu	Leu	Thr	Glu	Lys	Lys	Arg
		35					40					45			
Gly	Phe	Gln	Arg	Arg	Ser	Thr	Ser	Gln	Val	Phe	Trp	Asn	Val	Gly	Leu
	50					55				60					
Leu	Glu	Met	Ile	Ser	Pro	Gly	Lys	Glu	Glu	Gln	Lys	Gly	Met	Leu	Gly
65					70				75					80	
Glu	Val	Thr	Gln	Ser	Ile										
					85										

<210> 1797

<211> 348

<212> DNA

<213> Homo sapiens

<400> 1797

aagcttcact atgttgccca ttccatgggc ggcgtgctgg tgcgtgacct gctggcggac  
 60  
 cggaatttgc cgatgtcatt gatcaggtea tctgtctggg ctgcccgcag cagggtctgc  
 120  
 gtgccgctaa tttgttggcg ccatttgctg gcggcgcata cgtcaaatgg tgtatcacag  
 180  
 cgactatgtg atgccgcttg cgccacgcc cggcagcgcg cgttggagcg ccatcaactc  
 240  
 acagatggac aacctggtgt tgccggtgac ctcggaatt ttaccgggaa tgacccatgt  
 300  
 ggcggtggat tacctggggc attgttcggt attgtacagc ccacgcgt  
 348

<210> 1798

<211> 108

<212> PRT

<213> Homo sapiens

&lt;400&gt; 1798

```

Met Gly Gly Val Leu Val Arg Asp Leu Leu Ala Asp Arg Asn Leu Pro
 1           5           10           15
Met Ser Leu Ile Arg Ser Ser Val Trp Ala Arg Arg Ser Arg Ala Arg
      20           25           30
Val Pro Leu Ile Cys Trp Arg His Leu Leu Ala Ala His Pro Ser Asn
      35           40           45
Gly Val Ser Gln Arg Leu Cys Asp Ala Ala Cys Ala His Ala Arg Gln
      50           55           60
Arg Ala Leu Glu Arg His Gln Leu Thr Asp Gly Gln Pro Gly Val Ala
      65           70           75           80
Gly Asp Leu Gly Asn Phe Thr Gly Asn Asp Pro Cys Gly Gly Gly Leu
      85           90           95
Pro Gly Ala Leu Phe Val Ile Val Gln Pro Thr Arg
      100           105

```

&lt;210&gt; 1799

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1799

```

acgcgctgcc tcctgctggt cgggattttc ctgctgtag ttaaccaaac caccggcgtc
60
aataccgtca tgtattacgc gcccaagggt ttggagttcg caggaatgag caccagggcg
120
tcgattattt cagaggtggc taatggagtc atgtctgtta ttggtgccgc tgcaggcttg
180
tggtcatcg aacggtttga tcgtcgtcac ctgcttatct tcgatgtcac gccggtcgggt
240
gtgtgtctcc ttggtattgc ggctactttc gggctggcaa ttgctcctca tgtgggtcaa
300
gggggtaccga agtgggcgcc tattctcgtg ctgctcctga tgagtatctt catgcttacc
360
gtgcac
366

```

&lt;210&gt; 1800

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1800

```

Thr Arg Arg Leu Leu Leu Val Gly Ile Phe Leu Ala Val Val Asn Gln
 1           5           10           15
Thr Thr Gly Val Asn Thr Val Met Tyr Tyr Ala Pro Lys Val Leu Glu
      20           25           30
Phe Ala Gly Met Ser Thr Gln Ala Ser Ile Ile Ser Glu Val Ala Asn
      35           40           45
Gly Val Met Ser Val Ile Gly Ala Ala Ala Gly Leu Trp Leu Ile Glu
      50           55           60
Arg Phe Asp Arg Arg His Leu Leu Ile Phe Asp Val Thr Ala Val Gly
      65           70           75           80
Val Cys Leu Leu Gly Ile Ala Ala Thr Phe Gly Leu Ala Ile Ala Pro

```



```

      85              90              95
His Val Gly Gln Gly Val Pro Lys Trp Ala Pro Ile Leu Val Leu Val
      100              105              110
Leu Met Ser Ile Phe Met Leu Ile Val His
      115              120

```

<210> 1801  
 <211> 597  
 <212> DNA  
 <213> Homo sapiens

<400> 1801  
 aatttctcct tcggtgacta cttcaagaac gaggccattc agtacgcatg ggagctcgtc  
 60  
 actaagccgg cagaacaggg cggattgggt ttcgacctg ccagcatctg ggtgacggtc  
 120  
 cttggacctg ggtttcaccc tgactatccg gagggcgaca ttgaggcgcg cgaggcgtgg  
 180  
 cgtgctgagg gtatccctga cgagcagatt cagggtcgct cccttaagga caactactgg  
 240  
 catatggggg ttcccgggcc cggcggcccg tgctcgaaa tctacatcga tcgtggccca  
 300  
 gcctatggtc ccgacgggtg tccagaagca gatgaggacc gttaccttga gatctggaac  
 360  
 ctggtattcg agaccgagga tctctcagcg gtgcgcgcta aagatgactt cgacatcgca  
 420  
 ggccattgac gcagccttaa catcgacact ggtgccggtc tcgaacgtat tgcctaccta  
 480  
 ctccagggcg tcgacaatat gtacgagact gaccaggtat tccctgtcat tgagaaagcg  
 540  
 tccgagatgt cgggcaagcg gtacggcggt cgccacgacg acgacgtccg actacgc  
 597

<210> 1802  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<400> 1802  
 Asn Phe Ser Phe Gly Asp Tyr Phe Lys Asn Glu Ala Ile Gln Tyr Ala  
 1 5 10 15  
 Trp Glu Leu Val Thr Lys Pro Ala Glu Gln Gly Gly Leu Gly Phe Asp  
 20 25 30  
 Pro Ala Ser Ile Trp Val Thr Val Leu Gly Pro Gly Phe His Pro Asp  
 35 40 45  
 Tyr Pro Glu Gly Asp Ile Glu Ala Arg Glu Ala Trp Arg Ala Ala Gly  
 50 55 60  
 Ile Pro Asp Glu Gln Ile Gln Gly Arg Ser Leu Lys Asp Asn Tyr Trp  
 65 70 75 80  
 His Met Gly Val Pro Gly Pro Gly Gly Pro Cys Ser Glu Ile Tyr Ile  
 85 90 95  
 Asp Arg Gly Pro Ala Tyr Gly Pro Asp Gly Gly Pro Glu Ala Asp Glu  
 100 105 110  
 Asp Arg Tyr Leu Glu Ile Trp Asn Leu Val Phe Glu Thr Glu Asp Leu

```

      115      120      125
Ser Ala Val Arg Ala Lys Asp Asp Phe Asp Ile Ala Gly Pro Leu Arg
      130      135      140
Ser Leu Asn Ile Asp Thr Gly Ala Gly Leu Glu Arg Ile Ala Tyr Leu
145      150      155      160
Leu Gln Gly Val Asp Asn Met Tyr Glu Thr Asp Gln Val Phe Pro Val
      165      170      175
Ile Glu Lys Ala Ser Glu Met Ser Gly Lys Arg Tyr Gly Val Arg His
      180      185      190
Asp Asp Asp Val Arg Leu Arg
      195

```

<210> 1803  
 <211> 708  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1803
cccacaacga tggccgtcat ggtggatggg gaagtgcctg aggaggtcac acctaaggac
60
ctcatcctgg ccctcatctc cgagatcggc accggtgggg gacaaggcca tatggtcgag
120
tatcgccggcg aggccatcga gaagatgtcg atggagggtc gcatgacgat ctgcaatatg
180
tcgattgagt ggggagctcg cgtcggcatg gttgcttctg atgagaccac cttcacctac
240
ctcaaggatc gtccgcacgc tccgcgtggt gcacagtggg acaaggctgt cgcgtactgg
300
cgactctgc gtactgacga cgatgcgacc tttgacgctg agatccatgt ggacgcctcg
360
aatctcgccc ccttcgttac ctgggggtacc aaccgggggc agggatcccc cctaggcggt
420
gtggtgccgg cgcgcgaaga ctttgaggac gaggtagctc gcagcgcagc gtttgaggta
480
catggatttg accccgacga gatcgggtcc cggtttgctg acatctttcg caataactct
540
gcgaacaacg gcttggtact ggctcaggtt gatcccaagg tcgtcggaga gttgtgggac
600
tttgccgagc agcatcctgg tgagcagctc accctctccc tcgagaatcg gacgattaac
660
cttcggggtc gcacgacctc cccgttccat attgatgaag tcacgcgt
708

```

<210> 1804  
 <211> 236  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1804
Pro Thr Thr Met Ala Val Met Val Asp Gly Glu Val Pro Glu Glu Val
1      5      10      15
Thr Pro Lys Asp Leu Ile Leu Ala Leu Ile Ser Glu Ile Gly Thr Gly
      20      25      30
Gly Gly Gln Gly His Met Val Glu Tyr Arg Gly Glu Ala Ile Glu Lys

```

```

<210> 1805
<211> 833
<212> DNA
<213> Homo sapiens
<400> 1805
nccgcagtggtg tgtgggacaa gaacaccgggt gagccggttt ataacgccat cgtgtggcag
60
gacacgcgcga ctcaaaagat ctgtaacgaa ctagctggtg acaagggcgc cgaccgctac
120
aaggagatct gtggtctggg cctgtcgacc tatttctctg gccgaaggt caaatggatt
180
ctcgacaacg ttgaggggagc ccgtgcgagg gccgaggccg gcgatctgct cttcggtaac
240
atggacactt ggggtgctgtg gaacctgact ggcggtacta acggtggcgt gcacatcacc
300
gatccgacca acgcgtcccg aaccatgctc atggacgtcc gaaagctgca gtgggacgac
360
tcgatgtgcg aggtcatggg aattccaaag tccatgcttc ctgagatcaa gtctctctcc
420
gagatctacg gctatggctg caagaacggc ctgctgatcg ataccccgat ctccggcatt
480
cttggcgatc agcaggccgc cacctttggc caggcttgct tccaaaaggg catggcgaag
540
aacacgtacg gcaccggctg cttcatgctc atgaacacag gtgaggaggc catcttctcc
600
gagaacggtc tgctgaccac cgtctgctac aagattggtg accagcccac cgtctatgcc
660

```

ctggaagggtt cgatcgccgt cgctggatcg ctggtacagt ggctgcgcga caacctcaag  
 720  
 atgttcgaga ccgccccgca aatcgaagcc ctgcaccaaca ccgtcgagga caatgggtggc  
 780  
 gcctactttg tgccggcctt ctctggcctg ttgcgcgcgt actggcggtcc gga  
 833

<210> 1806

<211> 277

<212> PRT

<213> Homo sapiens

<400> 1806

Xaa	Ala	Val	Val	Trp	Asp	Lys	Asn	Thr	Gly	Glu	Pro	Val	Tyr	Asn	Ala
1				5					10					15	
Ile	Val	Trp	Gln	Asp	Thr	Arg	Thr	Gln	Lys	Ile	Cys	Asn	Glu	Leu	Ala
			20					25					30		
Gly	Asp	Lys	Gly	Ala	Asp	Arg	Tyr	Lys	Glu	Ile	Cys	Gly	Leu	Gly	Leu
		35					40					45			
Ser	Thr	Tyr	Phe	Ser	Gly	Pro	Lys	Val	Lys	Trp	Ile	Leu	Asp	Asn	Val
	50					55					60				
Glu	Gly	Ala	Arg	Ala	Arg	Ala	Glu	Ala	Gly	Asp	Leu	Leu	Phe	Gly	Asn
65					70					75					80
Met	Asp	Thr	Trp	Val	Leu	Trp	Asn	Leu	Thr	Gly	Gly	Thr	Asn	Gly	Gly
			85						90					95	
Val	His	Ile	Thr	Asp	Pro	Thr	Asn	Ala	Ser	Arg	Thr	Met	Leu	Met	Asp
			100					105					110		
Val	Arg	Lys	Leu	Gln	Trp	Asp	Asp	Ser	Met	Cys	Glu	Val	Met	Gly	Ile
		115					120					125			
Pro	Lys	Ser	Met	Leu	Pro	Glu	Ile	Lys	Ser	Ser	Ser	Glu	Ile	Tyr	Gly
	130					135						140			
Tyr	Gly	Arg	Lys	Asn	Gly	Leu	Leu	Ile	Asp	Thr	Pro	Ile	Ser	Gly	Ile
145					150					155					160
Leu	Gly	Asp	Gln	Gln	Ala	Ala	Thr	Phe	Gly	Gln	Ala	Cys	Phe	Gln	Lys
			165						170					175	
Gly	Met	Ala	Lys	Asn	Thr	Tyr	Gly	Thr	Gly	Cys	Phe	Met	Leu	Met	Asn
			180					185					190		
Thr	Gly	Glu	Glu	Ala	Ile	Phe	Ser	Glu	Asn	Gly	Leu	Leu	Thr	Thr	Val
		195					200						205		
Cys	Tyr	Lys	Ile	Gly	Asp	Gln	Pro	Thr	Val	Tyr	Ala	Leu	Glu	Gly	Ser
	210					215					220				
Ile	Ala	Val	Ala	Gly	Ser	Leu	Val	Gln	Trp	Leu	Arg	Asp	Asn	Leu	Lys
225					230					235					240
Met	Phe	Glu	Thr	Ala	Pro	Gln	Ile	Glu	Ala	Leu	Ala	Asn	Thr	Val	Glu
			245						250					255	
Asp	Asn	Gly	Gly	Ala	Tyr	Phe	Val	Pro	Ala	Phe	Ser	Gly	Leu	Phe	Ala
			260					265					270		
Pro	Tyr	Trp	Arg	Pro											
			275												

<210> 1807

<211> 420

<212> DNA

<213> Homo sapiens

&lt;400&gt; 1807

```

nnntatcggc aaggtggtcg aaatggctct tgactatgtc aacggtgaca cgtgcgccgc
60
gaccgccccca ttcatttgtc gtttgacgtc gacgcgatgg accctagcgt ggccccgagc
120
acaggcacac cgggtgcgtgg tggcttcaca ttccgagaag gccactacat atgcgaggcg
180
gtagctgaga cgggctcggt ggtggctatg gatatggtag aagtcaaccc ccatcttgaa
240
aagcatgcgg ctgagcagac gatcgccgtg ggttggtccc tcattcgttc ggcgctgggg
300
gagacgcttc tgtaatgggt gcatgatggg ccggtgggtcc atagccatgc atagacactc
360
cgggcgctga tatgatgagt gacatagcac gtacgataaa tctcggtttt gagcacgcgt
420

```

&lt;210&gt; 1808

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1808

```

His Val Arg Arg Asp Arg Pro Ile His Leu Ser Phe Asp Val Asp Ala
1           5           10           15
Met Asp Pro Ser Val Ala Pro Ser Thr Gly Thr Pro Val Arg Gly Gly
20           25           30
Leu Thr Phe Arg Glu Gly His Tyr Ile Cys Glu Ala Val Ala Glu Thr
35           40           45
Gly Ser Leu Val Ala Met Asp Met Val Glu Val Asn Pro His Leu Glu
50           55           60
Lys His Ala Ala Glu Gln Thr Ile Ala Val Gly Cys Ser Leu Ile Arg
65           70           75           80
Ser Ala Leu Gly Glu Thr Leu Leu
85

```

&lt;210&gt; 1809

&lt;211&gt; 340

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1809

```

nnaccggtga tcgcatcggt gagcctcggc gcgatgcgcg tgttcgacct tcgccatcgc
60
cagaccggtg tcacgcatgc gtatcgccctc gggcatggca gcctcctcgt gatgcggggc
120
ccccaccagg ccgaatggca gcatcgcggtg ccgaaagcgc cgggtgtgca gggcgagcgc
180
gtgaacctga cgtttcggcg cgtgatgccg gtcgggtatgg gccggtaaca accgcgctcg
240
ccgaggtgcc cggatcgccg ggcgattcgc gccccgtttt cgcgattcat gcgcgatcga
300
tacgggcagg cggtcgcatg tgcggcacgt tgccgcacgn
340

```

<210> 1810  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

<400> 1810  
 Xaa Pro Val Ile Ala Ser Val Ser Leu Gly Ala Met Arg Val Phe Asp  
 1 5 10 15  
 Leu Arg His Arg Gln Thr Gly Val Thr His Ala Tyr Arg Leu Gly His  
 20 25 30  
 Gly Ser Leu Leu Val Met Arg Gly Pro Thr Gln Ala Glu Trp Gln His  
 35 40 45  
 Arg Val Pro Lys Ala Pro Gly Val Gln Gly Glu Arg Val Asn Leu Thr  
 50 55 60  
 Phe Arg Arg Val Met Pro Val Gly Met Gly Arg  
 65 70 75

<210> 1811  
 <211> 500  
 <212> DNA  
 <213> Homo sapiens

<400> 1811  
 nnacgcgtgc taggaatagc catggactca tcatcagata catgctggat ttataacttca  
 60  
 ctgggtggat tgtatgagct gtcgtaaaa gatgaggctc gcgatatgtg gcatttgttg  
 120  
 ctgaaacggt gcgactttga gaaggcacta acattttgtc gtgatgagac gtgtcggaag  
 180  
 caggtactgg aaaagaaggg cgatgcactg ctacacgcag gtcagctcat ggaggccgctc  
 240  
 gagtgtatg ctcaggccca gacaccggcc tttgaacagg ttgtgctttc tttgatggac  
 300  
 gtctgtgccg acaaggcatt gcgtcgatat gtcagactgc gtctcgacaa gatgccgaaa  
 360  
 caagctcgcg tgcctcgtct catgctggct acttggctca ttgaattgta tgtggccgccc  
 420  
 attcaagcgc atgaaccac ctccgaacat tatcagacac ttttgcgtga agcccaggag  
 480  
 acacttgagc ggcacatga  
 500

<210> 1812  
 <211> 166  
 <212> PRT  
 <213> Homo sapiens

<400> 1812  
 Xaa Arg Val Leu Gly Ile Ala Met Asp Ser Ser Ser Asp Thr Cys Trp  
 1 5 10 15  
 Ile Tyr Thr Ser Leu Gly Gly Leu Tyr Glu Leu Leu Val Lys Asp Glu  
 20 25 30  
 Ala Arg Asp Met Trp His Leu Leu Leu Lys Arg Cys Asp Phe Glu Lys

```

      35          40          45
Ala Leu Thr Phe Cys Arg Asp Glu Thr Cys Arg Lys Gln Val Leu Glu
      50          55          60
Lys Lys Gly Asp Ala Leu Leu His Ala Gly Gln Leu Met Glu Ala Val
      65          70          75          80
Glu Cys Tyr Ala Gln Ala Gln Thr Pro Ala Phe Glu Gln Val Val Leu
      85          90          95
Ser Leu Met Asp Val Cys Ala Asp Lys Ala Leu Arg Arg Tyr Val Arg
      100          105          110
Leu Arg Leu Asp Lys Met Pro Lys Gln Ala Arg Val Pro Arg Leu Met
      115          120          125
Leu Ala Thr Trp Leu Ile Glu Leu Tyr Val Ala Ala Ile Gln Ala His
      130          135          140
Glu Pro Thr Ser Glu His Tyr Gln Thr Leu Leu Leu Glu Ala Gln Glu
      145          150          155          160
Thr Leu Glu Arg His His
      165

```

&lt;210&gt; 1813

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1813

```

tctagagccg ttgtgatcgg tatccatggt tggatggggg tcatctcgat ggaggagtgt
60
gtcctgaggg gtggcagtga cctggtaggg gtgcctgcgg cgtcgcggct tgcgatcgct
120
ggttctcggg gatgactctc ggatgaatat agatctgcta agacgtcatt agattcgctt
180
ggcgcttggt tgggaacggg tgtgaagcag ccttctgatg gatgtatttt tgcgttggtg
240
aataaggttt caatattaat tgaatatggc gctagatgct ggtttaggat cagttgacgt
300
ccgctgtaga tcctccctat ggtcattctg gggccaggcg cttcgccagc tggccatcgc
360
aacaatggtg tggcgaaggg ttatgaggtg agtatggctg agcaagtcgt tggacaggcg
420
tctaca
426

```

&lt;210&gt; 1814

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1814

```

Met Thr Ile Gly Arg Ile Tyr Ser Gly Arg Gln Leu Ile Leu Asn Gln
1      5      10      15
His Leu Ala Pro Tyr Ser Ile Asn Ile Glu Thr Leu Phe Asn Asn Ala
      20      25      30
Lys Ile His Pro Ser Glu Gly Cys Phe Thr Pro Val Pro Asn Gln Ala
      35      40      45
Pro Ser Glu Ser Asn Asp Val Leu Ala Asp Leu Tyr Ser Ser Glu Ser

```

```

      50              55              60
His Pro Arg Glu Pro Ala Ile Ala Ser Arg Asp Ala Ala Gly Thr Pro
65              70              75              80
Thr Arg Ser Leu Pro Pro Leu Arg Thr His Ser Ser Ile Glu Met Asn
      85              90              95
Pro Ile Gln Pro Trp Ile Pro Ile Thr Thr Ala Leu
      100              105

```

<210> 1815  
 <211> 303  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1815
ggcgccacaca tggctacgct cgcaccgcgg cacaaggtaa gccgtagcgg cgggatcgag
60
cgccaggccg cgcattctcg catggagcgc gatcagttcg gccatcatcg cgtcgtcggg
120
cgtgccgata tcgaggggca acgccgcgcc gagccgcgaa gccagatcgg gcagcgcgat
180
ccgccagcca tcggcaaatt cgcgagtgat gacgagcaag ggccgcctgg tctcctgcgc
240
ccggttccag cagtggaaca cgttcgctc ggcagacgg gcggcatcgg cgatcacggt
300
acc
303

```

<210> 1816  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1816
Met Ala Thr Leu Ala Pro Arg His Lys Val Ser Arg Ser Gly Gly Ile
1      5      10      15
Glu Arg Gln Ala Ala His Leu Gly Met Glu Arg Asp Gln Phe Gly His
      20      25      30
His Arg Val Val Gly Arg Ala Asp Leu Glu Gly Gln Arg Arg Ala Glu
      35      40      45
Pro Arg Ser Gln Ile Gly Gln Arg Asp Pro Pro Ala Ile Gly Lys Phe
      50      55      60
Ala Ser Asp Asp Glu Gln Gly Pro Pro Gly Leu Leu Arg Pro Val Pro
65      70      75      80
Ala Val Glu His Val Arg Leu Gly Gln Thr Gly Gly Ile Gly Asp His
      85      90      95
Gly Thr

```

<210> 1817  
 <211> 413  
 <212> DNA  
 <213> Homo sapiens

<400> 1817



nncagcttgc aagaccgagg ccacacagtg tacatcttaa catcacattt cgatgcgtcg  
 60  
 catgcgtttg agccacacag cgatggcaca cttcagggtca ttcacgcaaa gacatggatc  
 120  
 ccgcgtcctt tatttcacat gctgcatctg cgatggccat tcgcagcagt tttttctctt  
 180  
 gtgatgcagg tcgtggtagc agcgtatgga tcgtcactcg cagccactt gccgcatgtg  
 240  
 tacagggcgt gacgcatgtc ccgtcaaact cgctcccaga cgtgtttgtt attgaccaac  
 300  
 ttccagcagc gataccccta atcaaactcc tgtgtgggag gcgtgtcatg tactactgtc  
 360  
 acttcctga caaagaaatc agcgtgctc tggctcgaca gcgaggcacg cgt  
 413

<210> 1818

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1818

Xaa	Ser	Leu	Gln	Asp	Arg	Gly	His	Thr	Val	Tyr	Ile	Leu	Thr	Ser	His
1				5					10					15	
Phe	Asp	Ala	Ser	His	Ala	Phe	Glu	Pro	Thr	Arg	Asp	Gly	Thr	Leu	Gln
		20						25					30		
Val	Ile	His	Ala	Lys	Thr	Trp	Ile	Pro	Arg	Ser	Leu	Phe	His	Met	Leu
		35					40					45			
His	Leu	Arg	Trp	Pro	Phe	Ala	Ala	Val	Phe	Ser	Leu	Val	Met	Gln	Val
	50					55					60				
Val	Val	Ala	Ala	Tyr	Gly	Ser	Ser	Leu	Ala	Arg	His	Leu	Pro	His	Val
65					70					75				80	
Tyr	Arg	Ala													

<210> 1819

<211> 343

<212> DNA

<213> Homo sapiens

<400> 1819

ggatccaaga gtggggcatc aggaacatgc catggttgctc gtgggtgctgg aatgagaaca  
 60  
 atcacaagac agataggcct tggcatgatc caacagatga acactgtttg ccctgaatgc  
 120  
 aaaggatcag gtgagatcat aagtgacaag gacaaatgcc caagctgtaa aggaaacaaa  
 180  
 gtagtccagg agaagaaggt gttagagggt catgtggaga aaggaatgca acataacca  
 240  
 aagattgtat tccagggtca ggctgatgaa gctcctgata cgggtacagg agacattggt  
 300  
 tttgtcttgc aacttaaaga ccatccaaaa ttaagagga tgt  
 343

<210> 1820

<211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 1820

```

Gly Ser Lys Ser Gly Ala Ser Gly Thr Cys His Gly Cys Arg Gly Ala
 1           5           10           15
Gly Met Arg Thr Ile Thr Arg Gln Ile Gly Leu Gly Met Ile Gln Gln
          20           25           30
Met Asn Thr Val Cys Pro Glu Cys Lys Gly Ser Gly Glu Ile Ile Ser
          35           40           45
Asp Lys Asp Lys Cys Pro Ser Cys Lys Gly Asn Lys Val Val Gln Glu
          50           55           60
Lys Lys Val Leu Glu Val His Val Glu Lys Gly Met Gln His Asn Gln
          65           70           75           80
Lys Ile Val Phe Gln Gly Gln Ala Asp Glu Ala Pro Asp Thr Gly Thr
          85           90           95
Gly Asp Ile Val Phe Val Leu Gln Leu Lys Asp His Pro Lys Phe Lys
          100          105          110
Arg Met
  
```

<210> 1821  
 <211> 285  
 <212> DNA  
 <213> Homo sapiens

<400> 1821

```

aagcttgagt tcagcaagat cttggaggct attaaggcaa acttcaacga caagttcgat
60
gaggtcggga agaagtgggg aggtggcatc atgggatcca agtcgcaggc caagaccaag
120
gcccgggaaa agttgctcgc caaggaggcc gccacgcgga tgacctagat tgtctactgc
180
tgtgtctgcc ctgtagtttg acggggaaga actgatgaac tcgtattgtg gttttccgaa
240
tctagtttca tatgtttctg tccaccagac catgtttaga agctt
285
  
```

<210> 1822  
 <211> 55  
 <212> PRT  
 <213> Homo sapiens

<400> 1822

```

Lys Leu Glu Phe Ser Lys Ile Leu Glu Ala Ile Lys Ala Asn Phe Asn
 1           5           10           15
Asp Lys Phe Asp Glu Val Gly Lys Lys Trp Gly Gly Gly Ile Met Gly
          20           25           30
Ser Lys Ser Gln Ala Lys Thr Lys Ala Arg Glu Lys Leu Leu Ala Lys
          35           40           45
Glu Ala Ala Gln Arg Met Thr
          50           55
  
```

<210> 1823  
 <211> 387  
 <212> DNA  
 <213> Homo sapiens

<400> 1823  
 ngttggctgc tgttgctggg cgttctgtcc ctgacgggct gcgcccgttc cgatgcgctg  
 60  
 tggggcgctgg tcgataagct ctgcatggcc aactatcagc aaaagcgcgga tccggccccg  
 120  
 tgtgagcaga tttatatgcc gcagggtaaa gcgcagggct ttagcgtgct gcaaaaacccg  
 180  
 cgttatccct atcatttcat tctgggtgccg acggcgccgc tttccggcat tgaaagccccg  
 240  
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<210> 1824  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

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 Gln Gln Lys Arg Asp Pro Ala Pro Cys Glu Gln Ile Tyr Met Pro Gln  
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 Gly Lys Ala Gln Gly Phe Ser Val Leu Gln Asn Pro Arg Tyr Pro Tyr  
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 His Phe Ile Leu Val Pro Thr Ala Pro Leu Ser Gly Ile Glu Ser Pro  
 65 70 75 80  
 Leu Leu Leu Ala Gly Glu Arg Thr Asp Tyr Phe Gly Tyr Ala Trp Leu  
 85 90 95  
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<210> 1825  
 <211> 413  
 <212> DNA  
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<210> 1826

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1826

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Trp	Ala	Pro	Arg	His	His	Val	Ala	Gly	Arg	His	Gly	His	Val	Gly	Val
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Val	Pro	Arg	Tyr	Ala	Arg	Pro	Phe	Leu	Leu	Ser	Val	Gly	Leu	Val	Cys
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Pro	Val	Gly	His	Ala	Ala	Gly	Ser	Gly	Leu	Arg	Cys	Val	Ala	Asp	Pro
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<210> 1827

<211> 345

<212> DNA

<213> Homo sapiens

<400> 1827

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<210> 1828  
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<400> 1828  
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 Gly Lys Ala Asn Arg Thr Ile Ser Ala Arg Lys Leu Tyr Ala Arg Met  
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 Met Arg Thr Leu Ala Glu Thr Gly Asn Gly Trp Met Thr Phe Lys Asp  
 65 70 75 80  
 Lys Cys Asn Arg Ala Ser Asn Gln Thr Leu Arg Pro Gly Asn Val Ile  
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<210> 1829  
 <211> 4457  
 <212> DNA  
 <213> Homo sapiens

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<210> 1830

<211> 1377

<212> PRT

<213> Homo sapiens

<400> 1830

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Ile	Leu	Gln	Ser	Ser	Asp	Ser	Gly	Cys	Ser	Gln	Ser	Ser	Ala	Gly	Asp
			20					25					30		
Asn	Leu	Ser	Tyr	Glu	Val	Asp	Pro	Glu	Thr	Val	Asn	Ala	Gln	Glu	Asp
		35					40					45			
Ser	Gln	Met	Pro	Lys	Glu	Ser	Ser	Pro	Asp	Asp	Asp	Val	Gln	Gln	Val
		50				55				60					
Val	Phe	Asp	Leu	Ile	Cys	Lys	Val	Val	Ser	Gly	Leu	Glu	Val	Glu	Ser
65					70				75				80		
Ala	Ser	Val	Thr	Ser	Gln	Leu	Glu	Ile	Glu	Ala	Met	Pro	Pro	Lys	Cys
			85						90				95		
Ser	Asp	Ile	Asp	Pro	Asp	Glu	Glu	Thr	Ile	Lys	Ile	Glu	Asp	Asp	Ser
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Ile	Arg	Gln	Ser	Gln	Asn	Ala	Leu	Leu	Ser	Asn	Glu	Ser	Ser	Gln	Phe
		115					120					125			
Leu	Ser	Val	Ser	Ala	Glu	Gly	Gly	His	Glu	Cys	Val	Ala	Asn	Gly	Ile
		130				135					140				
Ser	Arg	Asn	Ser	Ser	Ser	Pro	Cys	Ile	Ser	Gly	Thr	Thr	His	Thr	Leu
145				150					155					160	
His	Asp	Ser	Ser	Val	Ala	Ser	Ile	Glu	Thr	Lys	Ser	Arg	Gln	Arg	Ser
			165						170				175		
His	Ser	Ser	Ile	Gln	Phe	Ser	Phe	Lys	Glu	Lys	Leu	Ser	Glu	Lys	Val
		180					185					190			
Ser	Glu	Lys	Glu	Thr	Ile	Val	Lys	Glu	Ser	Gly	Lys	Gln	Pro	Gly	Ala
		195					200					205			
Lys	Pro	Lys	Val	Lys	Leu	Ala	Arg	Lys	Lys	Asp	Asp	Asp	Lys	Lys	Lys
		210				215					220				
Ser	Ser	Asn	Glu	Lys	Leu	Lys	Gln	Thr	Ser	Val	Phe	Phe	Ser	Asp	Gly



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Ile Glu Ser Asp Met Gly Ser Pro Gly Ser Arg Lys Ser Pro Asn Phe
          260          265          270
Asn Ile His Pro Leu Tyr Gln His Val Leu Leu Tyr Leu Gln Leu Tyr
          275          280          285
Asp Ser Ser Arg Thr Leu Tyr Ala Phe Ser Ala Ile Lys Ala Ile Leu
          290          295          300
Lys Thr Asn Pro Ile Ala Phe Val Asn Ala Ile Ser Thr Thr Ser Val
          305          310          315          320
Asn Asn Ala Tyr Thr Pro Gln Leu Ser Leu Leu Gln Asn Leu Leu Ala
          325          330          335
Arg His Arg Ile Ser Val Met Gly Lys Asp Phe Tyr Ser His Ile Pro
          340          345          350
Val Asp Ser Asn His Asn Phe Arg Ser Ser Met Tyr Ile Glu Ile Leu
          355          360          365
Ile Ser Leu Cys Leu Tyr Tyr Met Arg Ser His Tyr Pro Thr His Val
          370          375          380
Lys Val Thr Ala Gln Asp Leu Ile Gly Asn Arg Asn Met Gln Met Met
          385          390          395          400
Ser Ile Glu Ile Leu Thr Leu Leu Phe Thr Glu Leu Ala Lys Val Ile
          405          410          415
Glu Ser Ser Ala Lys Gly Phe Pro Ser Phe Ile Ser Asp Met Leu Ser
          420          425          430
Lys Cys Lys Val Gln Lys Val Ile Leu His Cys Leu Leu Ser Ser Ile
          435          440          445
Phe Ser Ala Gln Lys Trp His Ser Glu Lys Met Ala Gly Lys Asn Leu
          450          455          460
Val Ala Val Glu Glu Gly Phe Ser Glu Asp Ser Leu Ile Asn Phe Ser
          465          470          475          480
Glu Asp Glu Phe Asp Asn Gly Ser Thr Leu Gln Ser Gln Leu Leu Lys
          485          490          495
Val Leu Gln Arg Leu Ile Val Leu Glu His Arg Val Met Thr Ile Pro
          500          505          510
Glu Glu Asn Glu Thr Gly Phe Asp Phe Val Val Ser Asp Leu Glu His
          515          520          525
Ile Ser Pro His Gln Pro Met Thr Ser Leu Gln Tyr Leu His Ala Gln
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Pro Ile Thr Cys Gln Gly Met Phe Leu Cys Ala Val Ile Arg Ala Leu
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His Gln His Cys Ala Cys Lys Met His Pro Gln Trp Ile Gly Leu Ile
          565          570          575
Thr Ser Thr Leu Pro Tyr Met Gly Lys Val Leu Gln Arg Val Val Val
          580          585          590
Ser Val Thr Leu Gln Leu Cys Arg Asn Leu Asp Asn Leu Ile Gln Gln
          595          600          605
Tyr Lys Tyr Glu Thr Gly Leu Ser Asp Ser Arg Pro Leu Trp Met Ala
          610          615          620
Ser Ile Ile Pro Pro Asp Met Ile Leu Thr Leu Leu Glu Gly Ile Thr
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Ala Ile Ile His Tyr Cys Leu Leu Asp Pro Thr Thr Gln Tyr His Gln
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Leu Leu Val Ser Val Asp Gln Lys His Leu Phe Glu Ala Arg Ser Gly

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1419

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 1125 1130 1135  
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 Pro Thr Met Ile Thr Glu Leu Val Gln Val Phe Leu Leu Met Glu Gln  
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 Ala Gly Leu Glu Thr Thr Tyr Thr Gly Gly Asn Gly Phe Ser Thr Ser  
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 Val Arg Leu Ala Lys Leu Leu Arg Lys Arg Ala Lys Lys Asn Pro Glu  
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 Gly His Ser Gly Ser Pro Ile Leu Tyr Ser Asn Ala Phe Pro Asn Lys  
 1330 1335 1340  
 Asp Met Lys Leu Glu Asn His Lys Pro Cys Ser Ser Lys Ala Arg Gln  
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&lt;210&gt; 1831

&lt;211&gt; 508

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1831

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<210> 1832

<211> 169

<212> PRT

<213> Homo sapiens

<400> 1832

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			20					25					30		
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		35					40					45			
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	50					55					60				
Gln	Cys	Lys	Ile	Gly	Asp	Ala	Ala	Ala	Val	Ser	Tyr	Asp	Lys	Ala	Arg
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Gln	Lys	Ala	Met	Arg	Leu	Arg	Trp	Lys	Val	Glu	Trp	Gly	Gly	Asn	Pro
			85					90						95	
Leu	Glu	Glu	Arg	Gln	Ala	Leu	Arg	Ala	Val	Pro	Thr	Leu	Ala	Glu	Phe
			100					105					110		
Ile	Arg	Glu	Thr	Tyr	Val	Pro	His	Ile	His	Leu	His	Arg	Arg	Asn	Phe
		115					120					125			
Gln	Ser	Thr	Leu	Ser	Phe	Leu	Lys	Cys	His	Val	Leu	Pro	Arg	Phe	Gly
		130				135					140				
Ala	Lys	His	Leu	Asp	Glu	Ile	Thr	Thr	Asn	Met	Leu	Ala	Glu	Ala	His
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<210> 1833

<211> 430

<212> DNA

<213> Homo sapiens

<400> 1833

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acatctccgg cgctcctgct gtcaggcgct gaaggatcg aaagtcatgc gccgtgacaa  
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 aggaagatcg gcgacacagg agccgaagcg ccgccgctg caataagcgc gcgcgatcgc  
 420  
 aattgtcggg  
 430

<210> 1834

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1834

Met	Arg	Arg	Cys	Arg	Leu	Asn	Cys	Pro	Val	Pro	Arg	Gln	Thr	Met	Pro
1			5						10					15	
Arg	Arg	Ala	Ala	Lys	Gly	Arg	Arg	Arg	Ser	Val	Ala	Gln	Ser	Gly	
		20					25					30			
Asp	Asp	Arg	Val	Glu	Gln	Arg	Tyr	Ser	Ser	Gln	Arg	Ala	Asn	Gln	Gln
		35				40					45				
His	His	Gln	Val	Glu	Thr	Asp	Asp	Pro	Arg	Arg	Asp	Ala	Phe	Ser	Ala
	50					55					60				
Arg	Val	Trp	Gln	Arg	Leu	Gly	Leu	Gly	Phe	Pro	Ala	Phe	Arg	Arg	Arg
65				70				75						80	
Pro	Ala	Ile	Leu	Glu	Ile	Asp	Glu	His	Leu	Arg	Arg	Ser	Cys	Cys	Gln
			85					90					95		
Ala	Leu	Lys	Val	Ser	Lys	Val	Met	Arg	Arg	Asp	Lys	Gly	Arg	Ser	Ala
		100						105					110		
Thr	Gln	Glu	Pro	Lys	Arg	Arg	Arg	Leu	Gln						
		115					120								

<210> 1835

<211> 677

<212> DNA

<213> Homo sapiens

<400> 1835

nataactcaag gactttgacg gcacccgagc ccggttgctc cctgaggcca tcatgaaccc  
 60  
 ccagtgga cctatgcta ctgtggcacc cagcacttta gcccaccccc aggcccaggc  
 120  
 tctggccccg cagcaggccc tgcagcatgc acagaccctg gcccatgccc ctccccagac  
 180  
 gctgcagcac cctcagggtg tcccgcacc ccaggcactg tcccaccctc agagcctcca  
 240  
 gcagcctcag ggctggggc accctcagcc catggcccaa acccagggtg tggtcaccc  
 300  
 tcaggccctg gctcaccagg gtctccagca cccccacaat cccttgctgc atggaggccg  
 360  
 gaagatgcca gactcagatg ccccccgaa tgtgaccgtg tctacctcaa ctatccccct  
 420  
 ttcaatggcg gccactctgc agcacagcca gcctccggac ctgagtagca tcgtgcacca  
 480  
 gatcaaccag ttttgccaga cgagggcagg catcagcact acctcagtgt gtgagggcca  
 540

gacgcgccaac cccagcccca ttagtcgcag tctgctcatc aatgcaagca cccgggtgtc  
 600  
 gacccacagc gtccccacac caatgccttc atgtgtgggc aatcccatgg agcacacca  
 660  
 cgcgccacc gccgcgg  
 677

<210> 1836  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 1836  
 Gly His His Glu Pro Pro Ser Gly Thr Leu Cys Tyr Cys Gly Thr Gln  
 1 5 10 15  
 His Phe Ser Pro Pro Gly Pro Gly Ser Gly Pro Pro Ala Gly Pro  
 20 25 30  
 Ala Ala Cys Thr Asp Pro Gly Pro Cys Pro Ser Pro Asp Ala Ala Ala  
 35 40 45  
 Pro Ser Gly Tyr Pro Ala Thr Pro Gly Thr Val Pro Pro Ser Glu Pro  
 50 55 60  
 Pro Ala Ala Ser Gly Pro Gly Pro Pro Ser Ala His Gly Pro Asn Pro  
 65 70 75 80  
 Gly Leu Gly Pro Pro Ser Gly Pro Gly Ser Pro Gly Ser Pro Ala Pro  
 85 90 95  
 Pro Gln Ser Leu Ala Ala Trp Arg Pro Glu Asp Ala Arg Leu Arg Cys  
 100 105 110  
 Pro Pro Glu Cys Asp Arg Val Tyr Leu Asn Tyr Pro Pro Phe Asn Gly  
 115 120 125  
 Gly His Ser Ala Ala Gln Pro Ala Ser Gly Pro Glu  
 130 135 140

<210> 1837  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<400> 1837  
 nntctagaac actctgcccc tgaatctgta ccgggattgt ttggcccgtc acgaactcgt  
 60  
 acggtcgata tcaatatcac tgggttttct tcacagtatt taccgcgccc ctatggacca  
 120  
 attgctgcgg acgtcaaaca aacctgggcg tgggacccac aggatctgac gattgtctca  
 180  
 acttctgctg atcacgacca taacctccga tatgcagtac agcatttcgg cgcaagcccc  
 240  
 accccgatcc agtaaccttc gataacgcga aagccggcac cccacataac tcgngtgtac  
 300  
 accgaagtcc ctgccaacgt tccatccgac ataggggagt taactaaccg aattatcaag  
 360  
 gggaaatcta ccccgtaac caaggccatc gcgattcaaa actgggttcg tgacagcgct  
 420  
 cgattccatt acgacatcaa cgcacccgaa ggtgacggct atcaggtact ggaaaacttc  
 480

ctgctgcaca.cccaccgagg ttattgcac ctttcgcgg cgtcaatggc actcatggca  
 540  
 cgacttgaag gtattccgtc acgc  
 564

<210> 1838  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<400> 1838  
 Xaa Leu Glu His Ser Ala Pro Glu Ser Val Pro Gly Leu Phe Gly Pro  
 1 5 10 15  
 Ser Arg Thr Arg Thr Val Asp Ile Asn Ile Thr Gly Phe Ser Ser Gln  
 20 25 30  
 Tyr Leu Pro Ala Pro Tyr Gly Pro Ile Ala Ala Asp Val Lys Gln Thr  
 35 40 45  
 Trp Ala Trp Asp Pro Gln Asp Leu Thr Ile Val Ser Thr Ser Ala Asp  
 50 55 60  
 His Asp His Asn Leu Arg Tyr Ala Val Gln His Phe Gly Ala Ser Pro  
 65 70 75 80  
 Thr Pro Ile Gln

<210> 1839  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 1839  
 ncaatacggc tgaacaccgc tgatatcacc cgtactttcc ccgtcaacgg.aaaattttcc  
 60  
 gaagttcagg caaaggctta tcaggcgggtg ctggacgctg cagatgcggc atttaaggca  
 120  
 gccgttcctg gcaataaatt ccgcgacgtc catgctgcag cgatgaatgt tctcgctcc  
 180  
 cgctttagg actgggggct tatgccggtc agcgcgaagg tcgctctttc ggacgagggc  
 240  
 gggcaacacc gtcgttgat gccgcacggc accagccacc atctagggct ggatgtgcac  
 300

<210> 1840  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 1840  
 Xaa Ile Arg Leu Asn Thr Ala Asp Ile Thr Arg Thr Phe Pro Val Asn  
 1 5 10 15  
 Gly Lys Phe Ser Glu Val Gln Ala Lys Ala Tyr Gln Ala Val Leu Asp  
 20 25 30  
 Ala Ala Asp Ala Ala Phe Lys Ala Ala Val Pro Gly Asn Lys Phe Arg  
 35 40 45  
 Asp Val His Ala Ala Ala Met Asn Val Leu Ala Ser Arg Leu Glu Asp

```

      50              55              60
Trp Gly Leu Met Pro Val Ser Ala Lys Val Ala Leu Ser Asp Glu Gly
65              70              75              80
Gly Gln His Arg Arg Trp Met Pro His Gly Thr Ser His His Leu Gly
      85              90              95
Leu Asp Val His
      100

```

<210> 1841  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1841
nnctccaaga acgtcccga gtggggcccc agggcgctcg aactccccgg cgggcccgg
60
gtcgatccgg tggcgagat cggcggtccc ggtacgctag cccaatcgat ggtcgccccg
120
cgcgtcggcg cccatgtcgc cttgatcggc gtgcttnacg gggattgtcg ggcggtgagg
180
acggcgctgc tgatgagcaa gaatctgcgc gtgcaagggc tgccggtcgg cagccgcgcg
240
cagcaactcg cgatgatcgc gggggtcgag gcgaacggca tccgtccgat cctcgaccag
300
catttccgc tcgaaaatct ccccgacgcg
330

```

<210> 1842  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1842
Xaa Ser Lys Asn Val Pro Glu Trp Gly Pro Arg Ala Leu Glu Leu Pro
1      5      10      15
Gly Gly Pro Gly Val Asp Pro Val Val Glu Ile Gly Gly Pro Gly Thr
      20      25      30
Leu Ala Gln Ser Met Val Ala Pro Arg Val Gly Ala His Val Ala Leu
      35      40      45
Ile Gly Val Leu Xaa Gly Asp Cys Arg Ala Val Arg Thr Ala Leu Leu
      50      55      60
Met Ser Lys Asn Leu Arg Val Gln Gly Leu Pro Val Gly Ser Arg Ala
65      70      75      80
Gln Gln Leu Ala Met Ile Ala Gly Val Glu Ala Asn Gly Ile Arg Pro
      85      90      95
Ile Leu Asp Gln His Phe Pro Leu Glu Asn Leu Pro Asp Ala
      100      105      110

```

<210> 1843  
 <211> 473  
 <212> DNA  
 <213> Homo sapiens

<400> 1843



aagctttggc atctccagca aaagatgtgc tatttactga taccatcacc atgaaggcca  
 60  
 acagttttga gtccagatta acaccaagca ggttcatgaa agccttaagt tatgcatcat  
 120  
 tagataaaga agattttattg agtcctatta atcaaaatac cctgcaacga tcttctcag  
 180  
 tgcggtccat ggtgtccagt gccacatatg ggggttcaga tgattacatt ggtcttgctc  
 240  
 tcccgggtgga tataaatgat atattccagg taaaggatat tccctatttt cagacaaaaa  
 300  
 acataccacc acatgatgat cgagggtgcaa gagcatttgc ccatgatgca ggaggtcttc  
 360  
 catctggaac tggaggtctt gtaaaaaatt cttttcactt gctacgacag cagatgagtc  
 420  
 ttacggaaat aatgaattca atccattcag atgcctctcn cnnccnccccc ccc  
 473

<210> 1844

<211> 141

<212> PRT

<213> Homo sapiens

<400> 1844

Met	Lys	Ala	Asn	Ser	Phe	Glu	Ser	Arg	Leu	Thr	Pro	Ser	Arg	Phe	Met
1				5					10					15	
Lys	Ala	Leu	Ser	Tyr	Ala	Ser	Leu	Asp	Lys	Glu	Asp	Leu	Leu	Ser	Pro
			20					25					30		
Ile	Asn	Gln	Asn	Thr	Leu	Gln	Arg	Ser	Ser	Ser	Val	Arg	Ser	Met	Val
			35				40					45			
Ser	Ser	Ala	Thr	Tyr	Gly	Gly	Ser	Asp	Asp	Tyr	Ile	Gly	Leu	Ala	Leu
	50					55					60				
Pro	Val	Asp	Ile	Asn	Asp	Ile	Phe	Gln	Val	Lys	Asp	Ile	Pro	Tyr	Phe
65				70						75				80	
Gln	Thr	Lys	Asn	Ile	Pro	Pro	His	Asp	Asp	Arg	Gly	Ala	Arg	Ala	Phe
			85					90					95		
Ala	His	Asp	Ala	Gly	Gly	Leu	Pro	Ser	Gly	Thr	Gly	Gly	Leu	Val	Lys
		100					105						110		
Asn	Ser	Phe	His	Leu	Leu	Arg	Gln	Gln	Met	Ser	Leu	Thr	Glu	Ile	Met
		115				120						125			
Asn	Ser	Ile	His	Ser	Asp	Ala	Ser	Xaa	Xaa	Xaa	Xaa	Pro			
	130					135						140			

<210> 1845

<211> 390

<212> DNA

<213> Homo sapiens

<400> 1845

aagcttacga cgcctagctt tggagacctg aaccacttga tcagtgaac aatgagtgga  
 60  
 gtgacttgct gcctccgctt cccggggcag ctcaactcgg accttcggaa acttgcaagt  
 120  
 aacctgattc cattccctcg cctgcacttt tttatggctg gctttgcgcc actcacctcg  
 180

cgtaggctccc agcagtaccg tgctctcact gtccctgagc tgaccagca gatgtgggac  
 240  
 tccaagaaca tgatgtgtgc tgctgacccg cgtcatggcc gctacctcac agtatctgcc  
 300  
 atgttccgtg gaaagatgag caccaaggag gtggacgagc agatgctgaa cgtgcagaac  
 360  
 aagaactctt cctacttcgt ggagtggatc  
 390

<210> 1846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 1846

Lys	Leu	Thr	Thr	Pro	Ser	Phe	Gly	Asp	Leu	Asn	His	Leu	Ile	Ser	Ala
1				5				10					15		
Thr	Met	Ser	Gly	Val	Thr	Cys	Cys	Leu	Arg	Phe	Pro	Gly	Gln	Leu	Asn
		20						25					30		
Ser	Asp	Leu	Arg	Lys	Leu	Ala	Val	Asn	Leu	Ile	Pro	Phe	Pro	Arg	Leu
		35					40					45			
His	Phe	Phe	Met	Val	Gly	Phe	Ala	Pro	Leu	Thr	Ser	Arg	Gly	Ser	Gln
	50					55				60					
Gln	Tyr	Arg	Ala	Leu	Thr	Val	Pro	Glu	Leu	Thr	Gln	Gln	Met	Trp	Asp
65					70				75					80	
Ser	Lys	Asn	Met	Met	Cys	Ala	Ala	Asp	Pro	Arg	His	Gly	Arg	Tyr	Leu
			85					90						95	
Thr	Val	Ser	Ala	Met	Phe	Arg	Gly	Lys	Met	Ser	Thr	Lys	Glu	Val	Asp
			100					105					110		
Glu	Gln	Met	Leu	Asn	Val	Gln	Asn	Lys	Asn	Ser	Ser	Tyr	Phe	Val	Glu
		115					120						125		
Trp	Ile														
	130														

<210> 1847

<211> 343

<212> DNA

<213> Homo sapiens

<400> 1847

cagccgtgct ttcctgcgtc aactcgggaa cggtatatc gcgcagatcc aacagttcca  
 60  
 tggctcgaag agtagtaaaa atatcaataa ctggcagagc atcgcgtcaa gctggcgacc  
 120  
 ctggccgccc ccgcgttggc cgatcacgcc atgttgagc aggccttcca gctgttccag  
 180  
 caaaaaagtt gcggacaatc tcctgccgga tggctcgggtg ttcgacttca gggagcgcca  
 240  
 tgcaactcac tacgtcgtct atgacctgga gccgctggtt caggcgggccc tggcgggcaa  
 300  
 gccctaacgg tggaactgg ctgacttaca ccgccccac cgn  
 343

<210> 1848

<211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 1848  
 Met Ala Arg Arg Val Val Lys Ile Ser Ile Thr Gly Arg Ala Ser Arg  
 1 5 10 15  
 Gln Ala Gly Asp Pro Gly Arg Arg Arg Val Gly Arg Ser Arg His Val  
 20 25 30  
 Gly Ala Gly Leu Pro Ala Val Pro Ala Lys Lys Leu Arg Thr Ile Ser  
 35 40 45  
 Cys Arg Met Ala Arg Cys Ser Thr Ser Gly Ser Ala Met His Cys Thr  
 50 55 60  
 Thr Ser Ser Met Thr Trp Ser Arg Trp Phe Arg Arg Pro Trp Arg Ala  
 65 70 75 80  
 Ser Pro Asn Gly Gly Asn Trp Leu Thr Tyr Thr Ala Pro Thr  
 85 90

<210> 1849  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<400> 1849  
 cggaagaac aggttcagca aagagcaata gaatgttccc gggctctcag tgcgattctt  
 60  
 gacattgaac atggagaccc aaaagagaat gtactagggt cagcttttga catgaaacag  
 120  
 ctgaaggatg ctattgatga gactaaaata gctttgatgg gacattcttt tggaggagca  
 180  
 acagttcttc aagcccttag tgaggaccag agattcagat gtggagttgc tcttgatcca  
 240  
 tggatgtatc cggtgaacga agagctgtac tccagaaccc tccagcctct cctctttatc  
 300  
 aactctgcca aattccagac tccaaaggac atcgcaaaaa tgaaaaagtt ctaccagcct  
 360  
 gacaaggaaa ggaaanatga ttacaatcaa  
 390

<210> 1850  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 1850  
 Arg Lys Glu Gln Val Gln Gln Arg Ala Ile Glu Cys Ser Arg Ala Leu  
 1 5 10 15  
 Ser Ala Ile Leu Asp Ile Glu His Gly Asp Pro Lys Glu Asn Val Leu  
 20 25 30  
 Gly Ser Ala Phe Asp Met Lys Gln Leu Lys Asp Ala Ile Asp Glu Thr  
 35 40 45  
 Lys Ile Ala Leu Met Gly His Ser Phe Gly Gly Ala Thr Val Leu Gln  
 50 55 60  
 Ala Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Val Ala Leu Asp Pro

```

65              70              75              80
Trp Met Tyr Pro Val Asn Glu Glu Leu Tyr Ser Arg Thr Leu Gln Pro
              85              90              95
Leu Leu Phe Ile Asn Ser Ala Lys Phe Gln Thr Pro Lys Asp Ile Ala
              100             105             110
Lys Met Lys Lys Phe Tyr Gln Pro Asp Lys Glu Arg Lys Xaa Asp Tyr
              115             120             125
Asn Gln
              130

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&lt;210&gt; 1851

&lt;211&gt; 574

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1851

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nccgatcggag aggcctttccg cactggtgac ttggactcta agcccgaccc cagccggagc
60
ttcaggcctt accgagctga agacaatgat tcctatgcct ctgagatcaa ggagctgcag
120
ctggtgctgg ctgaggccca cgacagcctc cggggcttgc aagagcagct ctcccaggag
180
cggcagctac gaaaggagga ggccgacaat ttcaaccaga aaatgggtcca gctgaaggag
240
gaccagcaga gggcgctcct gaggcgggag tttgagctgc agagtctgag cctccagcgg
300
aggctggagc agaaattctg gagccaggag aagaacatgc tgggtgcagga gtcccagcaa
360
ttcaagcaca acttctgct gctcttcatg aagctcaggt gggttcctcaa gcgctggcgg
420
cagggcaagg ttttgcccag cgaaggggat gacttcctcg aggtgaacag catgaaggac
480
ctgtacttgc tgatggagga agacgagata aacgctcagc attctgataa caaggcctgc
540
acggggggaca gctggaccca gaacacgccc aatg
574

```

&lt;210&gt; 1852

&lt;211&gt; 191

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1852

```

Xaa Ile Gly Glu Ala Phe Arg Thr Gly Asp Leu Asp Ser Lys Pro Asp
1              5              10              15
Pro Ser Arg Ser Phe Arg Pro Tyr Arg Ala Glu Asp Asn Asp Ser Tyr
              20              25              30
Ala Ser Glu Ile Lys Glu Leu Gln Leu Val Leu Ala Glu Ala His Asp
              35              40              45
Ser Leu Arg Gly Leu Gln Glu Gln Leu Ser Gln Glu Arg Gln Leu Arg
              50              55              60
Lys Glu Glu Ala Asp Asn Phe Asn Gln Lys Met Val Gln Leu Lys Glu
65              70              75              80
Asp Gln Gln Arg Ala Leu Leu Arg Arg Glu Phe Glu Leu Gln Ser Leu

```

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<400> 1854
Met Pro His Pro Pro Trp Lys Arg Cys Arg Ser Ala Thr Ser Leu Arg
 1          5          10          15
Ser Ala Pro Ser Lys Leu Thr Cys Ser Ser Ala Arg Ser Ile His Ser
      20          25          30
Ser Leu Arg Arg Ala Trp His Phe Cys Ala Ser Arg Thr Thr Trp Met
    35          40          45
Ala Arg Ser Ala Arg Arg Phe Thr Trp Met Thr Met Ser Phe Leu Ser
 50          55          60
Arg His Arg Ser Ser Ala Gln Pro Arg Ala Ser Asp Ser Asn Thr Ser
65          70          75          80
Pro Ser Leu Trp Pro Ser Cys Ser Ser Ala Leu Leu His Arg Ile His
      85          90          95
Ile Pro Lys Leu
      100

```

<210> 1855  
 <211> 429  
 <212> DNA  
 <213> Homo sapiens

<400> 1855  
 gcgtccttcg cgtacgtgga cgagggcgagg caggtgttcg tccagtgcag caccagcac  
 60  
 ccgagcgaaa cgcaggaaat cgtggcgacac gtcttgacc tggacaacca cgaggtcacg  
 120  
 gtgcagtgtc tgcgcatggg cgggtggcttt ggcggtaagg aaatgcagcc gcacgggttc  
 180  
 gccgcgatcg cagcactcgg cgcgaccctg accgggcgac cggttcgact gcgactgacc  
 240  
 cgaaaccagg acatcaccat ctccgaaaag cgccacccat acctcgcgga gtgggacgtg  
 300  
 gccttcgacg acgacggccg cctccaggct ctgcgcgcca ccgtcaccag cgacggcggg  
 360  
 tggagcctgg acctctcgga gccgggtgatg cagcggacgg tgtgtcacat cgataactcc  
 420  
 tattggatc  
 429

<210> 1856  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 1856  
 Ala Ser Phe Ala Tyr Val Asp Glu Gly Gly Gln Val Phe Val Gln Cys  
 1 5 10 15  
 Ser Thr Gln His Pro Ser Glu Thr Gln Glu Ile Val Ala His Val Leu  
 20 25 30  
 Asp Leu Asp Asn His Glu Val Thr Val Gln Cys Leu Arg Met Gly Gly  
 35 40 45  
 Gly Phe Gly Gly Lys Glu Met Gln Pro His Gly Phe Ala Ala Ile Ala  
 50 55 60  
 Ala Leu Gly Ala Thr Leu Thr Gly Arg Pro Val Arg Leu Arg Leu Thr  
 65 70 75 80  
 Arg Asn Gln Asp Ile Thr Ile Ser Gly Lys Arg His Pro Tyr Leu Ala  
 85 90 95  
 Glu Trp Asp Val Ala Phe Asp Asp Asp Gly Arg Leu Gln Ala Leu Arg  
 100 105 110  
 Ala Thr Val Thr Ser Asp Gly Gly Trp Ser Leu Asp Leu Ser Glu Pro  
 115 120 125  
 Val Met Gln Arg Thr Val Cys His Ile Asp Asn Ser Tyr Trp Ile  
 130 135 140

<210> 1857  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 1857

gtgcacgccg ctgccccagc cgtcgccctac cgatcaacag acgcagccgc cgtgcgttga  
 60  
 gataccagcc gagcacgata atgctcagca tggtcagcag cagccagaac ggaaatcgca  
 120  
 gcaggcgctc gaacagctca ctgccaccca gcaccagcgg gattgccccg gccacgacca  
 180  
 gtgcgccgag gagcagccac catcgcccg ccatgctgcg gcactcgata ccaatacggt  
 240  
 gcgcttcaac caatcgatct tggtcgaggc atgccgacca ttttccaaca ggcgagtcac  
 300  
 cagactcagc cagtaacacc gcgaaaaatc gtggcgcatg tcgacagggt gcaaaccgag  
 360  
 acgcagcacg ggtgcctgtc ggtggcgggc gag  
 393

<210> 1858

<211> 104

<212> PRT

<213> Homo sapiens

<400> 1858

Met	Leu	Ser	Met	Val	Ser	Ser	Ser	Gln	Asn	Gly	Asn	Arg	Ser	Arg	Arg
1				5					10					15	
Ser	Asn	Ser	Ser	Leu	Pro	Pro	Ser	Thr	Ser	Gly	Ile	Ala	Pro	Ala	Thr
				20				25					30		
Thr	Ser	Ala	Pro	Arg	Ser	Ser	His	His	Arg	Pro	Leu	Met	Leu	Arg	His
				35			40					45			
Ser	Ile	Pro	Ile	Arg	Cys	Ala	Ser	Thr	Asn	Arg	Ser	Trp	Ser	Arg	His
				50			55				60				
Ala	Ala	His	Leu	Pro	Thr	Gly	Glu	Ser	Pro	Asp	Ser	Ala	Ser	Asn	Thr
65					70					75				80	
Ala	Lys	Asn	Arg	Gly	Ala	Cys	Arg	Gln	Gly	Ala	Asn	Arg	Asp	Ala	Ala
				85					90					95	
Arg	Val	Pro	Val	Gly	Gly	Gly	Arg								
				100											

<210> 1859

<211> 345

<212> DNA

<213> Homo sapiens

<400> 1859

nagatctggc gcctcgtcac caacttcctc tacttccgca agatggattt ggattttctg  
 60  
 ttccacatgt tttttctcgc acgatactgc aagcttctgg aggagaactc atttagagga  
 120  
 agaactgccg acttttttta catgctcttg tttggtgcta ctgtcctaac tagcattgtt  
 180  
 ctgatcggag ggatgatacc ttacatttcc gagacatttg ccagaattct gttcctgagc  
 240  
 aattcattga cgtttatgat ggtttatgtc tggagcaagc acaatcctat catccatag  
 300  
 agcaatctgg gcctgttcac ctttacggct gcatacttac catgg  
 345

<210> 1860  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 1860  
 Xaa Ile Trp Arg Leu Val Thr Asn Phe Leu Tyr Phe Arg Lys Met Asp  
 1 5 10 15  
 Leu Asp Phe Leu Phe His Met Phe Phe Leu Ala Arg Tyr Cys Lys Leu  
 20 25 30  
 Leu Glu Glu Asn Ser Phe Arg Gly Arg Thr Ala Asp Phe Phe Tyr Met  
 35 40 45  
 Leu Leu Phe Gly Ala Thr Val Leu Thr Ser Ile Val Leu Ile Gly Gly  
 50 55 60  
 Met Ile Pro Tyr Ile Ser Glu Thr Phe Ala Arg Ile Leu Phe Leu Ser  
 65 70 75 80  
 Asn Ser Leu Thr Phe Met Met Val Tyr Val Trp Ser Lys His Asn Pro  
 85 90 95  
 Ile Ile His Met Ser Asn Leu Gly Leu Phe Thr Phe Thr Ala Ala Tyr  
 100 105 110  
 Leu Pro Trp  
 115

<210> 1861  
 <211> 435  
 <212> DNA  
 <213> Homo sapiens

<400> 1861  
 gcgttgactg tagtgagtga cgaagctgat atacaaaatg cgccgggcgt tagaaaagcc  
 60  
 aatagtgagc ttcattcagt cggcttaggt gttatgaact tacatggcta tcttgctaaa  
 120  
 aacaaaattg gctatgagtc ggaagaagct aaagattttg ctaatatatt ctttatgatg  
 180  
 atgaattact attcacttga aagatcaatg caaatagcaa aagaaagaca ggaaacgttt  
 240  
 aaagactttg ataagtcaga ttatgcaaat ggaaaatatt tcgaatttta tacttcgcaa  
 300  
 tcatttgaac cgaaatacga aaaagtacgt aaattatttg atggttttaga aatcccaacg  
 360  
 cctgaagatt ggaaagcatt gcaaaaagaa gttgaaactc acggtttatt ccatgcttat  
 420  
 cgtttagcga ttgca  
 435

<210> 1862  
 <211> 145  
 <212> PRT  
 <213> Homo sapiens

<400> 1862  
 Ala Leu Thr Val Val Ser Asp Glu Ala Asp Ile Gln Asn Ala Pro Gly



```

      1           5           10           15
Val Arg Lys Ala Asn Ser Glu Leu His Ser Val Gly Leu Gly Val Met
      20           25           30
Asn Leu His Gly Tyr Leu Ala Lys Asn Lys Ile Gly Tyr Glu Ser Glu
      35           40           45
Glu Ala Lys Asp Phe Ala Asn Ile Phe Phe Met Met Met Asn Tyr Tyr
      50           55           60
Ser Leu Glu Arg Ser Met Gln Ile Ala Lys Glu Arg Gln Glu Thr Phe
      65           70           75           80
Lys Asp Phe Asp Lys Ser Asp Tyr Ala Asn Gly Lys Tyr Phe Glu Phe
      85           90           95
Tyr Thr Ser Gln Ser Phe Glu Pro Lys Tyr Glu Lys Val Arg Lys Leu
      100          105          110
Phe Asp Gly Leu Glu Ile Pro Thr Pro Glu Asp Trp Lys Ala Leu Gln
      115          120          125
Lys Glu Val Glu Thr His Gly Leu Phe His Ala Tyr Arg Leu Ala Ile
      130          135          140
Ala
145

```

&lt;210&gt; 1863

&lt;211&gt; 792

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1863

```

nggatacctca cgcccgccat catacgtggg atatcggtga gcaaatgcgt catgacgggg
60
tctccgctcgt gctcactacc cacaacatgg atgaggctca acggctggct gatcacgtct
120
ggatcgctcga tcgcggcagg gtcgcaactc atggaactgt gccagagctc accgctgagt
180
cgagtttgga agatgtgttc ctactcaca ctagtgaccg cgcagcaggg aggaattgac
240
atgacgacac tcgatctccg ccccgcacct caggccgcac cggctgctgc acgctgctc
300
aaccacgctc tcaccgaggt gcgtctggtg atgcgcaacg gtgagcagct gctactagct
360
ctcgtcattc ccatcgggat catcgtcgcc gggcgcttcc tgggcggccg ggtcggactg
420
acgatggacg tcttagcacc ctactgctg gcgctcgcca tctggtcgac atgtttcact
480
tcccaagcga tcatgaccgg ttttgaacgc cgttacgggg tgctcgaacg attgtccgca
540
accccgtagt gtcggtcggg tctgctagct ggcaaggcga tggcttattc cgttatcagt
600
ctcgtcagg tgatactgct tgtcatcatt tcttttagcg tgggctggca ccccccagg
660
tccggcctgg cctggctccc aaccctggtg agcgttgtgc tcgcatgat gacattcggg
720
ctcgcagcac tggcaatggc cggcgctggc aaagctgaag tcactctcgg actggccaac
780
ttggtataca tc
792

```

<210> 1864  
 <211> 264  
 <212> PRT  
 <213> Homo sapiens

<400> 1864  
 Xaa Ile Leu Thr Pro Ala Ile Ile Arg Gly Ile Ser Leu Ser Lys Cys  
 1 5 10 15  
 Val Met Thr Gly Ser Pro Ser Cys Ser Leu Pro Thr Thr Trp Met Arg  
 20 25 30  
 Leu Asn Gly Trp Leu Ile Thr Ser Gly Ser Ser Ile Ala Ala Gly Ser  
 35 40 45  
 Gln Leu Met Glu Leu Cys Gln Ser Ser Pro Leu Ser Arg Val Trp Lys  
 50 55 60  
 Met Cys Ser Ser Leu Thr Leu Val Thr Ala Gln Gln Gly Gly Ile Asp  
 65 70 75 80  
 Met Thr Thr Leu Asp Leu Arg Pro Ala Pro Gln Ala Ala Pro Ala Ala  
 85 90 95  
 Ala Arg Val Arg Asn His Ala Leu Thr Glu Val Arg Leu Val Met Arg  
 100 105 110  
 Asn Gly Glu Gln Leu Leu Leu Ala Leu Val Ile Pro Ile Gly Ile Ile  
 115 120 125  
 Val Ala Gly Arg Phe Leu Gly Gly Arg Val Gly Leu Thr Met Asp Val  
 130 135 140  
 Leu Ala Pro Ser Val Leu Ala Leu Ala Ile Trp Ser Thr Cys Phe Thr  
 145 150 155 160  
 Ser Gln Ala Ile Met Thr Gly Phe Glu Arg Arg Tyr Gly Val Leu Glu  
 165 170 175  
 Arg Leu Ser Ala Thr Pro Leu Gly Arg Ser Gly Leu Leu Ala Gly Lys  
 180 185 190  
 Ala Met Ala Tyr Ser Val Ile Ser Leu Ala Gln Val Ile Leu Leu Val  
 195 200 205  
 Ile Ile Ser Leu Ala Leu Gly Trp His Pro His Gly Ser Gly Leu Ala  
 210 215 220  
 Trp Leu Pro Thr Leu Val Ser Val Val Leu Ala Met Met Thr Phe Gly  
 225 230 235 240  
 Leu Ala Ala Leu Ala Met Ala Gly Ala Gly Lys Ala Glu Val Thr Leu  
 245 250 255  
 Gly Leu Ala Asn Leu Val Tyr Ile  
 260

<210> 1865  
 <211> 717  
 <212> DNA  
 <213> Homo sapiens

<400> 1865  
 ngccggctga tcaacaact cacagacatg ggcttcccgga gagagccagc tgaggaggcc  
 60  
 ttgaagagta acaatatgaa tcttgatcag gccatgagcg ctctgctgga aaagaagggtg  
 120  
 gacgtggaca agcgtgggct gggagtgacc gaccataatg gaatggccgc caagcccctc  
 180

ggctgccgcc cgccaatctc caaagagtct tccgtggacc gcccaccct tcttgacaag  
 240  
 gatggcggcc tcgtggaaga gcccacgcct tcaccgttct tgccttcccc aagcctgaag  
 300  
 ctcccccttt cacacagtgc actccccagt caggccctgg gtgggggttg ctccgggctg  
 360  
 ggcatgcaaa acttgaattc ttctagacag ataccgagtg gcaatctggg tatgtttggc  
 420  
 aatagtggag cagcacaagc caggaccatg cagcagccgc cacagccacc agtcagcct  
 480  
 cttaactctt cccagcccag tctccgtgct caagtgcctc agtttctatc ccctcaggtt  
 540  
 caagcacagc ttttgcaagt tgcagcaaaa aacattgggtc tcaaccctgc actattaacc  
 600  
 tcgccaatta atcctcaaca tatgacgatg ttgaaccagc tctatcagct gcagctggca  
 660  
 taccaacgtt taaaaatcca gcagcagatg ttacaggccc agcgtaatgt gtccgga  
 717

<210> 1866

<211> 239

<212> PRT

<213> Homo sapiens

<400> 1866

Xaa	Arg	Leu	Ile	Lys	Gln	Leu	Thr	Asp	Met	Gly	Phe	Pro	Arg	Glu	Pro
1				5					10					15	
Ala	Glu	Glu	Ala	Leu	Lys	Ser	Asn	Asn	Met	Asn	Leu	Asp	Gln	Ala	Met
			20					25					30		
Ser	Ala	Leu	Leu	Glu	Lys	Lys	Val	Asp	Val	Asp	Lys	Arg	Gly	Leu	Gly
		35					40					45			
Val	Thr	Asp	His	Asn	Gly	Met	Ala	Ala	Lys	Pro	Leu	Gly	Cys	Arg	Pro
	50				55					60					
Pro	Ile	Ser	Lys	Glu	Ser	Ser	Val	Asp	Arg	Pro	Thr	Leu	Leu	Asp	Lys
65					70				75					80	
Asp	Gly	Gly	Leu	Val	Glu	Glu	Pro	Thr	Pro	Ser	Pro	Phe	Leu	Pro	Ser
			85					90					95		
Pro	Ser	Leu	Lys	Leu	Pro	Leu	Ser	His	Ser	Ala	Leu	Pro	Ser	Gln	Ala
		100					105					110			
Leu	Gly	Gly	Val	Ala	Ser	Gly	Leu	Gly	Met	Gln	Asn	Leu	Asn	Ser	Ser
	115					120					125				
Arg	Gln	Ile	Pro	Ser	Gly	Asn	Leu	Gly	Met	Phe	Gly	Asn	Ser	Gly	Ala
	130				135				140						
Ala	Gln	Ala	Arg	Thr	Met	Gln	Gln	Pro	Pro	Gln	Pro	Pro	Val	Gln	Pro
145				150					155					160	
Leu	Asn	Ser	Ser	Gln	Pro	Ser	Leu	Arg	Ala	Gln	Val	Pro	Gln	Phe	Leu
		165					170					175			
Ser	Pro	Gln	Val	Gln	Ala	Gln	Leu	Leu	Gln	Phe	Ala	Ala	Lys	Asn	Ile
	180						185				190				
Gly	Leu	Asn	Pro	Ala	Leu	Leu	Thr	Ser	Pro	Ile	Asn	Pro	Gln	His	Met
	195					200					205				
Thr	Met	Leu	Asn	Gln	Leu	Tyr	Gln	Leu	Gln	Leu	Ala	Tyr	Gln	Arg	Leu
	210				215						220				
Gln	Ile	Gln	Gln	Gln	Met	Leu	Gln	Ala	Gln	Arg	Asn	Val	Ser	Gly	

```
<400> 1869
acgcgtcacc ttcctgctgg agctactggg agccctcgga cacctgcgtg cattgcccca
60
ccgtgacatg ccgagcaccg aaaccacact gtggattcgc gagctgagcc gcacgcaccg
120
```

cgacgtgtcg actgccaccc actttcgttg gagcgacgac ggcaccgtgc taggtcagac  
 180  
 gaccgacgat ggcaccgagc ctgaggttgt tgccctgcc a ggggtctact gccgtcgttg  
 240  
 cggccgcagc ggatggggag tccagctcgc cagcaccggc aataacctca gcgagaacaa  
 300  
 cgacagcatc cgacggaccc acgcggcaca cgacggtcgc ttccgagcct tgctttcggc  
 360  
 ccctcgagag ggagccagcg cggtcgacac cggcgaggcg aactgtcct tacgtcgggt  
 420  
 cgacaccgtc aacagg  
 436

<210> 1870

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1870

Met	Pro	Ser	Thr	Glu	Thr	His	Leu	Trp	Ile	Arg	Glu	Leu	Ser	Arg	Ile
1				5					10					15	
Asp	Arg	Asp	Val	Ser	Thr	Ala	Thr	His	Phe	Arg	Trp	Ser	Asp	Asp	Gly
			20					25					30		
Thr	Val	Leu	Gly	Gln	Thr	Thr	Asp	Asp	Gly	Thr	Glu	Pro	Glu	Val	Val
		35					40					45			
Ala	Leu	Pro	Ala	Val	Tyr	Cys	Arg	Arg	Cys	Gly	Arg	Ser	Gly	Trp	Gly
	50					55				60					
Val	Gln	Leu	Ala	Ser	Thr	Gly	Asn	Asn	Leu	Ser	Glu	Asn	Asn	Asp	Ser
65					70				75					80	
Ile	Arg	Arg	Thr	His	Ala	Ala	His	Asp	Gly	Arg	Phe	Arg	Ala	Leu	Leu
			85					90					95		
Ser	Ala	Pro	Arg	Glu	Gly	Ala	Ser	Ala	Val	Asp	Thr	Gly	Glu	Ala	Thr
		100					105					110			
Leu	Ser	Leu	Arg	Trp	Phe	Asp	Thr	Val	Asn	Arg					
		115					120								

<210> 1871

<211> 474

<212> DNA

<213> Homo sapiens

<400> 1871

nntgcagcgc cccgaggtcg atgtctccaa cgtctttgcc agccttgaca tggctagcga  
 60  
 gcccgacctc gtccgtaccc tgctgaggca agcccaacaa tgaccgggga acagctcgcg  
 120  
 cattggatcg aggagtgcac gtcgacggtg tttttcggcg gcgcgggaat gtccaccgaa  
 180  
 tcaggtattc cggactttcg ctcggtcggc gggctttaca ccaactcagca tgacctgccc  
 240  
 ttccccgcgg agtacatgct cagtcacagc tgtttggttg agcatcccgc ggagttcttc  
 300  
 gacttctacc gcacctacct catccatcct caggccagge ccaatgctgg tcatcgtgcg  
 360

ttggttgcc tggagcaggc tggggaactt tcgacgatca ttaccagaa tattgacggc  
 420  
 ctgcaccaag aagctgggtc tcgtcagggtc attgagttgc atgggtcggg gcac  
 474

<210> 1872  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 1872  
 Met Thr Gly Glu Gln Leu Ala His Trp Ile Glu Glu Ser Thr Ser Thr  
 1 5 10 15  
 Val Phe Phe Gly Gly Ala Gly Met Ser Thr Glu Ser Gly Ile Pro Asp  
 20 25 30  
 Phe Arg Ser Ala Gly Gly Leu Tyr Thr Thr Gln His Asp Leu Pro Phe  
 35 40 45  
 Pro Ala Glu Tyr Met Leu Ser His Ser Cys Leu Val Glu His Pro Ala  
 50 55 60  
 Glu Phe Phe Asp Phe Tyr Arg Thr Tyr Leu Ile His Pro Gln Ala Arg  
 65 70 75 80  
 Pro Asn Ala Gly His Arg Ala Leu Val Ala Leu Glu Gln Ala Gly Glu  
 85 90 95  
 Leu Ser Thr Ile Ile Thr Gln Asn Ile Asp Gly Leu His Gln Glu Ala  
 100 105 110  
 Gly Ser Arg Gln Val Ile Glu Leu His Gly Ser Val His  
 115 120 125

<210> 1873  
 <211> 338  
 <212> DNA  
 <213> Homo sapiens

<400> 1873  
 nacgcgtaga aatgaagccc cagctgggtca gagaccggaa atccggtagt gcacgggacg  
 60  
 gggtccctcg gggatctcgg aggggagacc cccaccggg aggactggag gcagcgccctc  
 120  
 tcccgccccg gcgcgcgcag cctatttccc tctttccaag gggccaatcc ccaccgcggc  
 180  
 ccgcaggggg cgcgctcaag gcaagggtccg cggcgagaac ggtgcccagt gggagcgaag  
 240  
 ggcgaggcca gcccttggtc cttggccggc agttcgggtc ccgcctccaa attttagtat  
 300  
 gcatatgagt caccaggaaa gttttttgaa acaaattt  
 338

<210> 1874  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 1874  
 Ser Pro Ser Trp Ser Glu Thr Gly Asn Pro Val Val His Gly Thr Gly

```

      1             5             10             15
Ser Leu Gly Asp Leu Gly Gly Glu Thr Pro Thr Arg Glu Asp Trp Arg
      20             25             30
Gln Arg Leu Ser Arg Pro Gly Ala Arg Ser Leu Phe Pro Ser Phe Gln
      35             40             45
Gly Ala Asn Pro His Arg Gly Pro Gln Gly Ala Arg Ser Arg Gln Gly
      50             55             60
Pro Arg Arg Glu Arg Cys Pro Val Gly Ala Lys Gly Glu Ala Ser Pro
      65             70             75             80
Trp Ser Leu Ala Gly Ser Ser Gly Pro Ala Ser Lys Phe
      85             90

```

&lt;210&gt; 1875

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1875

```

aagcttggcg tacaagtggg tcgtcgtttc tcaggtgggt gagccgtgta tcacgatatg
60
ggcaatatct gcttctgctt cattacagaa gatgatggcg atagcttcg tgattttgga
120
aaattcacag aaccctgat tgaagcactc cataaaatgg gagcaacagg ggcagagtta
180
caaggacgta acgaccttct catcgacgga aagaaattct ctggaaatgc gatgtactca
240
aacaatggcc gtttaacagc gcacggaaca ttaatgttgg atttagatgt gagcattttg
300
ccacaaattt tacgtccaaa acaagagaaa atcgagtcaa aaggaatcaa gtcggttcgt
360
tcacgc
366

```

&lt;210&gt; 1876

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1876

```

Lys Leu Gly Val Gln Val Val Arg Arg Phe Ser Gly Gly Gly Ala Val
      1             5             10             15
Tyr His Asp Met Gly Asn Ile Cys Phe Cys Phe Ile Thr Glu Asp Asp
      20             25             30
Gly Asp Ser Phe Arg Asp Phe Gly Lys Phe Thr Glu Pro Val Ile Glu
      35             40             45
Ala Leu His Lys Met Gly Ala Thr Gly Ala Glu Leu Gln Gly Arg Asn
      50             55             60
Asp Leu Leu Ile Asp Gly Lys Lys Phe Ser Gly Asn Ala Met Tyr Ser
      65             70             75             80
Asn Asn Gly Arg Leu Thr Ala His Gly Thr Leu Met Leu Asp Leu Asp
      85             90             95
Val Ser Ile Leu Pro Gln Ile Leu Arg Pro Lys Gln Glu Lys Ile Glu
      100            105            110
Ser Lys Gly Ile Lys Ser Val Arg Ser Arg

```

115

120

&lt;210&gt; 1877

&lt;211&gt; 357

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1877

acgcgtgagt ggtcgcaaat atgacgggca agaaacgctt agaaagaaac taccattaa  
 60  
 cgagggtatg caaattgcag aaatctctct atcggattgt ggctatatta tttcatcttt  
 120  
 ccaagctgct ggaccaaggg ctgtagggtt gcaacgacct attatatctg aacatttttt  
 180  
 tcaatttgac ccatttgata aacgacattg ggttgtctca catcatttac cacacgctgc  
 240  
 gacagctgct ttcacttccg gatttgaaga ttgcgctgga ttagtttcag atactgccgg  
 300  
 atcgaacact cttgatggaa aggactatgt tgaaagctgc tgcaatgcta ttccacg  
 357

&lt;210&gt; 1878

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1878

Met	Gln	Ile	Ala	Glu	Ile	Ser	Leu	Ser	Asp	Cys	Gly	Tyr	Ile	Ile	Ser
1				5					10					15	
Ser	Phe	Gln	Ala	Ala	Gly	Pro	Arg	Ala	Val	Gly	Leu	Gln	Arg	Pro	Ile
			20					25					30		
Ile	Ser	Glu	His	Phe	Phe	Gln	Phe	Asp	Pro	Phe	Asp	Lys	Arg	His	Trp
		35				40					45				
Val	Val	Ser	His	His	Leu	Pro	His	Ala	Ala	Thr	Ala	Ala	Phe	Thr	Ser
	50				55				60						
Gly	Phe	Glu	Asp	Cys	Ala	Gly	Leu	Val	Ser	Asp	Thr	Ala	Gly	Ser	Asn
65				70					75					80	
Thr	Leu	Asp	Gly	Lys	Asp	Tyr	Val	Glu	Ser	Cys	Cys	Asn	Ala	Ile	Pro
			85					90						95	

&lt;210&gt; 1879

&lt;211&gt; 1062

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1879

nacgcgtgga tgctccttgg acggcttttt cgtggttagag ggttcccggg gcgcgccgca  
 60  
 tccctgggaa gtagctgaag agaaggcaca ggaagagtcg cctccactga tggctctcct  
 120  
 gtccctccca caggctctga cgcccgtctt gcggcttcgg tgtttgaaca ggccacagtc  
 180  
 caggagcgct tacattcagg agctccgcgt agcacctgcc caaccaaact cagccctccg  
 240



ttaagatcct ggttccatgc cgcagtagga cagcaggccc aagtctgcac atcccagtga  
 300  
 tgcaccatgc caatagtga taagttgaag gaggcctga aaccggccg caaggactcg  
 360  
 gctgatgatg gagaactggg gaagcttctt gcctcctctg ccaagaaggt ctttttacag  
 420  
 aaaatcgagt tcgagccagc cagcaagagc ttctcctacc agctggaggc cttaaagagc  
 480  
 aaatatgtgt tgctcaaccc caaacagag ggagctagtc gccacaagag tggagatgac  
 540  
 ccaccggcca ggagacaggg cagtgaacac acgtatgaga gctgtggtga cggagtccca  
 600  
 gccccgcaga aagtgccttt cccacaggag cgactgtctc tgaggtggga gcgggtcttc  
 660  
 cgcgtgggcg caggactcca caacctggc aacacctgct ttctcaatgc caccatccag  
 720  
 tgcttgacct acacaccacc tctagccaac tacctgctct ccaaggagca tgctgcagc  
 780  
 tgccaccagg gaagcttctg catgctgtgt gtcatgcaga accacattgt ccaggccttc  
 840  
 gccaacagcg gcaacgccat caagcccgtc tccttcaccc gagacctgaa aaagatcgcc  
 900  
 cgacacttcc gctttgggaa ccaggaggac gcgcatgagt tcctgcggta caccatcgac  
 960  
 gccatgcaga aagcctgcct gaatggctgt gccaaattgg atcgtcaaac gcaggctact  
 1020  
 accttggtcc atcaaatttt tggagggtat ctcagatcac gc  
 1062

&lt;210&gt; 1880

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1880

Met	Pro	Ile	Val	Asp	Lys	Leu	Lys	Glu	Ala	Leu	Lys	Pro	Gly	Arg	Lys
1				5					10					15	
Asp	Ser	Ala	Asp	Asp	Gly	Glu	Leu	Gly	Lys	Leu	Leu	Ala	Ser	Ser	Ala
		20						25					30		
Lys	Lys	Val	Leu	Leu	Gln	Lys	Ile	Glu	Phe	Glu	Pro	Ala	Ser	Lys	Ser
		35					40					45			
Phe	Ser	Tyr	Gln	Leu	Glu	Ala	Leu	Lys	Ser	Lys	Tyr	Val	Leu	Leu	Asn
	50					55					60				
Pro	Lys	Thr	Glu	Gly	Ala	Ser	Arg	His	Lys	Ser	Gly	Asp	Asp	Pro	Pro
65				70					75					80	
Ala	Arg	Arg	Gln	Gly	Ser	Glu	His	Thr	Tyr	Glu	Ser	Cys	Gly	Asp	Gly
			85					90					95		
Val	Pro	Ala	Pro	Gln	Lys	Val	Leu	Phe	Pro	Thr	Glu	Arg	Leu	Ser	Leu
		100					105						110		
Arg	Trp	Glu	Arg	Val	Phe	Arg	Val	Gly	Ala	Gly	Leu	His	Asn	Leu	Gly
	115					120					125				
Asn	Thr	Cys	Phe	Leu	Asn	Ala	Thr	Ile	Gln	Cys	Leu	Thr	Tyr	Thr	Pro
	130				135						140				
Pro	Leu	Ala	Asn	Tyr	Leu	Leu	Ser	Lys	Glu	His	Ala	Arg	Ser	Cys	His

```

145             150             155             160
Gln Gly Ser Phe Cys Met Leu Cys Val Met Gln Asn His Ile Val Gln
             165             170             175
Ala Phe Ala Asn Ser Gly Asn Ala Ile Lys Pro Val Ser Phe Ile Arg
             180             185             190
Asp Leu Lys Lys Ile Ala Arg His Phe Arg Phe Gly Asn Gln Glu Asp
             195             200             205
Ala His Glu Phe Leu Arg Tyr Thr Ile Asp Ala Met Gln Lys Ala Cys
             210             215             220
Leu Asn Gly Cys Ala Lys Leu Asp Arg Gln Thr Gln Ala Thr Thr Leu
225             230             235             240
Val His Gln Ile Phe Gly Gly Tyr Leu Arg Ser Arg
             245             250

```

<210> 1881  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

```

<400> 1881
natcaccatg gatggacgcc ggcaaagcaa catcaatcga tgtcaagcca cagacatctc
60
aaatccctgc agaaccgcaa agtttggcag agaagaagga tgaatgggag atcgcataca
120
tcaacacgaa gattaacgac gtctacaacc ctctcaacaa caatgtggac tggttaagca
180
cgagaattga tctgctacag caagatttgg acaccactcg caagaaggat ctaaaaccag
240
ccacatcgat cgatatctgc accatcacat cgatcgatag caagttcgta gccatggaag
300
atagggtaca atcttataag gatatgcacg accgtttcac ctcacctatc aggcgata
358

```

<210> 1882  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1882
Met Asp Ala Gly Lys Ala Thr Ser Ile Asp Val Lys Pro Gln Thr Ser
1             5             10             15
Gln Ile Pro Ala Glu Pro Gln Ser Leu Ala Glu Lys Lys Asp Glu Trp
             20             25             30
Glu Ile Ala Tyr Ile Asn Thr Lys Ile Asn Asp Val Tyr Asn Pro Leu
             35             40             45
Asn Asn Asn Val Asp Trp Leu Ser Thr Arg Ile Asp Leu Leu Gln Gln
             50             55             60
Asp Leu Asp Thr Thr Arg Lys Lys Asp Leu Lys Pro Ala Thr Ser Ile
65             70             75             80
Asp Ile Cys Thr Ile Thr Ser Ile Asp Ser Lys Phe Val Ala Met Glu
             85             90             95
Asp Arg Leu Gln Ser Tyr Lys Asp Met His Asp Arg Phe Thr Ser Pro
             100            105            110
Ile Arg Arg

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115

<210> 1883  
 <211> 367  
 <212> DNA  
 <213> Homo sapiens

<400> 1883  
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 60  
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 120  
 tgctgaaggc gatgagtctg tatttgtcaa ctccaattca aacagctcga tggcgcctcc  
 180  
 tgtcctggag aacaatgctg ttgatctcac tgatgggctg acagatttgg aatcctatat  
 240  
 gaggtttctt atggatggcg gngcaagtga ttcaattgat agccttctga accttgatgg  
 300  
 atcacaggat cttggtagca atatggacct ctggaccttc gatgacatgc ccacgcgtgg  
 360  
 cgatttn  
 367

<210> 1884  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 1884  
 Met Asn Leu His Ser Asp Gln Gly Ser Asn Ser Leu Gly Cys Ser Asp  
 1 5 10 15  
 Leu Gly Trp Glu Asn Asp Thr Lys Thr Pro Asp Ile Thr Ser Ile Ala  
 20 25 30  
 Pro Ile Pro Thr Ile Ala Glu Gly Asp Glu Ser Val Phe Val Asn Ser  
 35 40 45  
 Asn Ser Asn Ser Ser Met Val Pro Pro Val Leu Glu Asn Asn Ala Val  
 50 55 60  
 Asp Leu Thr Asp Gly Leu Thr Asp Leu Glu Ser Tyr Met Arg Phe Leu  
 65 70 75 80  
 Met Asp Gly Gly Ala Ser Asp Ser Ile Asp Ser Leu Leu Asn Leu Asp  
 85 90 95  
 Gly Ser Gln Asp Leu Gly Ser Asn Met Asp Leu Trp Thr Phe Asp Asp  
 100 105 110  
 Met Pro Ile Ala Gly Asp Xaa  
 115

<210> 1885  
 <211> 392  
 <212> DNA  
 <213> Homo sapiens

<400> 1885  
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 60

gttcgacgat ctccgcatgt tgggaacccg gtgatttctc gcctgcggcg cacctcgtgg  
 120  
 ctgcgtagta cagctgctgt tgccgccggg gccgcgaccg gtaccggggt ccaaccactg  
 180  
 aactgggtgga tcctcgctcat tcccgggtctc gctgcgctca tcctgctggg gcgcaacgcc  
 240  
 actggtcggg ccgcggcagg actgggggat ctcttcggca tcggctctgt taccaccacc  
 300  
 atttcctggg taggcgtcat cggcccgccg gtggcgatac ttctcatcgc tgtcatggcg  
 360  
 ttgtggtgtc tgctggccgg gtggacgatt cg  
 392

<210> 1886

<211> 130

<212> PRT

<213> Homo sapiens

<400> 1886

Xaa	Ala	Tyr	Ser	Gln	Arg	Met	Ser	Leu	Arg	His	Arg	Asp	Ser	Arg	Arg
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Pro	Arg	His	His	Val	Arg	Arg	Ser	Arg	His	Val	Gly	Asn	Pro	Val	Ile
			20					25				30			
Ser	Arg	Leu	Arg	Arg	Thr	Ser	Trp	Leu	Arg	Ser	Thr	Ala	Ala	Val	Ala
		35					40				45				
Ala	Gly	Ala	Ala	Thr	Gly	Thr	Gly	Phe	Gln	Pro	Leu	Asn	Trp	Trp	Ile
	50					55				60					
Leu	Val	Ile	Pro	Gly	Leu	Ala	Ala	Leu	Ile	Leu	Leu	Val	Arg	Asn	Ala
65				70					75				80		
Thr	Gly	Arg	Ala	Ala	Gly	Leu	Gly	Tyr	Leu	Phe	Gly	Ile	Gly	Leu	
			85				90					95			
Phe	Thr	Thr	Thr	Ile	Ser	Trp	Val	Gly	Val	Ile	Gly	Pro	Pro	Val	Ala
			100				105					110			
Ile	Leu	Leu	Ile	Ala	Val	Met	Ala	Leu	Trp	Cys	Leu	Leu	Ala	Gly	Trp
		115					120					125			
Thr	Ile														
	130														

<210> 1887

<211> 363

<212> DNA

<213> Homo sapiens

<400> 1887

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 120  
 gctgccaata tcaagagtca ccataatgtt ggtgggctcc ctgacgacct ccagttcagt  
 180  
 ctcgttgagc cattgcgcac cctctttaag gacgaggtgc gagccgtcgg actcgaactt  
 240  
 ggtctgcccg aggacatcgt ctggcgctcag cccttcccgg gcccggggct ggctatccgc  
 300

attattggcg aagtcaccgc ggagcgtctg gaggtgctac gcactgccga tgccatcacg  
 360  
 cgt  
 363

<210> 1888  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 1888  
 Arg Glu Phe Ile Arg Thr Phe Glu Asp Val Ala Lys Arg Leu Asn Gly  
 1 5 10 15  
 Asp Gln Pro Ile Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val  
 20 25 30  
 Val Glu Ser Gly Gly Gly Glu Gly Ala Ala Asn Ile Lys Ser His His  
 35 40 45  
 Asn Val Gly Gly Leu Pro Asp Asp Leu Gln Phe Ser Leu Val Glu Pro  
 50 55 60  
 Leu Arg Thr Leu Phe Lys Asp Glu Val Arg Ala Val Gly Leu Glu Leu  
 65 70 75 80  
 Gly Leu Pro Glu Asp Ile Val Trp Arg Gln Pro Phe Pro Gly Pro Gly  
 85 90 95  
 Leu Ala Ile Arg Ile Ile Gly Glu Val Thr Ala Glu Arg Leu Glu Val  
 100 105 110  
 Leu Arg Thr Ala Asp Ala Ile Thr Arg  
 115 120

<210> 1889  
 <211> 530  
 <212> DNA  
 <213> Homo sapiens

<400> 1889  
 gcaccagatc tgctcatggc gcgcattgcg acggcaacgc agtcgatccg gcttgggtct  
 60  
 ggtgggggtga tggccatgca ctacggggtcg ctgcaaatac cggaacgggtt ttcgaccctc  
 120  
 acagcgtctc tcggtgatcg tatcgacatg gggctgggccc gggctcccgg cggtgacatg  
 180  
 ctctccgccc atgccctcaa tcaggggcag gtcattccgc ctgaggccat taattccctc  
 240  
 atcgccgaaa cggtaggggt cgtgcgcgaa atgctaccgt cgaagcatcc gtacgcaaag  
 300  
 gtcgtcgtga ccccggcagg tcagatccag ccacagacgt ggctgctggg atcgtcgggc  
 360  
 cagtcagcag cgtggggtgg tgagcagggt atggactacg cctacgccc gtttttcacc  
 420  
 gggcgccagg acaccgggat catggatcac taccgcgcgc acctgtccga cggcttcccc  
 480  
 ggcaggaccc tctcagcagt gtgtgtatcg gctgctccga cgcgtccgga  
 530

<210> 1890

<211> 176  
 <212> PRT  
 <213> Homo sapiens

<400> 1890

Ala	Pro	Asp	Leu	Leu	Met	Ala	Arg	Ile	Ala	Thr	Ala	Thr	Gln	Ser	Ile
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Arg	Leu	Gly	Ser	Gly	Gly	Val	Met	Ala	Met	His	Tyr	Gly	Ser	Leu	Gln
		20						25				30			
Ile	Ala	Glu	Arg	Phe	Ser	Thr	Leu	Thr	Ala	Leu	Phe	Gly	Asp	Arg	Ile
	35						40				45				
Asp	Met	Gly	Leu	Gly	Arg	Ala	Pro	Gly	Gly	Asp	Met	Leu	Ser	Ala	His
	50					55				60					
Ala	Leu	Asn	Gln	Gly	Gln	Val	Ile	Arg	Pro	Glu	Ala	Ile	Asn	Ser	Leu
65				70					75					80	
Ile	Ala	Glu	Thr	Val	Gly	Phe	Val	Arg	Glu	Met	Leu	Pro	Ser	Lys	His
		85						90					95		
Pro	Tyr	Ala	Lys	Val	Val	Val	Thr	Pro	Ala	Gly	Gln	Ile	Gln	Pro	Gln
		100						105				110			
Thr	Trp	Leu	Leu	Gly	Ser	Ser	Gly	Gln	Ser	Ala	Ala	Trp	Ala	Gly	Glu
	115						120					125			
Gln	Gly	Met	Asp	Tyr	Ala	Tyr	Ala	Gln	Phe	Phe	Thr	Gly	Arg	Gln	Asp
	130					135					140				
Thr	Gly	Ile	Met	Asp	His	Tyr	Arg	Ala	His	Leu	Ser	Asp	Gly	Phe	Pro
145				150					155					160	
Gly	Arg	Thr	Leu	Ser	Ala	Val	Cys	Val	Ser	Ala	Ala	Pro	Thr	Arg	Pro
			165						170					175	

<210> 1891  
 <211> 423  
 <212> DNA  
 <213> Homo sapiens

<400> 1891

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120
cgtcaattta cagaggcagc ccagcttcct atcaactttc tggcctggct taacggtgta
180
atgggcaggg ggcaaggcct tgaccacact catgtttctc ccccggcctc ctccactctg
240
ggattttgta ccggtatggg gaggcactac ggttgcagat ttagcttttc agcgtggata
300
caagcaccca agtgtcccag accacagcag aaaccgtggt gctgccgttt ccaacctgct
360
gatttgggtct cttgctgccg ttctgaccaa cagaattgct actgactgac aaatcccttg
420
tgc
423

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<210> 1892  
 <211> 121  
 <212> PRT

<213> Homo sapiens

<400> 1892

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Met Trp Ala Pro Leu Pro Gln Ser Ser Ile Cys Thr Arg Leu Pro Thr
 1           5           10           15
Leu Gln Met Ala Pro Ala Cys Arg Glu Ile Gln Arg Gln Phe Thr Glu
 20           25           30
Ala Ala Gln Leu Pro Ile Asn Phe Leu Ala Trp Leu Asn Gly Val Met
 35           40           45
Gly Arg Gly Gln Gly Leu Asp His Thr His Val Ser Pro Pro Ala Ser
 50           55           60
Ser Thr Leu Gly Phe Cys Thr Gly Met Gly Arg His Tyr Gly Cys Arg
 65           70           75           80
Phe Ser Phe Ser Ala Trp Ile Gln Ala Pro Lys Cys Pro Arg Pro Gln
 85           90           95
Gln Lys Pro Cys Cys Cys Arg Phe Gln Pro Ala Asp Leu Val Ser Cys
100           105           110
Cys Arg Ser Asp Gln Gln Asn Cys Tyr
115           120

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<210> 1893

<211> 886

<212> DNA

<213> Homo sapiens

<400> 1893

```

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catgacgctg aactcgtcga aaagatatgg ggcgacgacc tgcgccacgt cggggtcggt
120
gtggaataca tgggtggcat ggacgacctc gtcgggatcg tcgccgagtt taagcctggt
180
ccggggcatc gccttggcgt gttggttgac cacctcgttg ccgacaccaa agagtcacgg
240
gtagcggacg aagtacgtcg tgggtgggtat agcgagtatg tcatgattac cggtcacgac
300
tttattgaca tctggcaggc catcaaacct caacgaattg gccgtcaaga atggcctgag
360
gtccccgatg acgaagactt caaactcggc accctgaagc gtctgggcct gcctcactcg
420
accaagctg acgtcggtaa ggctggcag gccatgctgg cacgagtgcg cgactggcac
480
gatttagacc cccgctttaa cacggagatg gagaaactta tcgatttcgt cacgcgtgac
540
catgtcgacg agctggacaa tggggagatg gcatgagtat tgacgtcgac acggtgtctg
600
acctcatccg ggatgtgagt gccagggtta tcgatccccg gttccggacc ctccacgate
660
atcaaatacca ccagaaaaag cccggggact tcgttactga tgccgatcgt caggccgagt
720
gcgagctggg tgccgctgtg accaagtatg ccggcggtat tgtcgtgggg gaggaatcag
780
ccttcgccga cccaaccatc cttgatgccg tttccgatgc tgacctggcc tgggtcatcg
840

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acccattga tggcactaag aacttcgtgc acgggtctgt tgatca  
886

<210> 1894

<211> 191

<212> PRT

<213> Homo sapiens

<400> 1894

Thr Gly Gly Ala Glu Pro Ala Arg Val Ala Leu Pro Ser Arg Ile Tyr  
1 5 10 15  
Val Glu Gly Arg His Asp Ala Glu Leu Val Glu Lys Ile Trp Gly Asp  
20 25 30  
Asp Leu Arg His Val Gly Val Val Val Glu Tyr Met Gly Gly Met Asp  
35 40 45  
Asp Leu Val Gly Ile Val Ala Glu Phe Lys Pro Gly Pro Gly His Arg  
50 55 60  
Leu Gly Val Leu Val Asp His Leu Val Ala Asp Thr Lys Glu Ser Arg  
65 70 75 80  
Val Ala Asp Glu Val Arg Arg Gly Gly Tyr Ser Glu Tyr Val Met Ile  
85 90 95  
Thr Gly His Arg Phe Ile Asp Ile Trp Gln Ala Ile Lys Pro Gln Arg  
100 105 110  
Ile Gly Arg Gln Glu Trp Pro Glu Val Pro Met Asp Glu Asp Phe Lys  
115 120 125  
Leu Gly Thr Leu Lys Arg Leu Gly Leu Pro His Ser Thr Gln Ala Asp  
130 135 140  
Val Gly Lys Ala Trp Gln Ala Met Leu Ala Arg Val Arg Asp Trp His  
145 150 155 160  
Asp Leu Asp Pro Arg Phe Asn Thr Glu Met Glu Lys Leu Ile Asp Phe  
165 170 175  
Val Thr Arg Asp His Val Asp Glu Leu Asp Asn Gly Glu Met Ala  
180 185 190

<210> 1895

<211> 2555

<212> DNA

<213> Homo sapiens

<400> 1895

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120  
cttcccctgt tgccaaggtc taactcactg tagtctggat gtgggtgtat gttcatgtac  
180  
acaacttttag aaagttgctt gcagaacaaa aaggctacac aaaagccac tggctctcaa  
240  
taccctcaag tggatggcag aggtctctgt tgaaagtggg caatttgcaa tctttgcatt  
300  
aggatttcag atgcatgccg ggtttccact gattgccaga actcgagatc actacacatg  
360  
gatcccaaaa atcaacatgg cagtggcagt tcgttagttg tgatccagca gccttctttg  
420



gatagccgtc agagattaga ctatgagaga gagattcagc ctactgctat tttgtcctta  
480  
gaccagatca aggccataag aggcagcaat gaatacacag aagggccttc ggtggtgaaa  
540  
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600  
ccaattaatg tgaataataa ctacgagcac agacacacaa gccacctggg acatgcagta  
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780  
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840  
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900  
gaacagtgtg ggaagtgaac gtgtggagaa tgcactgctc ccaggacct accatctgt  
960  
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1080  
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1200  
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1560  
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1620  
gtacatgaac atacaccac atccagacta cagtgtattt gagttgtttt gattgggtac  
1680  
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1740  
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1800  
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1920  
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1980  
tattggttgg accttgccca tcttactct agccttcgta tttgtgaagg actcagccac  
2040

cttccttctt caccocatgc ttctcaccaa atttttgttg tcattgaggg cacttggata  
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 actcaagttg atatttatag ctgatcaatc tatatgtgtc acagaactat gctgcctaaa  
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 2280  
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 2340  
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 2400  
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 2555

<210> 1896

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1896

Cys	Glu	Gln	Cys	Gly	Lys	Cys	Lys	Cys	Gly	Glu	Cys	Thr	Ala	Pro	Arg
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Thr	Leu	Pro	Ser	Cys	Leu	Ala	Cys	Asn	Arg	Gln	Cys	Leu	Cys	Ser	Ala
			20					25					30		
Glu	Ser	Met	Val	Glu	Tyr	Gly	Thr	Cys	Met	Cys	Leu	Val	Lys	Gly	Ile
		35					40					45			
Phe	Tyr	His	Cys	Ser	Asn	Asp	Asp	Glu	Gly	Asp	Ser	Tyr	Ser	Asp	Asn
	50					55				60					
Pro	Cys	Ser	Cys	Ser	Gln	Ser	His	Cys	Cys	Ser	Arg	Tyr	Leu	Cys	Met
65					70					75				80	
Gly	Ala	Met	Ser	Leu	Phe	Leu	Pro	Cys	Leu	Leu	Cys	Tyr	Pro	Pro	Ala
			85					90						95	
Lys	Gly	Cys	Leu	Lys	Leu	Cys	Arg	Arg	Cys	Tyr	Asp	Trp	Ile	His	Arg
		100					105						110		
Pro	Gly	Cys	Arg	Cys	Lys	Asn	Ser	Asn	Thr	Val	Tyr	Cys	Lys	Leu	Glu
		115				120						125			
Ser	Cys	Pro	Ser	Arg	Gly	Gln	Gly	Lys	Pro	Ser					
	130					135									

<210> 1897

<211> 938

<212> DNA

<213> Homo sapiens

<400> 1897

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 120

cacgcttccct ccctgagcaa acaccgggcc atccatcgtg gggagcggcc ccaccgctgt  
 180  
 ctggagtgtg gccgggcctt caccgagcgc tcggcgctga cttegcacct gcgcgtccac  
 240  
 accggcgaga aaccctatgg ctgcgccgac tgtggccgcc gcttcagcca gagctctgcc  
 300  
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 360  
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 540  
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 660  
 acaggtgaaa aacccaccca gtgccctagc tgtggacgtc gcttcgcta cccctcctg  
 720  
 ctggccagcc accggcgcgt gcactcgggc gagcggccct atgcctgcga cctttgctcc  
 780  
 aagcgttttg ctgagtggag ccacctggcc cagcaccagc tgctgcacac gggggagaag  
 840  
 cctttccctt gcctcgagtg tggccgggct tccgccagag gtggtctctg gctgtccaca  
 900  
 agtgtagccc caaggcccca aactgtagcc ctatgctt  
 938

&lt;210&gt; 1898

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1898

Arg	His	Gly	Cys	Tyr	Val	Cys	Gly	Lys	Ser	Phe	Ala	Trp	Arg	Ser	Thr
1				5				10					15		
Leu	Val	Glu	His	Val	Tyr	Ser	His	Thr	Gly	Glu	Lys	Pro	Phe	His	Cys
			20					25					30		
Thr	Asp	Cys	Gly	Lys	Gly	Phe	Gly	His	Ala	Ser	Ser	Leu	Ser	Lys	His
		35					40					45			
Arg	Ala	Ile	His	Arg	Gly	Glu	Arg	Pro	His	Arg	Cys	Leu	Glu	Cys	Gly
	50					55					60				
Arg	Ala	Phe	Thr	Gln	Arg	Ser	Ala	Leu	Thr	Ser	His	Leu	Arg	Val	His
65				70				75				80			
Thr	Gly	Glu	Lys	Pro	Tyr	Gly	Cys	Ala	Asp	Cys	Gly	Arg	Arg	Phe	Ser
			85					90				95			
Gln	Ser	Ser	Ala	Leu	Tyr	Gln	His	Arg	Arg	Val	His	Ser	Gly	Glu	Thr
			100					105				110			
Pro	Phe	Pro	Cys	Pro	Asp	Cys	Gly	Arg	Ala	Phe	Ala	Tyr	Pro	Ser	Asp
	115					120						125			
Leu	Arg	Arg	His	Val	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Pro	Cys
	130					135					140				
Pro	Asp	Cys	Gly	Arg	Arg	Phe	Ser	Ser	Ser	Ser	Leu	Leu	Val	Ser	His

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145          150          155          160
Arg Arg Ala His Ser Gly Glu Cys Pro Tyr Val Cys Asp Gln Cys Gly
          165          170          175
Lys Arg Phe Ser Gln Arg Lys Asn Leu Ser Gln His Gln Val Ile His
          180          185          190
Thr Gly Glu Lys Pro Tyr His Cys Pro Asp Cys Gly Arg Cys Phe Arg
          195          200          205
Arg Ser Arg Ser Leu Ala Asn His Arg Thr Thr His Thr Gly Glu Lys
          210          215          220
Pro His Gln Cys Pro Ser Cys Gly Arg Arg Phe Ala Tyr Pro Ser Leu
225          230          235          240
Leu Ala Ser His Arg Arg Val His Ser Gly Glu Arg Pro Tyr Ala Cys
          245          250          255
Asp Leu Cys Ser Lys Arg Phe Ala Gln Trp Ser His Leu Ala Gln His
          260          265          270
Gln Leu Leu His Thr Gly Glu Lys Pro Phe Pro Cys Leu Glu Cys Gly
          275          280          285
Arg Ala Ser Ala Arg Gly Gly Leu Trp Leu Ser Thr Ser Val Ala Pro
          290          295          300
Arg Pro Gln Thr Val Ala Leu Asp
305          310

```

<210> 1899  
<211> 508  
<212> DNA  
<213> Homo sapiens

```

<400> 1899
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60
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120
gaggaaatat caggccggct gcggagggaa ctggggccaaa gggacaggaa ccgggggagc
180
ctggaggcca ccctgctgca ggtgttgaaa aagggtggagg agtttcgaat caggatttga
240
gatgagatct ccaagcgac agacatggag ttcacctttg ttcagctgaa gaaggacctg
300
gatgcagagt gtcttcatcg gactgaactg gaaaccaagt taaaaagcct ggagagcttc
360
gtggagttga tgaaaacat ctatgagcag gagctgaagg acctggcagc acaggtgaag
420
gatgtgtcgg tgacctcgg catggacagc cgctgccaca tcgacctgag cggcatcgtg
480
gaggaggtga aggcccagta tgacgccg
508

```

<210> 1900  
<211> 79  
<212> PRT  
<213> Homo sapiens

```

<400> 1900
Lys Phe Ala Ser Leu Ile Gly Lys Val Gln Ala Leu Glu Gln Arg Asp

```

```

1           5           10           15
Gln Leu Leu Glu Thr Arg Trp Ser Phe Leu Gln Gly Gln Asp Ser Ala
      20           25           30
Ile Phe Asp Leu Gly His Leu Tyr Glu Glu Ile Ser Gly Arg Leu Arg
      35           40           45
Arg Glu Leu Gly Gln Arg Asp Arg Asn Arg Gly Gln Leu Glu Ala Thr
      50           55           60
Leu Leu Gln Val Leu Lys Lys Val Glu Glu Phe Arg Ile Arg Tyr
65           70           75

```

&lt;210&gt; 1901

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1901

```

acgcgtggac cacgatgcgc cggatcgggc tcggcgccat gcacacctcg gacctggcgg
60
cgggtgttcgg cgatgcgaag gcaacccgcg cttccaagtt cgacccttc cagccgcgcg
120
aggaattcga cgaggtcagc gccgccatgc agttccactg gggctccttc ttccacaacg
180
cgcatccggg cgagaagtgg ccggtctacg gtttccgcag cgacacggag cccggccgcg
240
cgaccgcgat cttcgcggcg aagtcctccg tggagtacga cccaaggcg gcgcagcgcc
300
gcgcgtggga gggctttgac atgcgcgaat ggggcatgca caggcaggac ctggtggaaa
360
cgctcaccga ttccatcgcc gacgagggca acgcttagcg acgccagcgc caccgagttt
420
agagaaatga aagaaatttt aatagagggt gga
453

```

&lt;210&gt; 1902

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1902

```

Thr Arg Gly Pro Arg Cys Ala Gly Ser Gly Ser Ala Pro Cys Thr Pro
1           5           10           15
Arg Thr Trp Arg Arg Cys Ser Ala Met Arg Arg Gln Pro Ala Leu Pro
      20           25           30
Ser Ser Thr Arg Ser Ser Arg Ala Arg Asn Ser Thr Arg Ser Ala Pro
      35           40           45
Pro Cys Ser Ser Thr Gly Ala Pro Ser Ser Thr Thr Arg Ile Arg Ala
      50           55           60
Arg Ser Gly Arg Ser Thr Val Ser Ala Ala Thr Arg Ser Pro Ala Ala
65           70           75           80
Arg Pro Arg Ser Ser Arg Arg Ser Pro Pro Trp Ser Thr Thr Pro Arg
      85           90           95
Arg Arg Ser Ala Ala Arg Gly Arg Ala Leu Thr Cys Ala Asn Gly Ala
      100          105          110
Cys Thr Gly Arg Thr Trp Trp Lys Arg Ser Pro Ile Pro Ser Pro Thr

```

115                      120                      125  
 Arg Ala Thr Leu Ser Asp Ala Ser Ala Thr Glu Phe Arg Glu Met Lys  
 130                      135                      140  
 Glu Ile Leu Ile Glu Gly Gly  
 145                      150

<210> 1903

<211> 531

<212> DNA

<213> Homo sapiens

<400> 1903

ccggcgaggg agctgttccg ggacgccgcc ttccccgccg cggactcctc gctcttctgc  
 60  
 gacttgctcta cgccgctggc ccagttccgc gaggacatca cgtggaggcg gcccagaga  
 120  
 atttgtgcca acccccgtt gtttccaaat gaccaacggg aagggcaggt gaagcagggg  
 180  
 ctgctggggg attgctggtt cctgtgtgcc tgcgccgcgc tgcagaagag caggcacctc  
 240  
 ctggaccagg tcattcctgc gggacagccg agctggggccg accaggagta ccggggctcc  
 300  
 ttcacctgtc gcttttggca gtttggacgg tgggtggagg gtccatgggt cccttcgagc  
 360  
 ccctgtgggc ggggcaggtg gcggatgccc tggtggacct gaccggcggc ctggcagaaa  
 420  
 gatggaacct gaagggcgta gcaggaagcg gaggccagca ggacaggcca ggccgctggg  
 480  
 agcacaggac ttgtcggcag ctgctccacc tgaaggacca gtgtctgatc a  
 531

<210> 1904

<211> 133

<212> PRT

<213> Homo sapiens

<400> 1904

Pro Ala Arg Glu Leu Phe Arg Asp Ala Ala Phe Pro Ala Ala Asp Ser  
 1                      5                      10                      15  
 Ser Leu Phe Cys Asp Leu Ser Thr Pro Leu Ala Gln Phe Arg Glu Asp  
 20                      25                      30  
 Ile Thr Trp Arg Arg Pro Gln Arg Ile Cys Ala Asn Pro Arg Leu Phe  
 35                      40                      45  
 Pro Asn Asp Gln Arg Glu Gly Gln Val Lys Gln Gly Leu Leu Gly Asp  
 50                      55                      60  
 Cys Trp Phe Leu Cys Ala Cys Ala Ala Leu Gln Lys Ser Arg His Leu  
 65                      70                      75                      80  
 Leu Asp Gln Val Ile Pro Ala Gly Gln Pro Ser Trp Ala Asp Gln Glu  
 85                      90                      95  
 Tyr Arg Gly Ser Phe Thr Cys Arg Phe Trp Gln Phe Gly Arg Trp Val  
 100                      105                      110  
 Glu Gly Pro Trp Val Pro Ser Ser Pro Cys Gly Arg Gly Arg Trp Arg  
 115                      120                      125  
 Met Pro Trp Trp Thr

130

<210> 1905  
 <211> 387  
 <212> DNA  
 <213> Homo sapiens

<400> 1905  
 acgcgtgggc tgatcggcat gctctgggca ctgggggtgg tggcggaagt gctgatgttc  
 60  
 ctggccatga gccggatcct cgcgcgcttt tcggtcctgc ggggtctgct ggccagtttc  
 120  
 ctcttgcccg ccgtgcgctg gttgctgctg ggcgcggttg ccgatcacct ggcgggtgctg  
 180  
 ttgttcgccc aggtgctgca cgcgcgacc ttgccagct ttcacgcctc tgccattcat  
 240  
 ttcgtgcaac gtagcttcgg cgcgcgcnca gcaaggccag ggcaggcggt atacgctgca  
 300  
 ctggccggta cgggcggggc tttggcgcg ttgtacgctg gttatagctg gaacagcctg  
 360  
 gggccgacct ggactttcag catcgct  
 387

<210> 1906  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<400> 1906  
 Thr Arg Gly Leu Ile Gly Met Leu Trp Ala Leu Gly Val Val Ala Glu  
 1 5 10 15  
 Val Leu Met Phe Leu Ala Met Ser Arg Ile Leu Ala Arg Phe Ser Val  
 20 25 30  
 Arg Arg Val Leu Leu Ala Ser Phe Leu Leu Ala Ala Val Arg Trp Leu  
 35 40 45  
 Leu Leu Gly Ala Leu Ala Asp His Leu Ala Val Leu Leu Phe Ala Gln  
 50 55 60  
 Val Leu His Ala Ala Thr Phe Ala Ser Phe His Ala Ser Ala Ile His  
 65 70 75 80  
 Phe Val Gln Arg Ser Phe Gly Ala Arg Xaa Ala Arg Pro Gly Gln Ala  
 85 90 95  
 Leu Tyr Ala Ala Leu Ala Gly Thr Gly Gly Ala Leu Gly Ala Leu Tyr  
 100 105 110  
 Ala Gly Tyr Ser Trp Asn Ser Leu Gly Pro Thr Trp Thr Phe Ser Ile  
 115 120 125  
 Val

<210> 1907  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 1907

acgcgttttcg accagcgcac ccgtgtcggc ggcatggcgg aaatcgtcgg cttcgacaag  
60  
aagctgcgcg ccgcgcgcgc cgaaacgctc gagatgtgcg tcaacgacct gttccccggg  
120  
ggcggcgaca cgtcgaaggc cacgttcttg acgggcctgc gcccgatgac gccggacggc  
180  
acgccgatcg tcggccgcac gccggtgtcg aacctgttcc tgaacaccgg ccacggcacg  
240  
ctcggctgga caatggtgtg cggctcgggc caactgctcg ccgacctgat ctccgggcaag  
300  
atgcccgcga tccaggccga cgacctgtct nnc  
333

<210> 1908

<211> 111

<212> PRT

<213> Homo sapiens

<400> 1908

Thr	Arg	Phe	Asp	Gln	Arg	Ile	Arg	Val	Gly	Gly	Met	Ala	Glu	Ile	Val
1				5					10					15	
Gly	Phe	Asp	Lys	Lys	Leu	Arg	Ala	Ala	Arg	Arg	Glu	Thr	Leu	Glu	Met
			20					25					30		
Cys	Val	Asn	Asp	Leu	Phe	Pro	Gly	Gly	Gly	Asp	Thr	Ser	Lys	Ala	Thr
		35					40				45				
Phe	Trp	Thr	Gly	Leu	Arg	Pro	Met	Thr	Pro	Asp	Gly	Thr	Pro	Ile	Val
	50					55				60					
Gly	Arg	Thr	Pro	Val	Ser	Asn	Leu	Phe	Leu	Asn	Thr	Gly	His	Gly	Thr
65				70					75					80	
Leu	Gly	Trp	Thr	Met	Val	Cys	Gly	Ser	Gly	Gln	Leu	Leu	Ala	Asp	Leu
			85				90						95		
Ile	Ser	Gly	Lys	Met	Pro	Ala	Ile	Gln	Ala	Asp	Asp	Leu	Ser	Xaa	
		100					105						110		

<210> 1909

<211> 2767

<212> DNA

<213> Homo sapiens

<400> 1909

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gaaggtggct gcggcgacaa aatgaagata ttcgtgggca acgtcgacgg gccggatacg  
120  
actccggagg agctggcagc cctctttgctg ccctacggca cggcatgag ctgcgccgtc  
180  
atgaaacagt tcgccttcgt gcacatgcgc gagaacgcgg gcgcgctgcg cgccatcgaa  
240  
gccctgcacg gccacgagct gcggccgggg cgcgcgctcg tgggtgaaat gtcgcgccca  
300  
aggcctctta atacttgga gattttcgtg ggcaatgtgt cggctgcatg cacgagccag  
360  
gaactgcgca gcctcttcga gcgcgcggga cgcgtcatcg agtgtgacgt ggtgaaagac  
420



tacgcggtttg ttcacatgga gaaggaagca gatgccaaag ccgcaatcgc gcagctcaac  
480  
ggcaaagaag tgaagggcaa gcgcatacaac gtggaactct ccaccaaggg tcagaagaag  
540  
gggcctggcc tggtgtcca gtctggggac aagaccaaga aaccaggggc tggggatacg  
600  
gccttccttg gaactggtgg cttctctgcc accttcgact accagcaggc ttttggcaac  
660  
agcactggtg gctttgatgg gcaagcccggt cagccacac cacccttctt tggtcgcgac  
720  
cgcagccctc tgcgcggttc acctccccga gcctcttatg tggctcctct gcagggccag  
780  
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840  
ttgctctctt tgggtgttgg ctatcggact cagcccatga cagcccaggc agcctcttac  
900  
cgcgctcagc cctctgtctc ccttggggca ccatacaggg gccagctggc tagtcctagc  
960  
tccagctctg ctgcagcttc ttaactcggc ccataatggtg gagcccagcc ctacgcctcg  
1020  
gccctttcct cctatggggg tcaggcagct gcagcttctt cgtcaactc ctatggggct  
1080  
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1140  
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1200  
ttaggtcctt acgggggtca ggcagcctcc tatggggccc agtctgcagc ctctcacta  
1260  
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1380  
gcacagccag ccacagctgc tgcctatgcc agccagccag cagcctacgc cgcacaagcc  
1440  
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1500  
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1560  
gccactggct cctatgggtgc cgcagcagcc tacggggccc aaccttctgc cactctggca  
1620  
gctccttacc gactcagtc atcagcctca ttggctgctt cctatgctgc ccagcagcat  
1680  
ccccaggctg ctgcctcta ccgcgccag ccaggcaatg cctacgatgg ggcaggtcag  
1740  
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1800  
ccgcccctatg agcgtaccgc cctctcccca cccggggcca gctacgacga tccctacaaa  
1860  
aaggctgtcg ccatgtcgaa aaggatggt tccgaccggc gtttagccga gctctctgat  
1920  
taccgcggtt tatcagagtc gcagctttcg ttccgcgct cgcgacaaa gtcctcgtg  
1980  
gattaccgtc gcctgcccga tgccattcc gattacgac gctattcggg ctctataat  
2040

gattacctgc gggcggetca gatgcactct ggctaccagc gccgcatgta gggccatcct  
 2100  
 gggatggggc accacagggg gggagggaga aaagaggtgg gtaggggttac agatccaggt  
 2160  
 tataactact ctggcccata cctttcctgg ttgtgggttt tcatgccctc taccatgtgg  
 2220  
 gccttcccca ggagatgata ctgttaagtg ttcggcagta acctactttg ttccttcgcc  
 2280  
 tcagcagcaa atcttgctac tggctctaga tctgcgggtt cccctctacc ctgcctcctg  
 2340  
 tctccccaga atgggaattt cttttatgtt tttatttttt tctgggctcc cttttatttt  
 2400  
 tgtgcgcgat atttaaggtc gtctggatgg ggaagcaacc tgcagctgag gtgcgcggcg  
 2460  
 cctttttcct tttagatggg aaggaggcca ggaaagggtc agcttaacca tttcctatgt  
 2520  
 gccaaagtgt gccagcagtc cagggtaacc tgactgtccc tctgtagact gttgagactg  
 2580  
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 2640  
 agctgatggg gaggcgacac gtcccacttc cccatctccc caagtaggtg gtgtagaaaa  
 2700  
 accttaattt tttttccctt ttgtatggac tacaaataaa acttggggca atttgagtt  
 2760  
 tggaaaa  
 2767

<210> 1910

<211> 669

<212> PRT

<213> Homo sapiens

<400> 1910

Met	Lys	Ile	Phe	Val	Gly	Asn	Val	Asp	Gly	Ala	Asp	Thr	Thr	Pro	Glu
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Glu	Leu	Ala	Ala	Leu	Phe	Ala	Pro	Tyr	Gly	Thr	Val	Met	Ser	Cys	Ala
			20					25					30		
Val	Met	Lys	Gln	Phe	Ala	Phe	Val	His	Met	Arg	Glu	Asn	Ala	Gly	Ala
		35					40					45			
Leu	Arg	Ala	Ile	Glu	Ala	Leu	His	Gly	His	Glu	Leu	Arg	Pro	Gly	Arg
		50				55					60				
Ala	Leu	Val	Val	Glu	Met	Ser	Arg	Pro	Arg	Pro	Leu	Asn	Thr	Trp	Lys
65					70					75				80	
Ile	Phe	Val	Gly	Asn	Val	Ser	Ala	Ala	Cys	Thr	Ser	Gln	Glu	Leu	Arg
			85					90					95		
Ser	Leu	Phe	Glu	Arg	Arg	Gly	Arg	Val	Ile	Glu	Cys	Asp	Val	Val	Lys
		100					105						110		
Asp	Tyr	Ala	Phe	Val	His	Met	Glu	Lys	Glu	Ala	Asp	Ala	Lys	Ala	Ala
		115					120				125				
Ile	Ala	Gln	Leu	Asn	Gly	Lys	Glu	Val	Lys	Gly	Lys	Arg	Ile	Asn	Val
		130				135					140				
Glu	Leu	Ser	Thr	Lys	Gly	Gln	Lys	Lys	Gly	Pro	Gly	Leu	Ala	Val	Gln
145					150					155				160	
Ser	Gly	Asp	Lys	Thr	Lys	Lys	Pro	Gly	Ala	Gly	Asp	Thr	Ala	Phe	Pro

165 170 175  
 Gly Thr Gly Gly Phe Ser Ala Thr Phe Asp Tyr Gln Gln Ala Phe Gly  
 180 185 190  
 Asn Ser Thr Gly Gly Phe Asp Gly Gln Ala Arg Gln Pro Thr Pro Pro  
 195 200 205  
 Phe Phe Gly Arg Asp Arg Ser Pro Leu Arg Arg Ser Pro Pro Arg Ala  
 210 215 220  
 Ser Tyr Val Ala Pro Leu Thr Ala Gln Pro Ala Thr Tyr Arg Ala Gln  
 225 230 235 240  
 Pro Ser Val Ser Leu Gly Ala Ala Tyr Arg Ala Gln Pro Ser Ala Ser  
 245 250 255  
 Leu Gly Val Gly Tyr Arg Thr Gln Pro Met Thr Ala Gln Ala Ala Ser  
 260 265 270  
 Tyr Arg Ala Gln Pro Ser Val Ser Leu Gly Ala Pro Tyr Arg Gly Gln  
 275 280 285  
 Leu Ala Ser Pro Ser Ser Gln Ser Ala Ala Ala Ser Ser Leu Gly Pro  
 290 295 300  
 Tyr Gly Gly Ala Gln Pro Ser Ala Ser Ala Leu Ser Ser Tyr Gly Gly  
 305 310 315 320  
 Gln Ala Ala Ala Ala Ser Ser Leu Asn Ser Tyr Gly Ala Gln Gly Ser  
 325 330 335  
 Ser Leu Ala Ser Tyr Gly Asn Gln Pro Ser Ser Tyr Gly Ala Gln Ala  
 340 345 350  
 Ala Ser Ser Tyr Gly Val Arg Ala Ala Ala Ser Ser Tyr Asn Thr Gln  
 355 360 365  
 Gly Ala Ala Ser Ser Leu Gly Ser Tyr Gly Ala Gln Ala Ala Ser Tyr  
 370 375 380  
 Gly Ala Gln Ser Ala Ala Ser Ser Leu Ala Tyr Gly Ala Gln Ala Ala  
 385 390 395 400  
 Ser Tyr Asn Ala Gln Pro Ser Ala Ser Tyr Asn Ala Gln Ser Ala Pro  
 405 410 415  
 Tyr Ala Ala Gln Gln Ala Ala Ser Tyr Ser Ser Gln Pro Ala Ala Tyr  
 420 425 430  
 Val Ala Gln Pro Ala Thr Ala Ala Ala Tyr Ala Ser Gln Pro Ala Ala  
 435 440 445  
 Tyr Ala Ala Gln Ala Thr Thr Pro Met Ala Gly Ser Tyr Gly Ala Gln  
 450 455 460  
 Pro Val Val Gln Thr Gln Leu Asn Ser Tyr Gly Ala Gln Ala Ser Met  
 465 470 475 480  
 Gly Leu Ser Gly Ser Tyr Gly Ala Gln Ser Ala Ala Ala Ala Thr Gly  
 485 490 495  
 Ser Tyr Gly Ala Ala Ala Ala Tyr Gly Ala Gln Pro Ser Ala Thr Leu  
 500 505 510  
 Ala Ala Pro Tyr Arg Thr Gln Ser Ser Ala Ser Leu Ala Ala Ser Tyr  
 515 520 525  
 Ala Ala Gln Gln His Pro Gln Ala Ala Ala Ser Tyr Arg Gly Gln Pro  
 530 535 540  
 Gly Asn Ala Tyr Asp Gly Ala Gly Gln Pro Ser Ala Ala Tyr Leu Ser  
 545 550 555 560  
 Met Ser Gln Gly Ala Val Ala Asn Ala Asn Ser Thr Pro Pro Pro Tyr  
 565 570 575  
 Glu Arg Thr Arg Leu Ser Pro Pro Arg Ala Ser Tyr Asp Asp Pro Tyr  
 580 585 590  
 Lys Lys Ala Val Ala Met Ser Lys Arg Tyr Gly Ser Asp Arg Arg Leu

595	600	605
Ala Glu Leu Ser Asp Tyr Arg Arg Leu Ser Glu Ser Gln Leu Ser Phe		
610	615	620
Arg Arg Ser Pro Thr Lys Ser Ser Leu Asp Tyr Arg Arg Leu Pro Asp		
625	630	635
Ala His Ser Asp Tyr Ala Arg Tyr Ser Gly Ser Tyr Asn Asp Tyr Leu		
645	650	655
Arg Ala Ala Gln Met His Ser Gly Tyr Gln Arg Arg Met		
660	665	

&lt;210&gt; 1911

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1911

```

nccgggtggc cggaatctac tcctagtgtc cagcttcctt cctcttctgt cttccctcg
60
ggtgcgcgga tgcgtttgcg cccctgctg cgttccgacg gtcattgagtg gcggcgtcag
120
cgcatcgacg atgaaagctt cctccgccca gttgagccga cccaagccgc accgtgggag
180
gcagcgcata gccagcaggc gtggtggaat cacctgaagt acctgcgcac cgccgcgcgt
240
gaagcactgg tgggtccgct cgtcattgag gtggagggga aattcgcagg gcaggttaacc
300
ctgggaaaca ttcagcatgg cagcattcgc gattgctgg
339

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&lt;210&gt; 1912

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1912

Xaa Gly Trp Pro Glu Ser Thr Pro Ser Val Gln Leu Pro Ser Ser Ser		
1	5	10
Val Phe Pro Ser Gly Ala Arg Met Arg Leu Arg Pro Leu Leu Arg Ser		
20	25	30
Asp Gly His Glu Trp Arg Arg Gln Arg Ile Asp Asp Glu Ser Phe Leu		
35	40	45
Arg Pro Val Glu Pro Thr Gln Ala Ala Pro Trp Ala Ala Ala His Ser		
50	55	60
Gln Gln Ala Trp Trp Asn His Leu Lys Tyr Leu Arg Thr Ala Ala Arg		
65	70	75
Glu Ala Leu Val Val Pro Leu Val Ile Glu Val Glu Gly Lys Phe Ala		
85	90	95
Gly Gln Val Thr Leu Gly Asn Ile Gln His Gly Ser Ile Arg Asp Cys		
100	105	110
Trp		

&lt;210&gt; 1913

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1913

gtgcacaccg gttcacagcg atatttcagg caaattgaaa gcgtcagttc gataggctga  
 60  
 atgcgaaatg ggggatttgt caccctcagg gaccggaagg aaggagagcag tccgatggca  
 120  
 gcgccagtac tcgatctcgt cctcccagcc ttgtccgaaa cctccgccaa tctcatcggc  
 180  
 cagaggttgc gccagggatg tcacacctcc atccccacat cgaatctacg gtgagcttcg  
 240  
 tcccagctgt cgggcagtag aaggcacctc ggatcaagct ttcttggcgt gaactgggtc  
 300  
 tggtacccat caatgccacc cacctgcact ccaatccccc acaagttgtc caacacgccg  
 360  
 cagaattgcy tcgcagccac ccggaccttg ccatcaaggt ggcccgcgcc accggaccag  
 420  
 caccggctct cctcaacctc gtcgatacgc gattgcgtct ggcagctcat cgcgtccatg  
 480  
 ccaggagct ggactcactc gtattgtctt cccctgatgg cggcgattta cgtggctcgg  
 540  
 caatgctgtc caggctgacc cggctgtggt ccagcacca ccaccttcg gtccgcatcg  
 600  
 ccaccaatcg tgggtgggct actgcggtcg aggaggtcgt cggccgcctg cgacaggagg  
 660  
 ggccgcgtca tatcgcatg ggaagcctgt ggatttgca cgacgagaat ttccgcatc  
 720  
 atactcgcca ggctttgcat gccggtgccg aggttgtcgc cgcaccg  
 767

&lt;210&gt; 1914

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1914

Met	Ser	His	Leu	His	Pro	His	Ile	Glu	Ser	Thr	Val	Ser	Phe	Val	Pro
1				5				10						15	
Ala	Val	Gly	Gln	Tyr	Lys	Ala	Pro	Arg	Ile	Lys	Leu	Ser	Trp	Arg	Glu
		20						25					30		
Leu	Val	Leu	Val	Pro	Ile	Asn	Ala	Thr	His	Leu	His	Ser	Asn	Pro	Pro
		35					40					45			
Gln	Val	Val	Gln	His	Ala	Ala	Glu	Leu	Arg	Arg	Ser	His	Pro	Asp	Leu
		50				55					60				
Ala	Ile	Lys	Val	Ala	Arg	Pro	Thr	Gly	Pro	Ala	Pro	Val	Leu	Leu	Asn
65					70					75				80	
Leu	Val	Asp	Thr	Arg	Leu	Arg	Leu	Ala	Ala	His	Arg	Val	His	Ala	Gln
			85						90					95	
Glu	Leu	Asp	Ser	Leu	Val	Leu	Ser	Ser	Pro	Asp	Gly	Gly	Asp	Leu	Arg
			100					105					110		
Gly	Ser	Ala	Met	Leu	Ser	Arg	Leu	Thr	Arg	Leu	Trp	Ser	Gln	His	His
		115					120					125			
His	Leu	Pro	Val	Arg	Ile	Ala	Thr	Asn	Arg	Gly	Gly	Ala	Thr	Ala	Val

130	135	140
Glu Glu Val Val Ala Arg	Leu Arg Gln Glu Gly Arg Arg His Ile Ala	
145	150	155
Val Gly Ser Leu Trp Ile Cys Asp Asp	Glu Asn Phe Arg Ile His Thr	160
	165	170
Arg Gln Ala Leu His Ala Gly Ala Glu Val Val Ala Ala Pro		175
	180	185
		190

<210> 1915  
 <211> 571  
 <212> DNA  
 <213> Homo sapiens

<400> 1915  
 acgcgtccca ggccccacag gcccctctg gctctcaggc ccccgccca gtggccagga  
 60  
 aggtgtgagc gcacgatggg cagtcacgcc gcacacacgc tctgctcatg tccctcccca  
 120  
 ggaccctctg accgggcaca agggcagctg tgaggacaag gccacagcca caaaccaacc  
 180  
 tggcacacac ggctcagggc gaggcactgc cccatggggc tgcattgatcc acgtcacag  
 240  
 gtgtcattgt ctatgctcag gggggcttgg caccatggga aaccacacca gaacacatgg  
 300  
 agaagccaca gcacaacctc agcggccgcc atgcaggacc ctgggtctca cccattgcac  
 360  
 ccaccgtgcg ggaccctgc gcctcaccgc gaacatccac agtgtgggac tgctgcgtct  
 420  
 caccactgc acctgccgtg caggatccct gactctcacc cgccgcaccc gccgtgcggg  
 480  
 atccctgagt ctacccgcc gcaccgccg tacctgccgc atccgccatg cgggacccct  
 540  
 gcgtctcacc caccgcaccc gccgtgcggg a  
 571

<210> 1916  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 1916  
 Met Gly Leu His Asp Pro Arg Ser Gln Val Ser Leu Ser Met Leu Arg  
 1 5 10 15  
 Gly Ala Trp His His Gly Lys Pro Thr Gln Asn Thr Trp Arg Ser His  
 20 25 30  
 Ser Thr Thr Ser Ala Pro Ala Met Gln Asp Pro Gly Ser His Pro Leu  
 35 40 45  
 His Pro Pro Cys Gly Thr Pro Ala Pro His Pro Glu His Pro Gln Cys  
 50 55 60  
 Gly Thr Ala Ala Ser His Pro Leu His Leu Pro Cys Arg Ile Pro Glu  
 65 70 75 80  
 Ser His Pro Pro His Pro Pro Cys Gly Ile Pro Glu Ser His Pro Pro  
 85 90 95  
 His Pro Pro Tyr Leu Pro His Pro Pro Cys Gly Thr Pro Ala Ser His

100 105 110  
 Pro Pro His Pro Pro Cys Gly  
 115

<210> 1917  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 1917  
 nnacgcgtga ccggcgaaga tctccgcacc ctatctgccg ggtacacgcc gggtgattcc  
 60  
 gatatgtctt gggctgccat caccttgtgg cgcggtgtcg ttgcctccgc cttggaccgt  
 120  
 catccctatg gcccggtgaa gtcggtaaag gtagcaggtc cggccggcca cccagccccc  
 180  
 gatttcgccg ccggatggtt gtcgaccgc ttggcagttc ccgtacatcg cacagtggcc  
 240  
 gactcccca ggagacactt cccggtgact catttgcagt tcaatcggga gacaaccac  
 300  
 gtagacgtcg atgtcattga cgagcgacg gttcgtgtat gtgttcggg ttcgccggaa  
 360

<210> 1918  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 1918  
 Xaa Arg Val Thr Gly Glu Asp Leu Arg Thr Leu Ser Ala Gly Tyr Thr  
 1 5 10 15  
 Pro Gly Asp Ser Asp Met Ser Trp Ala Ala Ile Thr Leu Trp Arg Gly  
 20 25 30  
 Val Val Ala Ser Ala Leu Asp Arg His Pro Tyr Gly Pro Val Lys Ser  
 35 40 45  
 Val Lys Val Ala Gly Pro Ala Gly His Pro Ala Pro Asp Phe Ala Ala  
 50 55 60  
 Gly Trp Leu Leu Asp Arg Leu Ala Val Pro Val His Arg Thr Val Ala  
 65 70 75 80  
 Asp Ser Pro Arg Arg His Phe Pro Val Thr His Leu Gln Phe Asn Arg  
 85 90 95  
 Glu Thr Thr His Val Asp Val Asp Val Ile Asp Glu Arg Thr Val Arg  
 100 105 110  
 Val Cys Val Pro Gly Ser Pro Glu  
 115 120

<210> 1919  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 1919  
 nncggccgca gctgtgtcca ctgcgctgtc cctgccacct cggccatctg cctctctctt  
 60

ccaggctgca gccatccctc ctgcactgct gaggcctggc cacgcgcac cgcgccacgc  
 120  
 ccacctccat cctctttggc ccttactaaa cactggggagc ccgcccgcgc gcgacaggcc  
 180  
 aggccagcgg gaaggtgtag acgaacagcc caaaggattc agcagtgtaa gtacccacc  
 240  
 tacgcactta caaagtgcag gccaccgccc agccccacct ccagacacag gcggaggcca  
 300  
 agctcgcggg caccgtatca tcccggtccg tctccacct acccctgcc attg  
 354

<210> 1920

<211> 118

<212> PRT

<213> Homo sapiens

<400> 1920

Xaa	Gly	Arg	Ser	Cys	Val	His	Cys	Ala	Val	Pro	Ala	Thr	Ser	Ala	Ile
1				5					10					15	
Cys	Leu	Ser	Leu	Pro	Gly	Cys	Ser	His	Pro	Ser	Cys	Thr	Ala	Glu	Ala
			20					25					30		
Trp	Pro	Arg	Ala	Ser	Arg	Pro	Arg	Pro	Pro	Pro	Ser	Ser	Leu	Pro	Leu
			35				40					45			
Thr	Lys	His	Trp	Glu	Pro	Ala	Arg	Pro	Arg	Gln	Ala	Arg	Pro	Ala	Gly
			50				55				60				
Arg	Cys	Arg	Arg	Thr	Ala	Gln	Arg	Ile	Gln	Gln	Cys	Lys	Tyr	Pro	Thr
					70					75				80	
Tyr	Ala	Leu	Thr	Lys	Cys	Arg	Pro	Pro	Pro	Ser	Pro	Thr	Ser	Arg	His
				85					90					95	
Arg	Arg	Arg	Pro	Ser	Ser	Arg	Ala	Pro	Tyr	His	Pro	Val	Pro	Ser	Pro
			100					105					110		
Pro	Tyr	Pro	Cys	Gln	Leu										
					115										

<210> 1921

<211> 357

<212> DNA

<213> Homo sapiens

<400> 1921

gaattcatct ggaggcagag agatggggaa gcgggtggga gaagagcaag aacggaaact  
 60  
 atttttaata caaatccagt catggtattg tatacacagc agcctctgtc ttccagaaac  
 120  
 ctacacggcc gccacaccaa agttaatgcc accaggcgtc atcacacaga tgtgaggtgc  
 180  
 aggtgccact ccacagccgt gggcagacct gggagcccag ctctctctgg tttcaccctc  
 240  
 cacatgccc accccatcct tctctcccag tctccactcc atcgaagcct ccagatgac  
 300  
 ttcattgtggg gacaggagaa ctacagatca tggctgagaa gggcgcnctg tngtcca  
 357

<210> 1922



<211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 1922  
 Met Val Leu Tyr Thr Gln Gln Pro Leu Ser Ser Arg Asn Leu His Gly  
 1 5 10 15  
 Arg His Thr Lys Val Asn Ala Thr Arg Arg His His Thr Asp Val Arg  
 20 25 30  
 Cys Arg Cys His Ser Thr Ala Val Gly Arg Pro Gly Ser Pro Ala Pro  
 35 40 45  
 Pro Gly Phe Thr Leu His Thr Ala His Pro Ile Leu Leu Ser Gln Ser  
 50 55 60  
 Pro Leu His Arg Ser Leu Pro Asp Asp Phe Met Trp Gly Gln Glu Asn  
 65 70 75 80  
 Tyr Arg Ser Trp Leu Arg Arg Ala Xaa Cys Xaa Pro  
 85 90

<210> 1923  
 <211> 368  
 <212> DNA  
 <213> Homo sapiens

<400> 1923  
 nattnaatta tgggtgagaaa aggcttatgc gttgcattgc tcgtgcttgc cacactgtca  
 60  
 ggtagtgcac agaagaaaga atgggttcagc aacattaaac tctcaggcta tggaatgacc  
 120  
 cagtatcaat atactgatca agaggggaagc aaaggccatt catttaatatc gcgattgttc  
 180  
 ccgttgccctt taaacggacg tatcttaaata gacttttatt ggaaggcaca ggcccaattc  
 240  
 aatggaaaca catcgacatt gggaagcagt ccacgtcttg tagacctatt tgtagagtgg  
 300  
 cagaaatatg attatttcaa ggtgaagtta ggccagttta agcgaccatt cacgtttgaa  
 360  
 aatcccag  
 368

<210> 1924  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 1924  
 Met Val Arg Lys Gly Leu Cys Val Ala Leu Leu Val Leu Val Thr Leu  
 1 5 10 15  
 Ser Gly Ser Ala Gln Lys Lys Glu Trp Phe Ser Asn Ile Lys Leu Ser  
 20 25 30  
 Gly Tyr Gly Met Thr Gln Tyr Gln Tyr Thr Asp Gln Glu Gly Ser Lys  
 35 40 45  
 Gly His Ser Phe Asn Leu Arg Leu Phe Pro Leu Pro Leu Asn Gly Arg  
 50 55 60  
 Ile Leu Asn Asp Phe Tyr Trp Lys Ala Gln Ala Gln Phe Asn Gly Asn

```

65              70              75              80
Thr Ser Thr Leu Gly Ser Ser Pro Arg Leu Val Asp Leu Phe Val Glu
              85              90              95
Trp Gln Lys Tyr Asp Tyr Phe Lys Val Lys Leu Gly Gln Phe Lys Arg
              100              105              110
Pro Phe Thr Phe Glu Asn Pro
              115

```

&lt;210&gt; 1925

&lt;211&gt; 427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1925

```

actagtgttt ccagcaggca gcgatttaat tgttcttgca ttgaaaccca gtgtggcaag
60
ccccctgtg atttgaggct aatccctccc caccctgttc tggcacatgt gcggtgccca
120
gggtccccc caggctgtga gcagataaag ccctgcgtgg cttcacaaca gtgactgggt
180
ctgagaaaca ggtccttgta caagcgacag ggagtgtca caccagatgt ggcagcccct
240
ccacgccagg ctgtgtggtg cagccgctg gtatatgtgt ccatcgtga tgaaaacagc
300
gttggtggt gcattgactgt tgtctgtttt cttcatggaa acaaggaaac ctaagcatta
360
aaacaacacc atccacgtct gggttccttag agcaaattga agcaccaggc tctggtgcac
420
ggcgcgc
427

```

&lt;210&gt; 1926

&lt;211&gt; 104

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1926

```

Met His His Thr Thr Leu Phe Ser Ser Ala Met Asp Thr Tyr Thr Arg
1              5              10              15
Arg Leu His His Thr Ala Trp Arg Gly Gly Ala Ala Thr Ser Gly Val
              20              25              30
Ser Thr Pro Cys Arg Leu Tyr Lys Asp Leu Phe Leu Arg Thr Ser His
              35              40              45
Cys Cys Glu Ala Thr Gln Gly Phe Ile Cys Ser Gln Pro Gly Gly Ser
              50              55              60
Pro Gly His Arg Thr Cys Ala Arg Thr Gly Trp Gly Gly Ile Ser Leu
65              70              75              80
Lys Ser Gln Gly Gly Leu Pro His Trp Val Ser Met Gln Glu Gln Leu
              85              90              95
Asn Arg Cys Leu Leu Glu Thr Leu
              100

```

&lt;210&gt; 1927

&lt;211&gt; 516

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1927

```

nntctagaag actccaccta cttttcccca gactttcagc tctattctgg gaggcatagaa
60
acatctgctt tgacggtgga ggcaaccagt agcatcaggg aaaaagttgt tgaagatcct
120
ctttgtaact tccactcccc aaacttcctg aggatctcag aggtggaaat gagaggttcc
180
gaggatgagg cagctggaac agtattgcag cggtgatcc aggaacaact gcggtatggc
240
acccaacccg agaacatgaa cttgctggcc attcagcacc aggccacagg gagtgcagga
300
ccagcccatc ctacaaacaa cttttcttcc acggaaaacc tcaactcaaga agaccacaaa
360
atggtctacc agtcagcacg ccaagaaccg cagggtcaag aacaccagng tgganncaat
420
acggtgatgg agaaacaggt ccggtccacg cagcctcagc agaacaacga ggaactgccc
480
acttacgagg aggccaaagc acagcccttc acgcgt
516

```

&lt;210&gt; 1928

&lt;211&gt; 172

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1928

```

Xaa Leu Glu Asp Ser Thr Tyr Phe Ser Pro Asp Phe Gln Leu Tyr Ser
 1             5             10             15
Gly Arg His Glu Thr Ser Ala Leu Thr Val Glu Ala Thr Ser Ser Ile
          20             25             30
Arg Glu Lys Val Val Glu Asp Pro Leu Cys Asn Phe His Ser Pro Asn
      35             40             45
Phe Leu Arg Ile Ser Glu Val Glu Met Arg Gly Ser Glu Asp Ala Ala
      50             55             60
Ala Gly Thr Val Leu Gln Arg Leu Ile Gln Glu Gln Leu Arg Tyr Gly
      65             70             75             80
Thr Pro Thr Glu Asn Met Asn Leu Leu Ala Ile Gln His Gln Ala Thr
          85             90             95
Gly Ser Ala Gly Pro Ala His Pro Thr Asn Asn Phe Ser Ser Thr Glu
          100            105            110
Asn Leu Thr Gln Glu Asp Pro Gln Met Val Tyr Gln Ser Ala Arg Gln
          115            120            125
Glu Pro Gln Gly Gln Glu His Gln Xaa Gly Xaa Asn Thr Val Met Glu
          130            135            140
Lys Gln Val Arg Ser Thr Gln Pro Gln Gln Asn Asn Glu Glu Leu Pro
          145            150            155            160
Thr Tyr Glu Glu Ala Lys Ala Gln Pro Phe Thr Arg
          165            170

```

&lt;210&gt; 1929

&lt;211&gt; 843

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1929

```

nnccgcggac actcagggtc tggggtcctt cttccccaag aggcctgact gcctgggtgt
60
tctccaggta catgtccttc aaggagaaat acacttcctg gcctgggcct gggccagggg
120
ccttctgggc cttgtctgga gtgcccacag cagaggctgg cttcctggta ctatctgtgc
180
cagaggaccc agggccccgt gcagccctgc ctctgggctg ggtctgaacc tgctccacgc
240
ccacgggccc ctgagtccca caggagtcag gctcgtctga gctggggatg cagttttctg
300
aagaacggcg gctttgggct gccttctcta actctggctt ccgcaccttg cttggattcc
360
tcattcttct ttttcttctt ggccccactc tcctctttga gggctctctg agggccccagc
420
tccatggcgt cacagatgta tgtcagcaag ccatgctctc cgtcctctcc attctcgggg
480
gcagcctccc cgttggtggt cacttctcca gaagcaaact gttgatcagg cccaaacctg
540
agtgtgagc agtctcagtc tctccctcct gccaaagccgc cagggtccca ccctcaggct
600
ccctggtagg gaccgagggg cccggcgctt gagccccgct caatcgccgc tttcgtgga
660
agcggtcggg gctgagcttg cgcagagtgt cgacctccc aggcaccgcc ttctcgtgct
720
tccagctctg ctgatctcg cgcagctttg ccgcagcctt gcgcttcaac ttggcgaacc
780
agcgtggtg gatcttgtag tcagtcatgg tgcccacctc ccaggaccct gagcaggaca
840
caa
843

```

&lt;210&gt; 1930

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1930

```

Leu Pro Gly Cys Ser Pro Gly Thr Cys Pro Ser Arg Arg Asn Thr Leu
1          5          10          15
Pro Gly Leu Gly Leu Gly Gln Gly Pro Ser Gly Pro Cys Leu Glu Cys
20          25          30
Pro Gln Gln Arg Leu Ala Ser Trp Tyr Tyr Leu Cys Gln Arg Thr Gln
35          40          45
Ala Pro Val Gln Pro Cys Leu Trp Ala Gly Ser Glu Pro Ala Pro Arg
50          55          60
Pro Arg Ala Pro Glu Ser His Arg Ser Gln Ala Arg Leu Ser Trp Gly
65          70          75          80
Cys Ser Phe Leu Lys Asn Gly Gly Phe Gly Leu Pro Ser Leu Thr Leu
85          90          95
Ala Ser Ala Pro Cys Leu Asp Ser Ser Ser Phe Phe Phe Phe Leu Ala

```

100 105 110  
 Pro Leu Ser Ser Leu Arg Ala Leu  
 115 120

<210> 1931  
 <211> 719  
 <212> DNA  
 <213> Homo sapiens

<400> 1931  
 acgcgtaggc ctgagccgct ccacagccct ggggagggca gaaaaggagg aaagtaggca  
 60  
 gtgcaagaaa caggaggaaa cccccagag cgcagcctcc tggaagcgga agggagcact  
 120  
 gaagaggagg tggtagtggtgtgtcagaagc tgctgagaag ccagttagat aaagcggaga  
 180  
 agcttcctac taggacagct tcctcccagc ccagtgtggc cacgctgggtg tcctcgggtga  
 240  
 ccagacacgt ggccatgaat ttctcagtgt gctttattgt tgattaaatg cagtcggctc  
 300  
 acgaggctga ctttggaac aggaggtccg tgggtcgtgg aataagaaaag ggcatcatgg  
 360  
 ttgcagagga aggaaggaa gccacggct gccttgggga gctttctgaa aggcaggtct  
 420  
 gatcatgect ctctgggcta cggctcctc acggtggctc ctggttgga ctgaagtgtg  
 480  
 ccccttggtc cctctctccc atctcagcat tagccaggac ttttggttg ggggccccag  
 540  
 cagggtgcc cccttgcaac acttcttttc ccacatgac gtgccttcca aacctacttc  
 600  
 cagcgtcgcc ctcttcagg agcctttcat aaccacctct ccctccact ggctaaagat  
 660  
 gaggttgagc aactgcagga cttgggacct tgttcctgcc cctgtggctg cctggatcc  
 719

<210> 1932  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 1932  
 Met Pro Leu Trp Ala Thr Val Ser Ser Arg Trp Leu Leu Val Gly Thr  
 1 5 10 15  
 Glu Val Val Pro Leu Val Pro Leu Ser His Leu Ser Ile Ser Gln Asp  
 20 25 30  
 Phe Trp Leu Gly Gly Pro Ser Arg Ala Ala Pro Leu Gln His Phe Phe  
 35 40 45  
 Ser His Met Ile Val Pro Ser Lys Pro Thr Ser Ser Val Ala Leu Phe  
 50 55 60  
 Arg Glu Pro Phe Ile Thr Thr Ser Pro Phe His Trp Leu Lys Met Arg  
 65 70 75 80  
 Leu Ser Asn Cys Arg Thr Trp Asp Leu Val Pro Ala Pro Val Ala Ala  
 85 90 95  
 Trp Ile

&lt;210&gt; 1933

&lt;211&gt; 295

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1933

```

ggcgccgagc tgtgggcggc catggagcgc atgcctgccg acctgattat cctcgacctg
60
atgctgccgg gggataacgg cctcttctgtg tgccagcgcc tgcgccagca atacgcaaca
120
ccagtgatca tgctgaccgc catgggcgaa ctgagtgatc gcgtgggggg cctggaaatg
180
ggcgccgatg actacctgaa caaacctttc gatgcccggtg aattacttgc ccgggtgcgc
240
gctgtactgc gtccggcggtg tgaaaaccga ccgacgttgg gcgacgtgtc gcgcc
295

```

&lt;210&gt; 1934

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1934

```

Gly Ala Glu Leu Trp Ala Ala Met Glu Arg Met Pro Ala Asp Leu Ile
 1           5           10           15
Ile Leu Asp Leu Met Leu Pro Gly Asp Asn Gly Leu Leu Leu Cys Gln
      20           25           30
Arg Leu Arg Gln Gln Tyr Ala Thr Pro Val Ile Met Leu Thr Ala Met
      35           40           45
Gly Glu Leu Ser Asp Arg Val Gly Gly Leu Glu Met Gly Ala Asp Asp
      50           55           60
Tyr Leu Asn Lys Pro Phe Asp Ala Arg Glu Leu Leu Ala Arg Val Arg
65           70           75           80
Ala Val Leu Arg Pro Ala Cys Glu Asn Arg Pro Thr Leu Gly Asp Val
      85           90           95
Ser Arg

```

&lt;210&gt; 1935

&lt;211&gt; 298

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1935

```

accggtgtgg cgggcgcggc cttcaccacc atcggtcca ccgggccgac ggccgggttcg
60
caatacatcg tcgatacctt cctggtagtg gtgttcgggg gggcccaaag cctgttcggc
120
cccacgcct cggcgcttcgt gattgcccag acccaatcgc tgctcgagtt tttcctcagt
180
ggctcgatgg ccaagtgct gaccttgctg tcggtgattc tgatcctgat gctgcgccg
240

```

caagggttgt tctccatcaa agtgcgcaag taaaggcgag cagataaggg ttttaagca  
298

<210> 1936

<211> 90

<212> PRT

<213> Homo sapiens

<400> 1936

Thr	Gly	Val	Ala	Gly	Ala	Ala	Phe	Thr	Thr	Ile	Gly	Ser	Thr	Gly	Pro
1				5				10						15	
Thr	Ala	Gly	Ser	Gln	Tyr	Ile	Val	Asp	Thr	Phe	Leu	Val	Val	Val	Phe
			20					25					30		
Gly	Gly	Ala	Gln	Ser	Leu	Phe	Gly	Pro	Ile	Ala	Ser	Ala	Phe	Val	Ile
		35					40					45			
Ala	Gln	Thr	Gln	Ser	Leu	Ser	Glu	Phe	Phe	Leu	Ser	Gly	Ser	Met	Ala
	50					55				60					
Lys	Val	Leu	Thr	Leu	Ser	Ser	Val	Ile	Leu	Ile	Leu	Met	Leu	Arg	Pro
65					70				75					80	
Gln	Gly	Leu	Phe	Ser	Ile	Lys	Val	Arg	Lys						
				85					90						

<210> 1937

<211> 513

<212> DNA

<213> Homo sapiens

<400> 1937

gcacggcgca cagtaacacc aactcgaaag agaccttatg aatgcaaggt gtgcgggaaa  
60  
gcctttaatt ctccaattt atttcaaata catcaaagaa ctcacactgg aaagagggtcc  
120  
tataaatgta gggaaatagt gagagccttc acagttttcca gtttctttcg aaaacatgga  
180  
aaaatgcata ctggagaaaa acgctatgaa tgtaaaatact gtggaaaacc tatcgattat  
240  
cccagtttat ttcaaattca tgtagaact cactctggag aaaaacccta caaatgtaaa  
300  
caatgtggta aagccttcat ttccgcaggt tacgttcgga cacatgaaat cagatctcac  
360  
gcgctggaga aatcccacca atgtcaggaa tgtgggaaga aactcagttg ttccagttcc  
420  
cttcacagac atgaaagaac tcatagtgga ggaaaactct acgaatgtca aaaatgtgac  
480  
caagtcttta gatgtccac gtcccttcac gcg  
513

<210> 1938

<211> 171

<212> PRT

<213> Homo sapiens

<400> 1938

Ala Arg Arg Thr Val Thr Pro Thr Arg Lys Arg Pro Tyr Glu Cys Lys

1				5					10					15				
Val	Cys	Gly	Lys	Ala	Phe	Asn	Ser	Pro	Asn	Leu	Phe	Gln	Ile	His	Gln			
			20						25					30				
Arg	Thr	His	Thr	Gly	Lys	Arg	Ser	Tyr	Lys	Cys	Arg	Glu	Ile	Val	Arg			
		35					40					45						
Ala	Phe	Thr	Val	Ser	Ser	Phe	Phe	Arg	Lys	His	Gly	Lys	Met	His	Thr			
	50					55					60							
Gly	Glu	Lys	Arg	Tyr	Glu	Cys	Lys	Tyr	Cys	Gly	Lys	Pro	Ile	Asp	Tyr			
65				70					75					80				
Pro	Ser	Leu	Phe	Gln	Ile	His	Val	Arg	Thr	His	Ser	Gly	Glu	Lys	Pro			
			85					90					95					
Tyr	Lys	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Ile	Ser	Ala	Gly	Tyr	Val			
			100					105					110					
Arg	Thr	His	Glu	Ile	Arg	Ser	His	Ala	Leu	Glu	Lys	Ser	His	Gln	Cys			
		115					120					125						
Gln	Glu	Cys	Gly	Lys	Lys	Leu	Ser	Cys	Ser	Ser	Ser	Leu	His	Arg	His			
	130					135					140							
Glu	Arg	Thr	His	Ser	Gly	Gly	Lys	Leu	Tyr	Glu	Cys	Gln	Lys	Cys	Asp			
145					150					155				160				
Gln	Val	Phe	Arg	Cys	Pro	Thr	Ser	Leu	His	Ala								
			165					170										

&lt;210&gt; 1939

&lt;211&gt; 1233

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1939

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gccggcagcg ccgctcccca gggagggagt ccgcagcctg aggtcttctc caagaaaaaa
60
aaagaaaaaa aaacaacatg gctgcaaagg agaaactgga ggcagtgtta aatgtggccc
120
tgagggtgcc aagcatcatg ctgttggatg tctgtacag atgggatgtc agctcctttt
180
tccagcagat ccaaagaagt agccttagta ataaccctct tttccagtat aagtatttgg
240
ctcttaatat gcattatgta ggttatatct taagtgtggt gctgctaaca ttgccaggc
300
agcatctggt tcagctttat ctatatcttt tgactgctct gtcctctat gctggacatc
360
aaatttccag ggactatggt cggagtgaac tggggtttgc ctatgaggga ccaatgtatt
420
tagaacctct ctctatgaat cggtttacca cagccttaat aggtcagttg gtggtgtgta
480
ctttatgctc ctgtgtcatg aaaacaaagc agatttggct gttttcagct cacatgcttc
540
ctctgctagc acgactctgc cttgttcctt tggagacaat tgctatcatc aataaatttg
600
ctatgatttt tactggattg gaagtctctc attttcttgg gtctaattct ttggtacctt
660
ataaccttgc taaatctgca tacagagaat tggttcaggt agtggaggta tatggccttc
720
tcgccttggg aatgtccctg tggaatcaac tggtagtccc tgttcttttc atggttttct
780

```



ggctcgtctt atttgcctt cagatttact cctatttcag tactcgagat cagcctgcat  
 840  
 cacgtgagag gcttcttttc ctttttctga caaggtaatt aataagagcc tatgatacta  
 900  
 tatataacct tagaaagaga aaactttgat ctaggaatag taagttttgc agattacttt  
 960  
 tatcgttcat gttacacaac ttcgtatttt gttaagatag gattttcatt cactggatac  
 1020  
 ctaggttttg caatgcagag aggtgctaac ataataatgt ggtttatttg gctgcactat  
 1080  
 ggaccagagt gtagcaaatg atttgtggaa aggtacatag cacatcgtaa aagtattttt  
 1140  
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 1200  
 tattgagtat tttaaatgta ccataccatt naa  
 1233

<210> 1940

<211> 266

<212> PRT

<213> Homo sapiens

<400> 1940

Met	Ala	Ala	Lys	Glu	Lys	Leu	Glu	Ala	Val	Leu	Asn	Val	Ala	Leu	Arg
1			5						10					15	
Val	Pro	Ser	Ile	Met	Leu	Leu	Asp	Val	Leu	Tyr	Arg	Trp	Asp	Val	Ser
			20					25					30		
Ser	Phe	Phe	Gln	Gln	Ile	Gln	Arg	Ser	Ser	Leu	Ser	Asn	Asn	Pro	Leu
			35				40						45		
Phe	Gln	Tyr	Lys	Tyr	Leu	Ala	Leu	Asn	Met	His	Tyr	Val	Gly	Tyr	Ile
			50				55						60		
Leu	Ser	Val	Val	Leu	Leu	Thr	Leu	Pro	Arg	Gln	His	Leu	Val	Gln	Leu
65					70					75				80	
Tyr	Leu	Tyr	Phe	Leu	Thr	Ala	Leu	Leu	Leu	Tyr	Ala	Gly	His	Gln	Ile
			85						90					95	
Ser	Arg	Asp	Tyr	Val	Arg	Ser	Glu	Leu	Gly	Phe	Ala	Tyr	Glu	Gly	Pro
			100					105						110	
Met	Tyr	Leu	Glu	Pro	Leu	Ser	Met	Asn	Arg	Phe	Thr	Thr	Ala	Leu	Ile
			115					120					125		
Gly	Gln	Leu	Val	Val	Cys	Thr	Leu	Cys	Ser	Cys	Val	Met	Lys	Thr	Lys
			130				135					140			
Gln	Ile	Trp	Leu	Phe	Ser	Ala	His	Met	Leu	Pro	Leu	Leu	Ala	Arg	Leu
145					150					155				160	
Cys	Leu	Val	Pro	Leu	Glu	Thr	Ile	Ala	Ile	Ile	Asn	Lys	Phe	Ala	Met
				165					170					175	
Ile	Phe	Thr	Gly	Leu	Glu	Val	Leu	Tyr	Phe	Leu	Gly	Ser	Asn	Leu	Leu
			180					185					190		
Val	Pro	Tyr	Asn	Leu	Ala	Lys	Ser	Ala	Tyr	Arg	Glu	Leu	Val	Gln	Val
			195					200					205		
Val	Glu	Val	Tyr	Gly	Leu	Leu	Ala	Leu	Gly	Met	Ser	Leu	Trp	Asn	Gln
			210				215						220		
Leu	Val	Val	Pro	Val	Leu	Phe	Met	Val	Phe	Trp	Leu	Val	Leu	Phe	Ala
225					230					235				240	
Leu	Gln	Ile	Tyr	Ser	Tyr	Phe	Ser	Thr	Arg	Asp	Gln	Pro	Ala	Ser	Arg

```

<400> 1942
Met Met Gly Lys Leu Pro Leu Gly Val Val Ser Pro Tyr Val Lys Met
 1          5          10          15
Ser Ser Gly Gly Tyr Thr Asp Pro Leu Lys Phe Tyr Ala Thr Ser Tyr
      20          25          30
Cys Thr Ala Tyr Gly Arg Glu Asp Phe Lys Pro Arg Val Gly Ser His
      35          40          45
Val Gly Thr Gly Tyr Lys Ser Asn Phe Gln Pro Val Val Ser Cys Gln
      50          55          60
Ala Ser Leu Glu Ala Leu Asp Asn Pro Ala Arg Gly Glu Gln Ala Gln
65          70          75          80
Asp His Phe Gln Ser Val Ala Ser Gln Ser Tyr Arg Pro Leu Glu Val
      85          90          95
Pro Asp Gly Lys His Pro Leu Pro Trp Ser Met Arg Gln Thr Ser Ser
      100          105          110
Gly Tyr Gly Arg Glu Lys Pro Ser Ala Gly Pro Pro Thr Lys Glu Val
      115          120          125
Arg

```

```
<210> 1943
<211> 386
<212> DNA
<213> Homo sapiens
```

&lt;400&gt; 1943

nagaaacatt caggggtcca acaggggtgga aaacatgagg ctgcaggatg tttaacagga  
60  
gtctttgctg cagctcctct tggagccttt aacgagatac tatcatgcct atgaactgcc  
120  
acacagatgt acatggcata gcactgcccc aaagtatcag cccaaggaac cctactttcc  
180  
ccagcaacat ctaactcaga aatgctgac tttggcctca atctgggtccc aaaatacctc  
240  
caggggtat tgggcttcgg tgtgttcaca cacttggtca tgtaaactcg aacacagact  
300  
ctctctgcct tggcaagaac cccccacacc cccatagata attacaccct ttggttctcc  
360  
ctctgcaatc tcacctgcta gagacg  
386

&lt;210&gt; 1944

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1944

Met	Gly	Val	Trp	Gly	Val	Leu	Ala	Lys	Ala	Glu	Arg	Val	Cys	Val	Gln
1				5					10					15	
Ile	Tyr	Met	Thr	Lys	Cys	Val	Asn	Thr	Pro	Lys	Pro	Lys	Ile	Pro	Trp
			20					25					30		
Arg	Tyr	Phe	Gly	Thr	Arg	Leu	Arg	Pro	Lys	Ile	Ser	Ile	Ser	Glu	Leu
		35				40					45				
Asp	Val	Ala	Gly	Glu	Ser	Arg	Val	Pro	Trp	Ala	Asp	Thr	Phe	Gly	Gln
	50					55				60					
Cys	Tyr	Ala	Met	Tyr	Ile	Cys	Val	Ala	Val	His	Arg	His	Asp	Ser	Ile
65				70					75					80	
Ser	Leu	Lys	Ala	Pro	Arg	Gly	Ala	Ala	Lys	Thr	Pro	Val	Lys	His	
			85					90					95		
Pro	Ala	Ala	Ser	Cys	Phe	Pro	Pro	Cys	Trp	Ser	Pro	Glu	Cys	Phe	
		100					105						110		

&lt;210&gt; 1945

&lt;211&gt; 443

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1945

nacgcgtcac gaagcgcgct cgccccacgt ggctccaagg gcgtccacgc gcccctcctc  
60  
gaccgattgg tgtcgaacat ggcacgggtg catgcgacgc gcaccaagat ccagctcaag  
120  
ctcgcgatcc agcgantcgg catgctacag gagaaaaaag ccgcactgca taaaaaagtg  
180  
cgactggaaa ttgcggacnn tcgtagacgc caaaagcttg aatctgcgcg cgtcaaaacc  
240  
gaatcgctga tcatggacga tatacatctg gagttgcttg aactgcttga gctctactgt  
300

gagacactct atgccagatt cggattacta gaaggacgcg acaatgagcc tgatgatgcg  
 360  
 atccgcgagc cgatgatgcg cattattcat gcggctcatc gcacagaggt gaaggaacta  
 420  
 catgtgctcc aaaacatgct gaa  
 443

<210> 1946

<211> 147

<212> PRT

<213> Homo sapiens

<400> 1946

Xaa	Ala	Ser	Arg	Ser	Ala	Leu	Gly	Pro	Arg	Gly	Ser	Lys	Gly	Val	His
1				5					10					15	
Ala	Pro	Leu	Leu	Asp	Arg	Leu	Val	Ser	Asn	Met	Ala	Arg	Trp	His	Ala
		20						25					30		
Thr	Arg	Thr	Lys	Ile	Gln	Leu	Lys	Leu	Ala	Ile	Gln	Arg	Xaa	Gly	Met
		35					40					45			
Leu	Gln	Glu	Lys	Lys	Ala	Ala	Leu	His	Lys	Lys	Val	Arg	Leu	Glu	Ile
	50					55					60				
Ala	Asp	Xaa	Arg	Arg	Arg	Gln	Lys	Leu	Glu	Ser	Ala	Arg	Val	Lys	Thr
65					70					75				80	
Glu	Ser	Leu	Ile	Met	Asp	Asp	Ile	His	Leu	Glu	Leu	Leu	Glu	Leu	Leu
			85					90					95		
Glu	Leu	Tyr	Cys	Glu	Thr	Leu	Tyr	Ala	Arg	Phe	Gly	Leu	Leu	Glu	Gly
		100						105				110			
Arg	Asp	Asn	Glu	Pro	Asp	Asp	Ala	Ile	Arg	Glu	Pro	Met	Ile	Ala	Ile
		115					120					125			
Ile	His	Ala	Ala	His	Arg	Thr	Glu	Val	Lys	Glu	Leu	His	Val	Leu	Gln
	130					135					140				
Asn	Met	Leu													
145															

<210> 1947

<211> 472

<212> DNA

<213> Homo sapiens

<400> 1947

cggccgtgta ggccgtgacg gtgaccaaca gagccacagc gggcccgtg taggcgggag  
 60  
 gactgtgccg caggtgcagg agggtcagat ggaaacaaaa ggcgagggcg gcctccacaa  
 120  
 gcgccccgtg gggcacggat gtgcgagggg ccgagctgca gctctgggcc atgaggctct  
 180  
 gcagcaggtg caggtcactg agctcccagg ccagcagag gcgcgtcagg gtgcaggcgg  
 240  
 cctgcatgcc cagccctgt gccgccagct tcagcagcgt gccaggcaga gactcctcgg  
 300  
 ccatgaggaa ctctgcagg gacacgggtg ggttgccga gggcccgtcc aaggtgaccc  
 360  
 cgtgcgccag gaagagcagg aagagcaggg tgagcagcag gtcaggccca aagtcgccag  
 420

cccagggccccc gagctcgaaac agcgtcctca tctccaggaa gcaggccccg ag  
472

<210> 1948

<211> 150

<212> PRT

<213> Homo sapiens

<400> 1948

```

Met Arg Thr Leu Phe Glu Leu Gly Pro Trp Ala Gly Asp Phe Gly Pro
 1           5           10           15
Asp Leu Leu Leu Thr Leu Leu Phe Leu Leu Phe Leu Ala His Gly Val
      20           25           30
Thr Leu Asp Gly Ala Ser Ala Asn Pro Thr Val Ser Leu Gln Glu Phe
      35           40           45
Leu Met Ala Glu Glu Ser Leu Pro Gly Thr Leu Leu Lys Leu Ala Ala
      50           55           60
Gln Gly Leu Gly Met Gln Ala Ala Cys Thr Leu Thr Arg Leu Cys Trp
      65           70           75           80
Ala Trp Glu Leu Ser Asp Leu His Leu Leu Gln Ser Leu Met Ala Gln
      85           90           95
Ser Cys Ser Ser Ala Leu Arg Thr Ser Val Pro His Gly Ala Leu Val
      100          105          110
Glu Ala Ala Cys Ala Phe Cys Phe His Leu Thr Leu Leu His Leu Arg
      115          120          125
His Ser Pro Pro Ala Tyr Ser Gly Pro Ala Val Ala Leu Leu Val Thr
      130          135          140
Val Thr Ala Tyr Thr Ala
145           150

```

<210> 1949

<211> 395

<212> DNA

<213> Homo sapiens

<400> 1949

```

acgcgttgag ggaggcgaca tgcttcatga gcgcttgggc ccaactgctca agcgacatct
60
gcccttgct gatgttgcaa ggcggacagg acggcatgta attcgactcg acgtcacgct
120
cgggatgcct cgacgggacg ctcacaagct tccattggcc attcgcggtt cgcttggtct
180
cgaccgcgcg tacaaccggg tctacatggt cgccatgccca ccgatcgggc aatggcattc
240
cacagtaagc gcagcggccg tcgtatttgc gccggagccg atcgcgctgt gctttcgtea
300
gccggtcac gctttatgct ccacggcagg tgtggcagca tctggcagg cgactccaag
360
atccgcgcct gcgtccagct tgacggcgcc ggggtt
395

```

<210> 1950

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1950

```

Met Leu His Glu Arg Leu Ala Pro Leu Leu Lys Arg His Leu Pro Leu
 1             5             10             15
Ala Asp Val Ala Arg Arg Thr Gly Arg His Val Ile Arg Leu Asp Val
      20             25             30
Thr Leu Arg Met Pro Arg Arg Asp Ala His Lys Leu Pro Leu Ala Ile
      35             40             45
Arg Gly Ser Leu Gly Leu Asp Arg Ala Tyr Asn Arg Val Tyr Met Val
      50             55             60
Ala Met Pro Pro Ile Gly Gln Trp His Ser Thr Val Arg Ala Ala Ala
65             70             75             80
Val Val Phe Ala Pro Glu Pro Ile Ala Leu Cys Phe Arg Gln Pro Ala
      85             90             95
His Ala Leu Cys Ser Thr Ala Gly Val Ala Ala Ser Trp Gln Ala Thr
      100            105            110
Pro Arg Ser Ala Pro Ala Ser Ser Leu Thr Ala Pro Gly
      115            120            125

```

<210> 1951

<211> 363

<212> DNA

<213> Homo sapiens

<400> 1951

```

cggcgcgcgc ctctccgctc ccggggccccc gccgccaccg cgccccccgc gggagatgga
60
acagcggaac cggctcgggtg ccctcggata cctgccgcct ctgctgctgc atgccctgct
120
gctcttcgtg gccgacgctg cattcacaga agtccccaaa gatgtgacag tacgggaggg
180
agacgacatc gaaatgccct gcgcgttccg ggccagcgga gccacctcgt attcgtctga
240
gattcagtgg tggtagctca aggagccacc ccgggagctg ctgcacgagc tggcgctcag
300
cgtgccgggc gcccgagca aggtaacaaa taaggatgca actaaaatca gcaccgtacg
360
cgt
363

```

<210> 1952

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1952

```

Arg Pro Pro Pro Leu Arg Ser Arg Ala Pro Ala Ala Thr Ala Pro Pro
 1             5             10             15
Ala Gly Asp Gly Thr Ala Glu Pro Ala Arg Cys Pro Arg Ile Pro Ala
      20             25             30
Ala Ser Ala Ala Ala Cys Pro Ala Ala Leu Arg Gly Arg Arg Cys Ile
      35             40             45
His Arg Ser Pro Gln Arg Cys Asp Ser Thr Gly Gly Arg Arg His Arg

```

```

      50              55              60
Asn Ala Leu Arg Val Pro Gly Gln Arg Ser His Leu Val Phe Ala Gly
65              70              75              80
Asp Ser Val Val Val Pro Gln Gly Ala Thr Pro Gly Ala Ala Ala Arg
      85              90              95
Ala Gly Ala Gln Arg Ala Gly Arg Pro Glu Gln Gly Asn Lys
      100              105              110

```

<210> 1953  
 <211> 329  
 <212> DNA  
 <213> Homo sapiens

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<400> 1953
acgcgtcagc ctgagcccaa taactataaa agagtcgcaa ccatgactgt gctattgagt
60
gagcgcagcc agattttccg ggggtccgat gcctacgcgg tgctggacta cgtcaaccag
120
catgtgggca gccactgcat tcgcctgcct cccaagggcc ggccacgggc gagtatcagc
180
catcgcacct ttgccagcct ggacctgtgc cgcacagct acggcgctcc ggtacgggtc
240
acatcggtgg cgctggagac catctatcac ctgcagatcc tgttgagcgg gcattgccgc
300
tccagctccc gtggtgagga tgacgtggn
329

```

<210> 1954  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1954
Thr Arg Gln Pro Glu Pro Asn Asn Tyr Lys Arg Val Ala Thr Met Thr
1      5      10      15
Val Leu Leu Ser Glu Arg Ser Gln Ile Phe Arg Gly Ala Asp Ala Tyr
      20      25      30
Ala Val Ser Asp Tyr Val Asn Gln His Val Gly Ser His Cys Ile Arg
      35      40      45
Leu Pro Pro Lys Gly Arg Pro Arg Ala Ser Ile Ser His Arg Thr Phe
      50      55      60
Ala Ser Leu Asp Leu Cys Arg Ile Ser Tyr Gly Ala Pro Val Arg Val
65      70      75      80
Thr Ser Val Ala Leu Glu Thr Ile Tyr His Leu Gln Ile Leu Leu Ser
      85      90      95
Gly His Cys Arg Ser Ser Ser Arg Gly Glu Asp Asp Val
      100      105

```

<210> 1955  
 <211> 415  
 <212> DNA  
 <213> Homo sapiens

<400> 1955

acgcgtggct cgacgaaaac caagtacgag acatgcccga caaggtacta tcacacatgg  
 60  
 tggaatactg ctggggggcgc ttcacagaca acatcaaata cgctgtagct gcccaatatt  
 120  
 ggaaagggcc acacaagccc gatagtgacc atcaacggat cattgtaggc tatttcaaaa  
 180  
 ccgccaaca agccatgaac gcagcaaaac aattccactg gaacacccgg ctacaacaac  
 240  
 aatggaaaac atggatactc ccagtccaca acggcaccgt gtccgagttt ttcaccaac  
 300  
 aaaaaacttt gctagacgag caagacgata gcaatagcga gctgccggag catctacaaa  
 360  
 acgtcatgtg cggcaaaaaca ctccaccacc aagacgacac catatcgtgg tgcac  
 415

<210> 1956

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1956

Met	Pro	Asp	Lys	Val	Leu	Ser	His	Met	Val	Glu	Tyr	Cys	Trp	Gly	Arg
1				5					10					15	
Phe	Thr	Asp	Asn	Ile	Lys	Tyr	Ala	Val	Ala	Ala	Gln	Tyr	Trp	Lys	Gly
			20					25					30		
Pro	His	Lys	Pro	Asp	Ser	Asp	His	Gln	Arg	Ile	Ile	Val	Gly	Tyr	Phe
		35					40					45			
Lys	Thr	Ala	Lys	Gln	Ala	Met	Asn	Ala	Ala	Lys	Gln	Phe	His	Trp	Asn
	50					55				60					
Thr	Arg	Leu	Gln	Gln	Gln	Trp	Lys	Thr	Trp	Ile	Leu	Pro	Val	His	Asn
65				70					75					80	
Gly	Thr	Val	Ser	Glu	Phe	Phe	Thr	Gln	Gln	Lys	Thr	Leu	Leu	Asp	Glu
			85					90				95			
Gln	Asp	Asp	Ser	Asn	Ser	Glu	Leu	Pro	Glu	His	Leu	Gln	Asn	Val	Met
			100				105					110			
Cys	Gly	Lys	Thr	Leu	His	His	Gln	Asp	Asp	Thr	Ile	Ser	Trp	Cys	
		115					120					125			

<210> 1957

<211> 526

<212> DNA

<213> Homo sapiens

<400> 1957

acgcgttccg gagagatttt cctaacctct ctccgagctg ctgagccgat cggtgaccac  
 60  
 caggagctcc tcctgtgag gacaaagttc cagagtcggg gtcacgggcc ttacttattg  
 120  
 gggaggaggc ccgccggggc cgcagtgggc gaggggccct tggcgcgctc ctgggaggtc  
 180  
 agacctggca cagtgtggcg aaggtttcca gtgcgatccc gagtcgaggg cgcatttcgc  
 240  
 ggtgactgcc agcatgaacc gcagccgacc gagttctgcg atcgggcttc tccgcagagt  
 300



ggggaccctg gggaaggcgc caacttctct cctctgccca cctcactccc cgcgggcgtc  
 360  
 cctggggccgc ctgcccgggc cgcactgggc ggcctccatc gtcccttccc tctacctgca  
 420  
 ctgccccagg cgggagagag gccttgcccc nncgaggac cagctgcagc gggcagcggg  
 480  
 gtccctgtcc cccaaccccc gcccatggc acggggctga accggt  
 526

<210> 1958

<211> 175

<212> PRT

<213> Homo sapiens

<400> 1958

Thr	Arg	Ser	Gly	Glu	Ile	Phe	Leu	Thr	Ser	Leu	Arg	Ala	Ala	Glu	Pro
1				5					10					15	
Ile	Gly	Asp	His	Gln	Glu	Leu	Leu	Pro	Val	Arg	Thr	Lys	Phe	Gln	Ser
			20					25					30		
Arg	Gly	His	Gly	Pro	Tyr	Leu	Leu	Gly	Arg	Arg	Pro	Ala	Gly	Ala	Ala
			35				40					45			
Val	Gly	Glu	Gly	Pro	Leu	Ala	Arg	Ser	Trp	Glu	Val	Arg	Pro	Gly	Thr
			50			55				60					
Val	Trp	Arg	Arg	Phe	Pro	Val	Arg	Ser	Arg	Val	Glu	Gly	Ala	Phe	Arg
65					70					75				80	
Gly	Asp	Cys	Gln	His	Glu	Pro	Gln	Pro	Thr	Glu	Phe	Cys	Asp	Arg	Ala
			85					90					95		
Ser	Pro	Gln	Ser	Gly	Asp	Pro	Gly	Glu	Gly	Ala	Asn	Phe	Ser	Pro	Leu
			100				105						110		
Pro	Thr	Ser	Leu	Pro	Ala	Gly	Val	Pro	Gly	Pro	Pro	Ala	Arg	Ala	Ala
			115				120					125			
Leu	Gly	Gly	Leu	His	Arg	Pro	Phe	Pro	Leu	Pro	Ala	Leu	Pro	Gln	Ala
			130			135					140				
Gly	Glu	Arg	Pro	Trp	Pro	Xaa	Glu	Gly	Pro	Ala	Ala	Ala	Gly	Ser	Gly
145				150						155				160	
Val	Leu	Leu	Pro	Gln	Pro	Pro	Pro	His	Gly	Thr	Gly	Leu	Asn	Arg	
			165					170					175		

<210> 1959

<211> 378

<212> DNA

<213> Homo sapiens

<400> 1959

gtgcaccgga cggtcctcc aacggatcat ggcacggccc agcgggaaggc tcacccgagt  
 60  
 cgtcagaagg atcagggcgc ttgtcgtcgt cagacttcag gacatccac gacatggtga  
 120  
 acggctggga ggagaccttg tccccgtcgg tcttggcgcc gacaacaaca ccgctcatgg  
 180  
 tgtattttcc ggcattgagt aagaaccagt gggcatgctg atgacccttg atcggcagt  
 240  
 aggctccttt gaccacctga tatgtgtcat cagcgaggaa ggtgccgagt ttggcgttct  
 300

cgtctgcctc gggatgaattg ccgaggaggt acatcttgcc tggaccgta atcgcggtga  
 360  
 agtcgacgcg caacgcgt  
 378

<210> 1960  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 1960  
 Met Tyr Leu Leu Gly Asn Ser Pro Glu Ala Asp Glu Asn Ala Lys Leu  
 1 5 10 15  
 Gly Thr Phe Leu Ala Asp Asp Thr Tyr Gln Val Val Lys Gly Ala Ser  
 20 25 30  
 Leu Pro Ile Lys Gly His Gln His Ala His Trp Phe Phe Thr His Ala  
 35 40 45  
 Gly Lys Tyr Thr Met Ser Gly Val Val Val Gly Ala Lys Thr Asp Gly  
 50 55 60  
 Asp Lys Val Ser Ser Gln Pro Phe Thr Met Ser Trp Asp Val Leu Lys  
 65 70 75 80  
 Ser Asp Asp Asp Lys Arg Pro Asp Pro Ser Asp Asp Ser Gly Glu Pro  
 85 90 95  
 Ser Ala Gly Pro Ser His Asp Pro Leu Glu Glu Pro Ser Gly Ala  
 100 105 110

<210> 1961  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

<400> 1961  
 ggatccaccc cggaaaccgg caggatgaag ggggcaagtg aggagaagct ggcattctgtg  
 60  
 tccaacctgg tcaactgtgtt tgagaatagc aggacccag aagcagcacc cagaggccag  
 120  
 aggcctagagg acgtgcatca ccgccctgag tgcaggcctc ccgagtcacc aggaccacgg  
 180  
 gagaagacga atgtcgggga ggccgtgggg tctgagccca ggacagtcag caggaggtag  
 240  
 ctgaactccc tgaagaacaa gctgtccagc gaagcctgga ggaaatcttg ccagcctgtg  
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 accctctcag gatcggggac gcaggagcca gagaagaaga tcgtccagga gctgctggag  
 360  
 acagagcagg cctatgtggc gcgc  
 384

<210> 1962  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 1962  
 Gly Ser Thr Pro Glu Thr Gly Arg Met Lys Gly Ala Ser Glu Glu Lys

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1           5           10           15
Leu Ala Ser Val Ser Asn Leu Val Thr Val Phe Glu Asn Ser Arg Thr
           20           25           30
Pro Glu Ala Ala Pro Arg Gly Gln Arg Leu Glu Asp Val His His Arg
           35           40           45
Pro Glu Cys Arg Pro Pro Glu Ser Pro Gly Pro Arg Glu Lys Thr Asn
           50           55           60
Val Gly Glu Ala Val Gly Ser Glu Pro Arg Thr Val Ser Arg Arg Tyr
65           70           75           80
Leu Asn Ser Leu Lys Asn Lys Leu Ser Ser Glu Ala Trp Arg Lys Ser
           85           90           95
Cys Gln Pro Val Thr Leu Ser Gly Ser Gly Thr Gln Glu Pro Glu Lys
           100          105          110
Lys Ile Val Gln Glu Leu Leu Glu Thr Glu Gln Ala Tyr Val Ala Arg
           115          120          125

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<210> 1963  
 <211> 323  
 <212> DNA  
 <213> Homo sapiens

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<400> 1963
nnncccttcc taccctccca tactccccac cctcttctct cccctgtgac tgagcttgca
60
ggcatgaaac acccacctgg cctctctccc tctgttttgc ccttctgtc gtctctctcc
120
cacagctgcc tggctcttcg gcgtcagtc accaccttct gcagctctcc ctcacctgg
180
cgaccactca ggcatgcac tcgcggggcc ccttcagacc tctcggggtc atcttcccc
240
tcctgggcca ttatttttct tcatctgggc tgggcccggg ggggcgttcc ccccttctc
300
cttctttctt tttttttctc ttt
323

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<210> 1964  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

```

<400> 1964
Xaa Pro Phe Leu Pro Ser His Thr Pro His Pro Ser Ser Ser Pro Cys
1           5           10           15
Ala Glu Leu Ala Gly Met Lys His Pro Pro Gly Leu Ser Pro Ser Val
           20           25           30
Leu Pro Leu Leu Ser Ser Leu Ser His Ser Cys Leu Ala Leu Arg Arg
           35           40           45
Gln Ser Thr Thr Phe Cys Ser Ser Pro Ser Pro Trp Arg Pro Leu Arg
           50           55           60
His Ala Ser Arg Gly Pro Pro Ser Asp Leu Ser Gly Ser Ser Ser Pro
65           70           75           80
Ser Leu Ala Ile Ile Phe Leu His Leu Gly Trp Ala Arg Arg Gly Val
           85           90           95
Pro Pro Leu Pro Leu Leu Ser Phe Phe Phe Ser

```

100

105

&lt;210&gt; 1965

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1965

cggctggggc aggagctgga cgacgccacc atggacctgg agcagcagcg gcagcttggt  
60  
agcacccctgg agaagaagca gcgcaagttt gaccagcttc tggcagagga gaaggcagct  
120  
gtacttcggg cagtggagga acgtgagcgg gccgaggcag agggccggga gcgtgaggct  
180  
cgggccctgt cactgacacg ggactggag gaggagcagg aggcacgtga ggagctggag  
240  
cggcagaacc gggccctgcg ggctgagctg gaggcactgc tgagcagcaa ggatgacgtc  
300  
ggcaagagcg tgcattgagct ggaacgagcc tgccgggtag cagaacaggc agccaatgat  
360  
ctgcgagcac aggtgacaga actggaggat gactgacag cggccgagga tgccaagctg  
420  
cgtctggagg tgactgtgca ggctctcaag actcagcatg agcgtgacct gcagggccgt  
480  
gatgaggctg gtgaagagag gcggaggcag ctggccaagc agctgagaga tgcaagggtg  
540  
gagcgggatg aggagcggaa gcagcgcaact ctggccgtgg ctgcccga aaagctggag  
600  
ggagagctgg aggagctgaa ggctcagatg gcctctgccg gccagggcaa ggaggaggcg  
660  
gtgaagcagc ttcgcaagat gcaggcccag atgaaggagc tatggcggga ggtggaggag  
720  
acacgcacct cccgggagga gatcttctcc cagaatcggg aaagtga aaa gcgcctcaag  
780  
ggcctggagg ctgagggtgt gcggctgcag gaggaaactgg ccgcctcgga ccgtgtctcg  
840  
cggcaggccc agcaggaccg ggatgagatg gcagatgagg tggccaatgg taaccttagc  
900  
aaggcagcca ttctggagga gaagcgtcag ctggaggggc gcctggggca gttggaggaa  
960  
gagctggagg aggagcagac anactcagag ctgctcaatg accgctaccg caagctgtct  
1020  
ctgcaggtag agtcactgac cacagagctg tcagctgagc gcagtttctc agccaaggca  
1080  
gagagcgggc ggcagcagct ggaacggcag atccaggagc tacggggacg cctgggtgag  
1140  
gaggatgctg gggccctgct ccgccacaag atgaccattg ctgcccttga gtctaagttg  
1200  
gccagggctg aggagcagct agagcaagag accagagagc gcattcctctc tggaaagctg  
1260  
gtgccccaaa gtaagaagcg gtttaaagag gtggtgctcc aggtggagga ggagcggagg  
1320  
gtggctgacc agctccggga ccagctggag aagggaacc ttcgagtcaa gcagctgaag  
1380

cggcagctgg aggaggccga ggaggaggca tcccgg  
1416

<210> 1966

<211> 472

<212> PRT

<213> Homo sapiens

<400> 1966

Arg	Leu	Gly	Gln	Glu	Leu	Asp	Asp	Ala	Thr	Met	Asp	Leu	Glu	Gln	Gln
1				5					10					15	
Arg	Gln	Leu	Val	Ser	Thr	Leu	Glu	Lys	Lys	Gln	Arg	Lys	Phe	Asp	Gln
			20					25					30		
Leu	Leu	Ala	Glu	Glu	Lys	Ala	Ala	Val	Leu	Arg	Ala	Val	Glu	Glu	Arg
		35					40					45			
Glu	Arg	Ala	Glu	Ala	Glu	Gly	Arg	Glu	Arg	Glu	Ala	Arg	Ala	Leu	Ser
	50					55					60				
Leu	Thr	Arg	Ala	Leu	Glu	Glu	Gln	Glu	Ala	Arg	Glu	Glu	Leu	Glu	
65				70					75					80	
Arg	Gln	Asn	Arg	Ala	Leu	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Leu	Ser	Ser
			85						90					95	
Lys	Asp	Asp	Val	Gly	Lys	Ser	Val	His	Glu	Leu	Glu	Arg	Ala	Cys	Arg
			100					105					110		
Val	Ala	Glu	Gln	Ala	Ala	Asn	Asp	Leu	Arg	Ala	Gln	Val	Thr	Glu	Leu
		115					120					125			
Glu	Asp	Glu	Leu	Thr	Ala	Ala	Glu	Asp	Ala	Lys	Leu	Arg	Leu	Glu	Val
	130						135					140			
Thr	Val	Gln	Ala	Leu	Lys	Thr	Gln	His	Glu	Arg	Asp	Leu	Gln	Gly	Arg
145					150					155					160
Asp	Glu	Ala	Gly	Glu	Glu	Arg	Arg	Arg	Gln	Leu	Ala	Lys	Gln	Leu	Arg
			165						170					175	
Asp	Ala	Glu	Val	Glu	Arg	Asp	Glu	Glu	Arg	Lys	Gln	Arg	Thr	Leu	Ala
			180					185					190		
Val	Ala	Ala	Arg	Lys	Lys	Leu	Glu	Gly	Glu	Leu	Glu	Glu	Leu	Lys	Ala
		195					200					205			
Gln	Met	Ala	Ser	Ala	Gly	Gln	Gly	Lys	Glu	Glu	Ala	Val	Lys	Gln	Leu
	210					215					220				
Arg	Lys	Met	Gln	Ala	Gln	Met	Lys	Glu	Leu	Trp	Arg	Glu	Val	Glu	Glu
225				230						235				240	
Thr	Arg	Thr	Ser	Arg	Glu	Glu	Ile	Phe	Ser	Gln	Asn	Arg	Glu	Ser	Glu
			245						250					255	
Lys	Arg	Leu	Lys	Gly	Leu	Glu	Ala	Glu	Val	Leu	Arg	Leu	Gln	Glu	Glu
		260						265					270		
Leu	Ala	Ala	Ser	Asp	Arg	Ala	Arg	Gln	Ala	Gln	Gln	Asp	Arg	Arg	Asp
		275					280					285			
Glu	Met	Ala	Asp	Glu	Val	Ala	Asn	Gly	Asn	Leu	Ser	Lys	Ala	Ala	Ile
	290					295					300				
Leu	Glu	Glu	Lys	Arg	Gln	Leu	Glu	Gly	Arg	Leu	Gly	Gln	Leu	Glu	Glu
305					310				315					320	
Glu	Leu	Glu	Glu	Glu	Gln	Thr	Xaa	Ser	Glu	Leu	Leu	Asn	Asp	Arg	Tyr
			325						330					335	
Arg	Lys	Leu	Leu	Leu	Gln	Val	Glu	Ser	Leu	Thr	Thr	Glu	Leu	Ser	Ala
		340						345					350		
Glu	Arg	Ser	Phe	Ser	Ala	Lys	Ala	Glu	Ser	Gly	Arg	Gln	Gln	Leu	Glu

```

      355      360      365
Arg Gln Ile Gln Glu Leu Arg Gly Arg Leu Gly Glu Glu Asp Ala Gly
      370      375      380
Ala Arg Ala Arg His Lys Met Thr Ile Ala Ala Leu Glu Ser Lys Leu
385      390      395      400
Ala Gln Ala Glu Glu Gln Leu Glu Gln Glu Thr Arg Glu Arg Ile Leu
      405      410      415
Ser Gly Lys Leu Val Pro Lys Ser Lys Lys Arg Phe Lys Glu Val Val
      420      425      430
Leu Gln Val Glu Glu Glu Arg Arg Val Ala Asp Gln Leu Arg Asp Gln
      435      440      445
Leu Glu Lys Gly Asn Leu Arg Val Lys Gln Leu Lys Arg Gln Leu Glu
      450      455      460
Glu Ala Glu Glu Glu Ala Ser Arg
465      470

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&lt;210&gt; 1967

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1967

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aaatttgaat cctggaaagc tgatctcgat aagtcgtttg tcgagctggt tcggcgcttg
60
ccgacgcgcc taatttggat cgtgcagtaa gagcttctcc attcctcggc gccaaaggga
120
tgcattcacat ctgcggcca gtcagctccc ctgggcttgc actcgtcggg gatgctggcc
180
ttgcaccaga tcctctgtgg ggcgtcgggt gtggctgggc attccagtcg gcagcttggt
240
tagtggactg taccggatct catttggtg accggaccgc cttagatagg gcgcttcgca
300
gttatcatcg ataccaccgg cattctcttg ggtggcatga acgcctcatc tctagatatg
360
caaacggccg gggttttcat gcgctcgaga agctgatgct g
401

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&lt;210&gt; 1968

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1968

```

Met His His Ile Ser Arg Pro Val Ser Ser Pro Gly Leu Ala Leu Val
1      5      10      15
Gly Asp Ala Gly Leu Ala Pro Asp Pro Leu Trp Gly Val Gly Cys Gly
      20      25      30
Trp Ala Phe Gln Ser Ala Ala Trp Leu Val Asp Cys Thr Gly Ser His
      35      40      45
Leu Ala Asp Arg Thr Ala Leu Asp Arg Ala Leu Arg Ser Tyr His Arg
      50      55      60
Tyr His Arg His Ser Leu Gly Trp His Glu Arg Leu Ile Ser Arg Tyr
65      70      75      80
Ala Asn Gly Arg Gly Phe His Ala Leu Glu Lys Leu Met Leu

```

85

90

&lt;210&gt; 1969

&lt;211&gt; 464

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1969

```

nncatcgacg cgcactggac tcattctgggt gacggccac agatggacac tctgcgcgag
60
gaggctcgccg ttcaccgcgt cacggatgct gtcaccctgc tcggtcacgt cgccaacacc
120
caggctcatgg cgaccagcg tgatctcaaa ccgtcagtat tcgtcaacct ctctcctcg
180
gaaggacttc ctgtatcaat gatggaggtt gcttcctcg gtatcccat tatcgcgact
240
ggcgtcggcg gagtaggaga aatcgtctcg tctgacaacg ggcattctatt gcctgccgag
300
ttcaccgaca cccaggcatc tgacgcgtta gtgcagctgg cacgtctgtc tgaggacgag
360
taccagcagg tgtgtcaggc ctcccgccag gtgtgggaag aaaagtccg cgcctctgtc
420
gtctaccccc aattctgtcg cgagtgtctgg ggcgacgtg atca
464

```

&lt;210&gt; 1970

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1970

```

Xaa Ile Asp Ala His Trp Thr His Leu Gly Asp Gly Pro Gln Met Asp
 1           5           10           15
Thr Leu Arg Glu Val Ala Val His Arg Val Thr Asp Ala Val Thr
      20           25           30
Leu Leu Gly His Val Ala Asn Thr Gln Val Met Ala Thr Gln Arg Asp
      35           40           45
Leu Lys Pro Ser Val Phe Val Asn Leu Ser Ser Ser Glu Gly Leu Pro
      50           55           60
Val Ser Met Met Glu Val Ala Ser Leu Gly Ile Pro Ile Ile Ala Thr
      65           70           75           80
Gly Val Gly Gly Val Gly Glu Ile Val Ser Ser Asp Asn Gly His Leu
      85           90           95
Leu Pro Ala Glu Phe Thr Asp Thr Gln Ala Ser Asp Ala Leu Val Gln
      100          105          110
Leu Ala Arg Leu Ser Glu Asp Glu Tyr Gln Gln Val Cys Gln Ala Ser
      115          120          125
Arg Gln Val Trp Glu Glu Lys Phe Arg Ala Ser Val Val Tyr Pro Glu
      130          135          140
Phe Cys Arg Glu Cys Trp Gly Asp Ala Asp
145          150

```

&lt;210&gt; 1971

&lt;211&gt; 520

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1971

accggttgta ggtgtacaaa cactgctgac atcagccagc tcctgagtgt caggagagac  
 60  
 acagaagtac tcaggttggt tgtgtgttga ccgagagaac agctcagatt gaggaacgag  
 120  
 acagacgacg acaaaaacaa ttagagcatc agttgataca atacaaatgg aatataatgc  
 180  
 atctaacatt tcaaattcaa gacatgattc tgatgaaatc agtggtaaaa tgaatacata  
 240  
 tatgaattct acgacttcta agaaggatac tgggtgtgcaa acagatgact taaatatagg  
 300  
 aatattcacc aatgcagaat cacattgtgg atcattaatg gagagggaca tcacaaattg  
 360  
 ttcattctct gagatttcgg cagaacttat tggacagttt agcaccaaga aaaacaagca  
 420  
 agaactaact caggataaag gagccagctt agaaaaagaa aacaatcggg gtaatgacca  
 480  
 gtgtaatcag ttcacaagaa ttgagaaaca aacaaaacag  
 520

&lt;210&gt; 1972

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1972

Met	Glu	Tyr	Asn	Ala	Ser	Asn	Ile	Ser	Asn	Ser	Arg	His	Asp	Ser	Asp
1				5					10					15	
Glu	Ile	Ser	Gly	Lys	Met	Asn	Thr	Tyr	Met	Asn	Ser	Thr	Thr	Ser	Lys
			20					25					30		
Lys	Asp	Thr	Gly	Val	Gln	Thr	Asp	Asp	Leu	Asn	Ile	Gly	Ile	Phe	Thr
			35				40					45			
Asn	Ala	Glu	Ser	His	Cys	Gly	Ser	Leu	Met	Glu	Arg	Asp	Ile	Thr	Asn
			50			55					60				
Cys	Ser	Ser	Pro	Glu	Ile	Ser	Ala	Glu	Leu	Ile	Gly	Gln	Phe	Ser	Thr
65				70					75					80	
Lys	Lys	Asn	Lys	Gln	Glu	Leu	Thr	Gln	Asp	Lys	Gly	Ala	Ser	Leu	Glu
			85					90						95	
Lys	Glu	Asn	Asn	Arg	Cys	Asn	Asp	Gln	Cys	Asn	Gln	Phe	Thr	Arg	Ile
			100					105						110	
Glu	Lys	Gln	Thr	Lys	Gln										
			115												

&lt;210&gt; 1973

&lt;211&gt; 331

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1973

acgcgtacct atgcccagcg catggcggat cagttgaccg cggcactagg cagctactta  
 60



tccgcagggtc aaaagaaatc ggacggcctc ggatccttct tcgtggccac tacccttgaa  
 120  
 gagctacaag cgatgaacag cgatactcgc ttcaccacga gcgtgggaat cgacctatcc  
 180  
 cccgctcgat ctttctccgc ttgggcgctg cgcggaacga ctttttctgc gccgtcgatg  
 240  
 acaaaggctt cccgctcgag ctccggccga ccaagcgcac cgcgtcgctg tggcaaaagc  
 300  
 tggcgctcgc cgccagtga atcgtgtgca c  
 331

<210> 1974

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1974

Met	Ala	Asp	Gln	Leu	Thr	Ala	Ala	Leu	Gly	Ser	Tyr	Leu	Ser	Ala	Gly
1				5					10					15	
Gln	Lys	Lys	Ser	Asp	Gly	Leu	Gly	Ser	Phe	Phe	Val	Ala	Thr	Thr	Leu
			20					25					30		
Glu	Glu	Leu	Gln	Ala	Met	Asn	Ser	Asp	Thr	Arg	Phe	Thr	Thr	Ser	Val
		35					40					45			
Gly	Ile	Asp	Leu	Ser	Pro	Ala	Arg	Ser	Phe	Ser	Ala	Trp	Ala	Leu	Arg
	50					55				60					
Gly	Thr	Thr	Phe	Ser	Ala	Pro	Ser	Met	Thr	Lys	Ala	Ser	Arg	Ser	Ser
65				70						75				80	
Ser	Ala	Ala	Pro	Ser	Ala	Pro	Arg	Arg	Cys	Gly	Lys	Ser	Trp	Arg	Ser
			85						90					95	
Pro	Pro	Val	Lys	Ser	Cys	Ala									
					100										

<210> 1975

<211> 370

<212> DNA

<213> Homo sapiens

<400> 1975

acgcgtcggg ccaatcgctc gtggagctgc aaaccgcgct gcaagcccg c gacgagcaac  
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 gtctgacggc ttggaccgat gcgctgggtg caatggggcg caagctgagc caggcgtggg  
 120  
 agaaggcggg tgccgacacg gcgagccgct agcaggagat ttgcgatgcg ctggcgagcaga  
 180  
 ctgcgcgcga catctcttcg caaacacagg cccacgcca caacacgatc gccgagattt  
 240  
 ctgactgggt gcaggccgcc tcggaggcgc caaaggctgc tgccgaagtg gttgccgagc  
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 tgcgccagaa gctgtccgac agcatgggtcc gcgacacggg cgatgctgga agaacgcacg  
 360  
 cgcgtgctgg  
 370

<210> 1976

<211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 1976

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Met Arg Val Arg Ser Ser Ser Ile Ala Arg Val Ala Asp His Ala Val
 1           5           10           15
Gly Gln Leu Leu Ala Gln Leu Gly Asn His Phe Gly Ser Ser Leu Trp
           20           25           30
Arg Leu Arg Gly Gly Leu His Gln Ser Arg Asn Leu Gly Asp Arg Val
           35           40           45
Val Gly Val Gly Leu Cys Leu Arg Arg Asp Val Ala Arg Ser Leu Arg
           50           55           60
Gln Arg Ile Ala Asn Leu Leu Leu Thr Ala Arg Arg Val Gly Thr Arg
65           70           75           80
Leu Leu Pro Arg Leu Ala Gln Leu Gly Ala His Cys Thr Gln Arg Ile
           85           90           95
Gly Pro Ser Arg Gln Thr Leu Leu Val Ala Gly Leu Gln Arg Gly Leu
           100          105          110
Gln Leu His Glu Arg Leu Ala Arg Arg
           115          120

```

<210> 1977  
 <211> 551  
 <212> DNA  
 <213> Homo sapiens

<400> 1977

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ccgcgggcag gtggcatgtg ggctgagccc cgaagaaagt caaaagataa ggaagaggac
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aggtttctag gaagaagttg gctgagcagg agttgggcag gttaagagct gggtagggg
120
agagaggaga caggcagcca ggctgttaca caggaggagg cacaggaggt gcacgggagg
180
agccaagcgg gagggcaggc aatggccagg ttggaagatc tgcacctccc tggttactgg
240
aggaatgaaa ctggttggaac tgactgcagg gagaggctcc agttgaaaca tgagagaagt
300
actggatgaa aaaggtgcca caactgagac cagaaggcag attcctgaac tggtaggggtg
360
ccaaggatgc atatcaaaga ctgctggaac atgtgggtat caagattgaa gacagtgaag
420
gttaaaatgg cctgatccaa agctggaggg ggggtggagt gactggtgac tgctcttccc
480
acggacaggc attcaggcaa gctttcaaac tgagctctaa attctgctct gggttctaag
540
cagactcatg a
551

```

<210> 1978  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 1978

Met His Pro Trp His Pro Thr Ser Ser Gly Ile Cys Leu Leu Val Ser  
 1 5 10 15  
 Val Val Ala Pro Phe Ser Ser Ser Thr Ser Leu Met Phe Gln Leu Glu  
 20 25 30  
 Pro Leu Pro Ala Val Ser Pro Thr Ser Phe Ile Pro Pro Val Thr Arg  
 35 40 45  
 Glu Val Gln Ile Phe Gln Pro Gly His Cys Leu Pro Ser Arg Leu Ala  
 50 55 60  
 Pro Pro Val His Leu Leu Cys Ser Ser Leu Cys Asn Ser Leu Ala Ala  
 65 70 75 80  
 Cys Leu Leu Ser Pro Leu Thr Gln Leu Leu Thr Cys Pro Thr Pro Ala  
 85 90 95  
 Gln Pro Thr Ser Ser  
 100

&lt;210&gt; 1979

&lt;211&gt; 5530

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1979

ncttgactca atcctgcaag caagtgtgtg tgtgtcccca tccccgccc cgtaaacttc  
 60  
 atagcaaata acaaataccc ataaagtccc agtcgcgag cccctcccc cgggcagcgc  
 120  
 actatgctgc tcgggtgggc gtccctgctg ctgtgcgctg tccgctgccc cctggccgcg  
 180  
 gtcggccccg ccgcgacacc tgcccaggat aaagccgggc agcctccgac tgctgcagca  
 240  
 gccgcccagc cccgccggcg gcagggggag gaggtgcagg agcgagccga gcctccccgc  
 300  
 caccgcacc cctggcgca gcggcgagg agcaaggggc tggcgagaa catcgaccaa  
 360  
 ctctactccg gcggcgga ggtgggctac ctgctctacg cggcgggcg gaggttcctc  
 420  
 ttggacctgg agcgagatgg ttcggtgggc attgctggct tcgtgcccgc aggaggcggg  
 480  
 acgagtgcgc cctggcgcca ccggagccac tgcttctatc ggggcacagt ggacgctagt  
 540  
 ccccgctctc tggctgtctt tgacctctgt gggggtctcg acggcttctt cgcggtcaag  
 600  
 cagcgcgct acaccctaaa gccactgctg cgcggaccct gggcgaggga agaaaagggg  
 660  
 cgcgtgtacg gggatgggtc cgcacggatc ctgcacgtct acaccgcag ggcttcagct  
 720  
 tcgaggccct gccgccgc gccagctgcg aaacccccgc gtccacaccg gagggccacg  
 780  
 agcatgctcc ggcgcacagc aaccggagcg gacgcgcagc acgcctcgca gctcttggac  
 840  
 cagtccgctc tctcgcccgc tgggggctca ggaccgcaga cgtgggtggcg gcggcggcgc  
 900  
 cgctccatct cccgggcccg ccaggtggag ctgcttctgg tggctgacgc gtccatggcg  
 960

cggttgtatg gccggggcct gcagcattac ctgctgaccc tggcctccat cgccaatagg  
1020  
ctgtacagcc atgctagcat cgagaaccac atccgcctgg ccgtgggtgaa ggtgggtggtg  
1080  
ctaggcgaca aggacaagag cctggaagtg agcaagaacg ctgccaccac actcaagaac  
1140  
ttttgcaagt ggcagcacca acacaaccag ctgggagatg accatgagga gcactacgat  
1200  
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&lt;210&gt; 1980

&lt;211&gt; 929

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1980

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Gln Pro Pro Thr Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly			
35	40	45	
Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu			
50	55	60	
Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu			
65	70	75	80
Tyr Ser Gly Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg			
85	90	95	
Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly			
100	105	110	
Phe Val Pro Ala Gly Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser			
115	120	125	
His Cys Phe Tyr Arg Gly Thr Val Asp Ala Ser Pro Arg Ser Leu Ala			
130	135	140	
Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His			
145	150	155	160
Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu			
165	170	175	
Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val			
180	185	190	
Tyr Thr Arg Arg Ala Ser Ala Ser Arg Pro Cys Arg Arg Ala Pro Ala			
195	200	205	
Ala Lys Pro Pro Arg Pro His Arg Arg Pro Thr Ser Met Leu Arg Arg			
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Thr Ala Thr Arg Ala Asp Ala Gln His Ala Ser Gln Leu Leu Asp Gln			
225	230	235	240
Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp Arg			
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Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu Leu			
260	265	270	
Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln His			
275	280	285	
Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His Ala			
290	295	300	
Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val Leu			
305	310	315	320
Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr Thr			
325	330	335	
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340	345	350	
Asp His Glu Glu His Tyr Asp Ala Ala Ile Leu Phe Thr Arg Glu Asp			
355	360	365	
Leu Cys Gly His His Ser Cys Asp Thr Leu Gly Met Ala Asp Val Gly			
370	375	380	
Thr Ile Cys Ser Pro Glu Arg Ser Cys Ala Val Ile Glu Asp Asp Gly			
385	390	395	400
Leu His Ala Ala Phe Thr Val Ala His Glu Ile Gly His Leu Leu Gly			
405	410	415	
Leu Ser His Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser Thr			
420	425	430	
Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala Ser			

1497



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 Arg Thr Val Gln Cys Gln Asp Gly Asn Arg Lys Leu Ala Lys Gly Cys  
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 <211> 327  
 <212> DNA  
 <213> Homo sapiens

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    35                                      40                                      45  
 Ser Pro Pro Lys Ala Ala Gly Gly Gly Arg Cys Pro Gly Pro Cys Arg  
    50                                      55                                      60  
 Ile Met Ala Trp Pro Gly Gln Arg Ala Ser Ser Ser Gly Arg Gly Arg  
 65                                      70                                      75                                      80  
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 <211> 383  
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 383

&lt;210&gt; 1984

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1984

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			20					25					30		
Ala	Gln	Pro	Glu	Glu	Arg	Asn	Val	Pro	Lys	Arg	Asp	Ala	Ser	Val	Phe
		35				40					45				
Phe	Ile	Asp	Ile	Ile	Gly	Ser	Thr	Lys	Leu	Ser	Leu	Glu	Tyr	Asp	Ser
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Tyr	Thr	Val	Val	Asp	Leu	Leu	Asn	Arg	Phe	Tyr	Thr	Ile	Val	Val	Glu
65				70				75				80			
Glu	Val	Asn	Arg	Ala	Gly	Gly	Val	Val	Asn	Lys	Phe	Ala	Gly	Asp	Ala
			85			90					95				
Val	Leu	Ala	Ile	Phe	Asn	Val	Pro	His	Asp	His	Pro	Asp	Pro	Ala	Gly
		100				105					110				
Ala	Ser	Leu	Tyr	Cys	Ala	Arg	Val	Val	Met	Asn	Arg	Phe	Asp	His	
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&lt;210&gt; 1985

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1985

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<210> 1986

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1986

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		20					25						30		
Ile	Glu	Phe	Arg	Met	Gln	Asn	Ile	Ser	Ser	Val	Leu	Val	Gln	Met	Gly
		35				40						45			
Leu	Asp	Arg	Ile	Lys	Gly	Tyr	Lys	Ala	Cys	Glu	Pro	Met	Trp	Gly	Pro
	50				55					60					
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65				70					75					80	
Phe	Glu	Ser	Asp	Glu	Thr	Ala	Gln	Thr	Ala	Asp	Glu	Gln	Thr	Leu	Ile
			85					90					95		
Arg	Arg	Ala	Asn	Lys	Leu	Gln	Leu	Lys	Arg	Phe	Asp	Gln	Val	Pro	Asp
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<210> 1987

<211> 419

<212> DNA

<213> Homo sapiens

<400> 1987

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<210> 1988

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1988

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Ile Gly Phe Met Gly Val Arg Thr Met Ile Asn Arg Tyr Leu Leu Arg
      35           40           45
Thr Pro Asp Lys Gln Ala Leu Glu Val Pro Gln Tyr Phe Trp Met Arg
      50           55           60
Val Ala Met Gly Leu Ser Leu Thr Glu Asp Asp Pro Thr Ser Ser Ala
      65           70           75           80
Xaa Cys Leu Tyr Asp Ser Met Ser Asn Leu Arg His Leu Ala Ala Gly
      85           90           95
Ser Thr Leu Val Asn Ala Gly Thr His Xaa Ala Gln Leu Ser Asn Cys
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<210> 1989

<211> 10795

<212> DNA

<213> Homo sapiens

<400> 1989

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              1140              1145              1150
Ser Ser Pro Met Pro Ile Pro Asn Ser Ser Pro Leu Ala Ser Pro Val

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Pro Thr Thr Leu Pro Ala Pro Ala Ser Ala Pro Leu Thr Ile Pro Ile		
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Gly Leu Ala Thr Ala Pro Ser Leu Ser Ser Ser Gln Thr Pro Gly His		
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Pro Leu Leu Leu Ala Pro Thr Ser Ser His Val Pro Gly Leu Asn Ser		
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Thr Val Ala Pro Ala Cys Ser Pro Val Leu Val Pro Ala Ser Ala Leu		1280
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Leu Leu Ala Pro Ala Ser Ser Ala Ser Gln Ala Leu Ala Thr Pro Leu		
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Ala Pro Met Ala Ala Pro Gln Thr Ala Ile Leu Ala Pro Ser Pro Ala		
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Pro Pro Leu Ala Pro Leu Pro Val Leu Ala Pro Ser Pro Gly Ala Ala		
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Pro Val Leu Ala Ser Ser Gln Thr Pro Val Pro Val Met Ala Pro Ser		
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Ser Thr Pro Gly Thr Ser Leu Ala Ser Ala Ser Pro Val Pro Ala Pro		
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Thr Pro Val Leu Ala Pro Ser Ser Thr Gln Thr Met Leu Pro Ala Pro		
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Val Pro Ser Pro Leu Pro Ser Pro Ala Ser Thr Gln Thr Leu Ala Leu		
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Leu Ser Leu Gly Thr Gly Asn Pro Gln Gly Pro Phe Pro Thr Gln Thr		
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Leu Ser Leu Thr Pro Ala Ser Ser Leu Val Pro Thr Pro Ala Gln Thr		
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Pro Thr Leu Gly Pro Ala Ala Ala Gln Thr Leu Ala Leu Ala Pro Ala		
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Ser Thr Gln Ser Pro Ala Ser Gln Ala Ser Ser Leu Val Val Ser Ala		
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 Tyr Arg Leu Ile Ser Glu Arg Thr Val Glu Glu Asn Ile Leu Lys Lys  
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 Ala Asn Gln Lys Arg Met Leu Gly Asp Met Ala Ile Glu Gly Gly Asn  
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Ala	Gln	Thr	Cys	Leu	Val	Thr	Pro	Ser	Ser	Pro	Leu	Leu	Leu	Gly	Pro
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<212> PRT

<213> Homo sapiens

<400> 1992

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Leu	Leu	Gln	Gly	Gly	Asp	Glu	Lys	Lys	Val	Asn	Leu	Val	Leu	Gly	Asp
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Gly	Arg	Ser	Leu	Gly	Leu	Thr	Ile	Arg	Gly	Gly	Ala	Glu	Tyr	Gly	Leu
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Arg	His	Leu	Leu	Asn	Glu	Gln	Glu	His	Thr	Thr	Met	Ala	Tyr	Tyr	Leu

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Pro Gly Ala Gly Asp Thr Tyr Ser Met Val Ser Tyr Ser Asp Thr Gly		
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Ser Ser Thr Gly Ser His Gly Thr Ser Thr Thr Val Ser Ser Ala Arg		
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Gly Leu Ser Ser Phe Lys Pro Leu Pro Arg Pro Pro Pro Leu Ala Gln		
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Gly Asn Asp Leu Pro Leu Gly Gln Pro Arg Lys Leu Gly Arg Glu Asp		
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Thr Ser Ser Ala Gln Asp Leu Pro Ser Ser Pro Ile Tyr Ala Ser Val		
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Leu Leu Pro Pro Ser Pro Ser Gly His Pro Asp Gln Thr Gly Thr Asn		
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Gln His Phe Val Met Val Glu Val His Arg Pro Asp Ser Glu Pro Asp		
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Val Asn Glu Val Arg Ala Leu Pro Gln Thr Arg Thr Ala Ser Thr Leu		
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Ser Gln Leu Ser Asp Ser Gly Gln Thr Leu Ser Glu Asp Ser Gly Val		
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Asp Ala Gly Glu Ala Glu Ala Ser Ala Pro Gly Arg Gly Arg Gln Ser		
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Val Ser Thr Lys Ser Arg Ser Ser Lys Glu Leu Pro Arg Asn Glu Arg		
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625	630	635
Thr Leu Val Arg Val Lys Lys Ser Ala Ala Thr Leu Gly Ile Ala Ile		
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Glu Gly Gly Ala Asn Thr Arg Gln Pro Leu Pro Arg Ile Val Thr Ile		
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Gln Arg Gly Gly Ser Ala His Asn Cys Gly Gln Leu Lys Val Gly His		
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Val Ile Leu Glu Val Asn Gly Leu Thr Leu Arg Gly Lys Glu His Arg		

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Glu Ala Ala Arg Ile Ile Ala Glu Ala Phe Lys Thr Lys Asp Arg Asp				
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 ctgcgaccc cagcatgacc ctccgtgcct cagccgctga ccactccacc tggcggttgc  
 840  
 cggtagttgc tttcgtgtgc attgcaacca tcattctcga cgtcactggc ggtgccgtca  
 900  
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 957

<210> 1994  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 1994  
 Xaa Lys Thr Tyr Gly Met Thr Arg Ala Leu Asp His Ile Asp Ile Ala  
 1 5 10 15  
 Ile Pro Ala Gly Gln Ser Val Ala Val Met Gly Pro Ser Gly Ser Gly

```

      20      25      30
Lys Thr Thr Leu Leu His Cys Leu Ser Gly Ile Leu Ser Pro Asp Ser
      35      40      45
Gly Ser Ile Glu Leu Ala Leu Pro Asp Arg Thr Val Asn Val Glu Asn
      50      55      60
Leu Ser Asn Glu Gly Arg Ala Lys Leu Arg Arg Gln Ser Leu Gly Phe
      65      70      75      80
Val Phe Gln Gln Gly Met Leu Val Pro Glu Leu Thr Ala Val Glu Asn
      85      90      95
Thr Ala Leu Pro Leu Met Leu Asn Gly Val Ser Gln Thr Asp Ala Val
      100      105      110
Arg Tyr Ala Thr Gln Trp Leu Glu Ser Met Gly Leu Gly Gly Met Glu
      115      120      125
Asp Arg Arg Ile Gly Gln Leu Ser Gly Gly Gln Ala Gln Arg Val Thr
      130      135      140
Ile Ala Arg Ser Gln Val Ile Asp Pro Ser Ile Val Phe Ala Asp Glu
      145      150      155      160
Pro Thr Gly Ala Leu Asp Ser Ala Thr Ala Val Glu Val Met Ala Ile
      165      170      175
Leu Leu Ser Ala Thr Thr Gly Arg Gly Arg Thr Leu Val Val Val Thr
      180      185      190
His Asp Glu Asp Val Ala Arg Arg Cys Gln Arg Ile Leu His Leu His
      195      200      205
Asp Gly Arg Ile Val Ser Asp His Val Arg His Ser Asp Gly Arg Trp
      210      215      220

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&lt;210&gt; 1995

&lt;211&gt; 285

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1995

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catcaccacc attatcaaca ccatcatcac caccattatc acctttatca ccaccatcat
60
caccatcacc accatcatca ctaccaccat cacgcccac atcatgtgat gactctcaat
120
actgtcctca tcatgtgtga cttggactgt ggaccagccc ctggggtct gctctgctga
180
cctatattct ttgtctcttg ttctgagaa gctgggagtt gagaccagtt aagggtgtgt
240
acagacactt gtgaccccaa attccatgag acagaggacc tcccn
285

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&lt;210&gt; 1996

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1996

```

His His His His Tyr Gln His His His His His Tyr His Leu Tyr
1      5      10      15
His His His His His His His His His Tyr His His His Ala
20      25      30
His His His Val Met Thr Leu Asn Thr Val Leu Ile Met Cys Asp Leu

```

35                      40                      45  
 Asp Cys Gly Pro Ala Pro Arg Ala Leu Leu Cys  
 50                      55

<210> 1997  
 <211> 313  
 <212> DNA  
 <213> Homo sapiens

<400> 1997  
 ccgctgggtgg tgggtgctgct gattggcatg gccatctata ccttccgcaa gaaagacctg  
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 ggcaagctgc acaagccggg cagcatcggc cggcgcgaga tgctgggtggg gctggccatc  
 120  
 ggtggcggca tcggttttta cgacggcctg ttcggggccgg gtaccggcag tttcctgatg  
 180  
 ttcctgttcg tgcgggtttt gcggtttgat ttcttgcatt cttctgccgc ggccaagggt  
 240  
 gtcaacctgg ccaccaatgt ggcggcactg tgctttttca ttcccagcgg caatgtgctg  
 300  
 tatggctacg cgt  
 313

<210> 1998  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 1998  
 Pro Leu Val Val Val Leu Leu Ile Gly Met Ala Ile Tyr Thr Phe Arg  
 1                      5                      10                      15  
 Lys Lys Asp Leu Gly Lys Leu His Lys Pro Val Ser Ile Gly Arg Arg  
 20                      25                      30  
 Glu Met Leu Val Gly Leu Ala Ile Gly Gly Gly Ile Gly Phe Tyr Asp  
 35                      40                      45  
 Gly Leu Phe Gly Pro Gly Thr Gly Ser Phe Leu Met Phe Leu Phe Val  
 50                      55                      60  
 Arg Phe Leu Arg Phe Asp Phe Leu His Ala Ser Ala Ala Ala Lys Val  
 65                      70                      75                      80  
 Val Asn Leu Ala Thr Asn Val Ala Ala Leu Cys Phe Phe Ile Pro Ser  
 85                      90                      95  
 Gly Asn Val Leu Tyr Gly Tyr Ala  
 100

<210> 1999  
 <211> 399  
 <212> DNA  
 <213> Homo sapiens

<400> 1999  
 ccggggcgca agttggaatg gcaaaacatt ttcattcccg gcgagcaagg tagcttgagt  
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 tccactgcgc agagggcaga tgtgaagtac tccgggtactg ttcattttac cgggtgttggc  
 120



ggaagaatgg atcttactct cgctgaccct gagattgtcg ttaacaatgg cgatgatcat  
 180  
 gtgattatgt ctgtgaagtc caagactatg gtcgggcagt tgggtgacta tggccgtata  
 240  
 actttcgttg atatgaccgg ctctattacg caggggtcaaa acgatgcagc tcaggttggtg  
 300  
 gggaccaatg tcaagctgaa tagccaagcc gtcgatgcat tcgctggctt ctatcaagct  
 360  
 ggaaagccca tggatgacat cgattcgtcc ttaaagctt  
 399

<210> 2000

<211> 91

<212> PRT

<213> Homo sapiens

<400> 2000

Met	Asp	Leu	Thr	Leu	Ala	Asp	Pro	Glu	Ile	Val	Val	Asn	Asn	Gly	Asp
1				5				10				15			
Asp	His	Val	Ile	Met	Ser	Val	Lys	Ser	Lys	Thr	Met	Val	Gly	Gln	Leu
			20				25				30				
Val	Asp	Tyr	Gly	Arg	Ile	Thr	Phe	Val	Asp	Met	Thr	Gly	Ser	Ile	Thr
		35				40					45				
Gln	Gly	Gln	Asn	Asp	Ala	Ala	Gln	Val	Val	Gly	Thr	Asn	Val	Lys	Leu
	50				55					60					
Asn	Ser	Gln	Ala	Val	Asp	Ala	Phe	Ala	Gly	Phe	Tyr	Gln	Ala	Gly	Lys
65				70				75						80	
Pro	Met	Asp	Asp	Ile	Asp	Ser	Ser	Leu	Lys	Leu					
				85				90							

<210> 2001

<211> 1434

<212> DNA

<213> Homo sapiens

<400> 2001

nngaattgaag gacgtcataa tttgctgac agcagtgacg ctgactggag gagggacaaa  
 60  
 tttggcagga cccactgca ctatgcagct gctaacggta gctaccagtg tgcagtaaca  
 120  
 ttggtgactg ctggggcagg tgtcaacgag gccgactgta aaggctgctc tcccctccac  
 180  
 tacgctgccg cttctgacac ttacaggnag agcggaaacc catacacctt ccagccatga  
 240  
 tgccgaagag ganncgagcc actgaaggag tcccgcagga aggaggcctt cttctgtctg  
 300  
 gagttcttac tggataacgg tgcagacccc tccctgcggg acaggcaggg ctacacagct  
 360  
 gtgcactatg cagccgccta tggcaacaga cagaacctcg aactgctctt agaaatgtcc  
 420  
 tttaactgcc tggaggatgt ggagagcacc attccagtca gccctttgca cttagctgcc  
 480  
 tacaacggtc actgtgaagc cttgaagacg ctggcggaga cgctggtgaa tctggacgta  
 540

agggaccaca agggccggac cgcactcttc ctggccacgg agcgcggtc tactgagtgt  
 600  
 gtggaggtgc ttacagccca cggcgctctt gccctcatca aggagcgcaa gcgcaagtgg  
 660  
 acacccctgc acgccgctgc tgcctctggc cacactgact ccctgcactt gctgatcgac  
 720  
 agtggggaac gagctgacat cacagatgtc atggatgcct atggacagac cccactgatg  
 780  
 ctggccatca tgaatggcca tgtggactgt gtacatctgc tgctagagaa aggatccaca  
 840  
 gctgatgctg ctgacctccg gggccgcact gccctccacc gcggggcagt gactggctgt  
 900  
 gaggactgcc tggtgcctt gctggaccac gacgcatttg tgctgtgccg agactttaag  
 960  
 ggccgcacgc ccattcacct ggctcagcc tgtggccaca ctgcagtact gcggaccctg  
 1020  
 ctgcaggctg ccctttccac agatccctg gatgccgggg tggattacag cggatactcg  
 1080  
 cccatgcact gggcctccta cactggacat gaagattgtc tggagttggt acttgaacac  
 1140  
 agcccgtttt cgtacctgga aggaaacccc ttcactcctt tgcaactgtc agtgattaat  
 1200  
 aaccaagaca gcaccacaga gatgctactg ggagctctgg gtgccaagat tgtgaacagc  
 1260  
 cgagatgcca aaggacggac ccccttcac gccgctgcct tcgcggaaca tgtctctggg  
 1320  
 ctccggatgc tgctgcagca tcaagctgag gtgaacgcca ctgaccacac tggccgcact  
 1380  
 gcgctcatga cggcggtga gaacgggcag accgctgctg tgggaatttct gctg  
 1434

&lt;210&gt; 2002

&lt;211&gt; 79

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2002

Xaa	Asn	Glu	Gly	Arg	His	Asn	Leu	Leu	Ile	Ser	Ser	Ala	Ala	Asp	Trp
1				5					10					15	
Arg	Arg	Asp	Lys	Phe	Gly	Arg	Thr	Pro	Leu	His	Tyr	Ala	Ala	Ala	Asn
			20				25					30			
Gly	Ser	Tyr	Gln	Cys	Ala	Val	Thr	Leu	Val	Thr	Ala	Gly	Ala	Gly	Val
		35				40					45				
Asn	Glu	Ala	Asp	Cys	Lys	Gly	Cys	Ser	Pro	Leu	His	Tyr	Ala	Ala	Ala
	50				55				60						
Ser	Asp	Thr	Tyr	Arg	Xaa	Ser	Gly	Thr	Pro	Tyr	Thr	Phe	Gln	Pro	
65					70				75						

&lt;210&gt; 2003

&lt;211&gt; 688

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2003

ntcattgacta cggagacact gaagaaaatt cagattgata ggcagttttt cagcagatgtg  
 60  
 attgcagata ccattaagga gttgcaagat tcggccactt acaacagtct cctgcaagct  
 120  
 ttgagcaaag agaggggaaaa caaatgcat ttctatgaca tcatttccag ggaggaaaaa  
 180  
 ggaagaaaac agataatatc acttcaaaaa cagctaatta atttcaaaaa ggaatggcaa  
 240  
 tttgaagtcc agagtcagaa tgagtatatt gctaacctca aggaccaact gcaagagatg  
 300  
 aaggcaaaat ccaacttggg gaatcgctac atgaaaacca ataccgagct gcagattggc  
 360  
 cagacccaga aaaagtgtaa cagaacagag gaactcttgg tggaagagat tgagaaactc  
 420  
 aggatgaaaa ccgaagaaga ggcccgact catacagaga ttgaaatgtt ccttagaaaag  
 480  
 gagcagcagg tgggtcccca cagcttttct atgctttgac tttttttttg tactctgctt  
 540  
 atactgagga aacaaaaaga atattttgaa ggaaaaccaa ccatcattct ttcagcctaa  
 600  
 tgaactttag ctcatgtttt ctttcagggt tatgcatctg aatagatatc ttatatagct  
 660  
 gtaatttgag agagtgcagg taaaattg  
 688

&lt;210&gt; 2004

&lt;211&gt; 172

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2004

Xaa	Met	Thr	Thr	Glu	Thr	Leu	Lys	Lys	Ile	Gln	Ile	Asp	Arg	Gln	Phe
1				5					10					15	
Phe	Ser	Asp	Val	Ile	Ala	Asp	Thr	Ile	Lys	Glu	Leu	Gln	Asp	Ser	Ala
			20					25					30		
Thr	Tyr	Asn	Ser	Leu	Leu	Gln	Ala	Leu	Ser	Lys	Glu	Arg	Glu	Asn	Lys
		35				40						45			
Met	His	Phe	Tyr	Asp	Ile	Ile	Ser	Arg	Glu	Glu	Lys	Gly	Arg	Lys	Gln
	50					55					60				
Ile	Ile	Ser	Leu	Gln	Lys	Gln	Leu	Ile	Asn	Phe	Lys	Lys	Glu	Trp	Gln
65				70					75					80	
Phe	Glu	Val	Gln	Ser	Gln	Asn	Glu	Tyr	Ile	Ala	Asn	Leu	Lys	Asp	Gln
			85					90						95	
Leu	Gln	Glu	Met	Lys	Ala	Lys	Ser	Asn	Leu	Glu	Asn	Arg	Tyr	Met	Lys
			100					105					110		
Thr	Asn	Thr	Glu	Leu	Gln	Ile	Ala	Gln	Thr	Gln	Lys	Lys	Cys	Asn	Arg
		115				120						125			
Thr	Glu	Glu	Leu	Leu	Val	Glu	Glu	Ile	Glu	Lys	Leu	Arg	Met	Lys	Thr
	130					135					140				
Glu	Glu	Glu	Ala	Arg	Thr	His	Thr	Glu	Ile	Glu	Met	Phe	Leu	Arg	Lys
145				150					155					160	
Glu	Gln	Gln	Val	Gly	Pro	His	Ser	Phe	Ser	Met	Leu				
			165						170						

&lt;210&gt; 2005

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2005

gctagcacca agccaagggt atgtttcctt gcttgcattgt ggggtttctg gccagtcagc  
 60  
 caagtgaact gattgacccc cagccctgtg gggaatttca ggggggtatt gtcttgggtca  
 120  
 tcggagtcag ggggtggcctt tnagccaagg ctgcattaac ttttgggaaa agaaatggga  
 180  
 agcccgccgt gtcacagggt ctctgaccg gctgggtagg gtttggcctt atcttacagc  
 240  
 cagtgtgtg tttgtctaga tggacgcaca tggaaaccag gctaggatca tcttcccaat  
 300  
 gtctactccc tgctttggtc tgtcctgaaa acaattgcaa agacattgtg gctg  
 354

&lt;210&gt; 2006

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2006

Met	Phe	Pro	Cys	Leu	His	Val	Gly	Phe	Leu	Ala	Ser	Gln	Pro	Ser	Glu
1				5				10					15		
Leu	Ile	Asp	Pro	Gln	Pro	Cys	Gly	Glu	Phe	Gln	Gly	Gly	Ile	Val	Leu
		20					25					30			
Val	Ile	Gly	Val	Arg	Gly	Gly	Leu	Xaa	Ala	Lys	Ala	Ala	Leu	Thr	Phe
		35				40					45				
Gly	Lys	Arg	Asn	Gly	Lys	Pro	Ala	Val	Ser	Gln	Gly	Leu	Leu	Thr	Gly
	50				55				60						
Trp	Val	Gly	Phe	Gly	Leu	Ile	Leu	Gln	Pro	Val	Leu	Cys	Leu	Leu	Arg
65				70				75				80			
Trp	Thr	His	Met	Glu	Thr	Arg	Leu	Gly	Ser	Ser	Ser	Gln	Cys	Leu	Leu
		85				90					95				
Pro	Ala	Leu	Val	Cys	Pro	Glu	Asn	Asn	Cys	Lys	Asp	Ile	Val	Ala	
		100				105					110				

&lt;210&gt; 2007

&lt;211&gt; 335

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2007

nnacgcgtgc catgtgcatg tgtatatgca tgtatgtgcg tatgtgtgtg catgtgtgtg  
 60  
 tgtatatgca tgtgtgtatg tgcattgtacg tgttngtgca tatgcgtgtg catgcatgcg  
 120  
 tgtgcgtatg tgtgcatann catgtgcaca catgtacaca cgtgtacatg ttcattgcatg  
 180  
 tgcacgtgca tatgtgtaca cgtgtatgcg tgtacatgta tgagcatatg tacacgtgtg  
 240

gatgtgtgtg tatgcatgtg tgtgtgcaca gatatgcctt ttcctttcat acaggctggg  
 300  
 ttgagtattg ctggtaggca gggacaactt tccgt  
 335

<210> 2008  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 2008  
 Xaa Arg Val Pro Cys Ala Cys Val Tyr Ala Cys Met Cys Val Cys Val  
 1 5 10 15  
 Cys Met Cys Val Cys Ile Cys Met Cys Val Cys Ala Cys Thr Cys Xaa  
 20 25 30  
 Cys Ile Cys Val Cys Met His Ala Cys Ala Tyr Val Cys Ile Xaa Met  
 35 40 45  
 Cys Thr His Val His Thr Cys Thr Cys Ser Cys Met Cys Thr Cys Ile  
 50 55 60  
 Cys Val His Val Tyr Ala Cys Thr Cys Met Ser Ile Cys Thr Arg Val  
 65 70 75 80  
 Asp Val Cys Val Cys Met Cys Val Cys Thr Asp Met Pro Phe Pro Phe  
 85 90 95  
 Ile Gln Ala Gly Leu Ser Ile Ala Gly Arg Gln Gly Gln Leu Ser  
 100 105 110

<210> 2009  
 <211> 288  
 <212> DNA  
 <213> Homo sapiens

<400> 2009  
 gacatcaccc cgctgtggc caaccccaac ggtttctccg cagcgatcga ggaactggg  
 60  
 ctgcgttccc cacgcgacat cgacgtggc gtcggcatgg aggctcgcg cttcctcttc  
 120  
 gcagctccgg tcgccctggc catcggggca ggattcgtgc cggtcgcgcaa gccggggaag  
 180  
 ctccccggcc aggtgtattc cgagaccttt gccatggagt acggggagga gaccctcacc  
 240  
 gtccaccagt acgccatcaa gccgggggtcg cgcgtcatca tcgtcgac  
 288

<210> 2010  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 2010  
 Asp Ile Thr Pro Leu Leu Ala Asn Pro Asn Gly Phe Ser Ala Ala Ile  
 1 5 10 15  
 Glu Glu Leu Val Leu Arg Ser Pro Arg Asp Ile Asp Val Val Val Gly  
 20 25 30  
 Met Glu Ala Arg Gly Phe Leu Phe Ala Ala Pro Val Ala Leu Ala Ile

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<210> 2011
<211> 384
<212> DNA
<213> Homo sapiens
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<210> 2012
<211> 123
<212> PRT
<213> Homo sapiens
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<210> 2013  
<211> 309

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2013

gcgtatcccc acggctacgg catgaccgag cttatcgggc cggacctgtc caccgtcgaa  
60  
gccttgctcg cccaggtcca cagcacacaa accccggtgt acctggccaa tatcaatgcc  
120  
gataaccaga cggttatcgc gggcagcgac ggggcaatga aagcagtcgc caatctggtc  
180  
cgcggaacg gcgtcgccaa acgcttgccc gtcagcgtgc cgccccattg tgcgctgctg  
240  
gaaaaacctg ccgaaacact ggcccaagcc ttcgctgaag tgacgctgaa aacgccgnen  
300  
nnnccnncn  
309

&lt;210&gt; 2014

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2014

Ala	Tyr	Pro	His	Gly	Tyr	Gly	Met	Thr	Ala	Leu	Ile	Gly	Pro	Asp	Leu
1				5					10				15		
Ser	Thr	Val	Glu	Ala	Leu	Leu	Ala	Gln	Val	His	Ser	Thr	Gln	Thr	Pro
		20						25				30			
Val	Tyr	Leu	Ala	Asn	Ile	Asn	Ala	Asp	Asn	Gln	Thr	Val	Ile	Ala	Gly
		35					40				45				
Ser	Asp	Gly	Ala	Met	Lys	Ala	Val	Ala	Asn	Leu	Val	Arg	Gly	Asn	Gly
	50					55				60					
Val	Ala	Lys	Arg	Leu	Ala	Val	Ser	Val	Pro	Ser	His	Cys	Ala	Leu	Leu
65				70					75				80		
Glu	Lys	Pro	Ala	Glu	Thr	Leu	Ala	Gln	Ala	Phe	Ala	Glu	Val	Thr	Leu
				85				90					95		
Lys	Thr	Pro	Xaa	Xaa	Pro	Xaa									
				100											

&lt;210&gt; 2015

&lt;211&gt; 329

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2015

acgcgtgcca tgctcggtat ccgccgccac caccctgtct ttgggaccgg cgagttcacc  
60  
gatctaggcg ggccggacat ggcagtgatg tccttctctac gtcacaacga gcacgaaacg  
120  
gtcctgtgcc tggctaattct ctccgatact gagcggacgg ttgcccttca ccttccacaa  
180  
ttcgcgggcg tggcgggctc ttctctcatc catggtcagg acgcgcaacc agtaaaagct  
240  
gacggaacac tgtccgtacc gttgtggcca tatggctatc gatggctgca gatgtccggt  
300

gaggagaggt catgaccgct tgggaagac  
329

<210> 2016  
<211> 104  
<212> PRT  
<213> Homo sapiens

<400> 2016  
Thr Arg Ala Met Leu Gly Ile Arg Arg His His Pro Val Phe Gly Thr  
1 5 10 15  
Gly Glu Phe Thr Asp Leu Gly Gly Pro Asp Met Ala Val Met Ser Phe  
20 25 30  
Leu Arg His Asn Glu His Glu Thr Val Leu Cys Leu Ala Asn Leu Ser  
35 40 45  
Asp Thr Glu Arg Thr Val Ala Leu His Leu Pro Gln Phe Ala Gly Val  
50 55 60  
Ala Gly Ser Ser Leu Ile His Gly Gln Asp Ala Gln Pro Val Lys Ala  
65 70 75 80  
Asp Gly Thr Leu Ser Val Pro Leu Trp Pro Tyr Gly Tyr Arg Trp Leu  
85 90 95  
Gln Met Ser Gly Glu Glu Arg Ser  
100

<210> 2017  
<211> 457  
<212> DNA  
<213> Homo sapiens

<400> 2017  
accaaggtca gattcatggc ctcttttcct ccagcggcca gcaggaaacg cggggagccc  
60  
ttgatcatct ccgacatcaa gaaaggcagc gtggcacaca ggacgggcac cctggagcca  
120  
ggcgacaagc tactggccat tgacaatatc cgctggaca actgccccat ggaggacgcc  
180  
gtgcaaatcc tgccggcagt cgaggacctg gtgaagctga agatccggaa ggacgaggac  
240  
aactctgatg agctggagac cacaggtgcc gtcagttaca cagtggagct gaagcgctac  
300  
gggggtcccc tgggcatcac catttcgggc acggaggaac cttttgacct cattttcatc  
360  
tcaggcctcc ccaaactggg cctggctgag aggactggtg ccatccagtg ggggaaccgc  
420  
ttcggaccat aacaacgtta ttctcaggga cggacca  
457

<210> 2018  
<211> 143  
<212> PRT  
<213> Homo sapiens

<400> 2018  
Thr Lys Val Arg Phe Met Ala Ser Phe Pro Pro Ala Ala Ser Arg Lys



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      1           5           10           15
Arg Gly Glu Pro Leu Ile Ile Ser Asp Ile Lys Lys Gly Ser Val Ala
      20           25           30
His Arg Thr Gly Thr Leu Glu Pro Gly Asp Lys Leu Leu Ala Ile Asp
      35           40           45
Asn Ile Arg Leu Asp Asn Cys Pro Met Glu Asp Ala Val Gln Ile Leu
      50           55           60
Arg Gln Cys Glu Asp Leu Val Lys Leu Lys Ile Arg Lys Asp Glu Asp
      65           70           75           80
Asn Ser Asp Glu Leu Glu Thr Thr Gly Ala Val Ser Tyr Thr Val Glu
      85           90           95
Leu Lys Arg Tyr Gly Gly Pro Leu Gly Ile Thr Ile Ser Gly Thr Glu
      100          105          110
Glu Pro Phe Asp Pro Ile Phe Ile Ser Gly Leu Pro Lys Arg Gly Leu
      115          120          125
Ala Glu Arg Thr Gly Ala Ile Gln Trp Gly Asn Arg Phe Gly Pro
      130          135          140

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&lt;210&gt; 2019

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2019

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&lt;210&gt; 2020

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2020

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<210> 2022

<211> 135  
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 <213> Homo sapiens

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 Gly Trp Ser Leu Pro Leu His Tyr Phe Gln Val Val Thr Trp Ala Val  
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 Phe Val Gly Leu Ser Ser Ala Thr Phe Gly Ile Phe Ile Pro Phe Leu  
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 Pro His Ala Trp Lys Tyr Ile Ala Tyr Val Val Ser Phe Ser Ser Trp  
 65 70 75 80  
 His Gly Leu Ser Gly Arg Gly Ser Trp Arg Thr Leu Arg Trp Thr Trp  
 85 90 95  
 Leu Trp Gly Leu Gly His Gly Cys Pro Val Ala Pro Val Thr Cys Pro  
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 <211> 462  
 <212> DNA  
 <213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

<400> 2024  
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      20             25             30
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      35             40             45
His Ile Pro Val Asp Lys Ile Gly Glu Val Ile Gly Pro Lys Gly Lys
      50             55             60
Met Ile Asn Gln Ile Gln Asp Asp Thr Gly Ala Asn Ile Ser Ile Glu
      65             70             75             80
Asp Asp Gly Thr Ile Phe Ile Gly Ala Asp Asn Gly Asp Ser Ala Glu
      85             90             95
Ser Ala Arg Ser Met Ile Asn Ala Ile Ala Asn Pro Gln Met Pro Glu
      100            105            110
Val Gly Glu Arg Tyr Leu Gly Thr Val Val Lys Thr Thr Ser Phe Gly
      115            120            125
Ala Phe Val Ser Leu Leu Pro Gly Lys Asp Gly Leu Leu His Ile Ser
      130            135            140
Lys Met Arg Asp Leu Asn Asp Gly Lys Arg
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&lt;210&gt; 2025

&lt;211&gt; 872

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2025

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<211> 157

<212> PRT

<213> Homo sapiens

<400> 2026

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Asp	Ile	Lys	Pro	Glu	Asn	Phe	Ala	Ile	Arg	Ser	Asp	Phe	Thr	Val	Val
			20					25					30		
Ala	Ile	Asp	Val	Asp	Met	Ala	Phe	Phe	Glu	Pro	Lys	Met	Arg	Glu	Ile
			35				40					45			
Leu	Glu	Gln	Asn	Cys	Thr	Gly	Asp	Glu	Asp	Cys	Asn	Phe	Phe	Asp	Cys
	50					55				60					
Phe	Ser	Arg	Cys	Asp	Leu	Arg	Val	Asn	Lys	Cys	Gly	Ala	Gln	Arg	Val
65				70					75					80	
Asn	Asn	Asn	Leu	Gln	Val	Ile	Cys	Asp	Lys	Ile	Phe	Arg	His	Trp	Phe
			85					90						95	
Ser	Ala	Pro	Leu	Lys	Ser	Ser	Ala	Val	Ser	Phe	Gln	Leu	Gln	Leu	Gln
			100					105					110		
Leu	Gln	Glu	Ala	Val	Gln	Glu	Cys	Ala	Asp	Pro	Gly	Val	Pro	Ser	Gly
		115					120					125			
Asn	Thr	Arg	Arg	Ala	Ala	Ser	Ser	Val	Phe	Trp	Lys	Leu	Arg	Gln	Leu
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<210> 2027

<211> 721

<212> DNA

<213> Homo sapiens

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<210> 2028

<211> 114

<212> PRT

<213> Homo sapiens

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			20					25					30		
Lys	Leu	Phe	Phe	Cys	Gln	Leu	Cys	Ile	Thr	Ser	Asp	Asp	Ile	Gly	Tyr
		35					40					45			
Ser	Cys	Arg	Leu	Lys	Phe	Lys	Ile	Gln	Val	Ala	Pro	Tyr	Ser	Ile	Phe
	50					55					60				
Leu	His	Lys	Glu	Arg	Leu	His	Val	Leu	Ile	Leu	Cys	Gly	Leu	Cys	Tyr
65					70				75					80	
Leu	Arg	Ser	Asn	Gln	Glu	Ser	Leu	Ile	Leu	Ser	Gln	Lys	Cys	Leu	Leu
			85						90					95	
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<210> 2029

<211> 8028

<212> DNA

<213> Homo sapiens

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 aatattaaat caagagtga catgtacaca aagtgaatt ggaagtgggc taaaaattta  
 7140  
 gccccagct tcccagcagg caactcaaag aggtactga ggtaaatgt tccagctcag  
 7200  
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 7260  
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 7320  
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 7380  
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 7440  
 gtcctccatc ttcattggct gcaacttgat gagctacagc ctctttccta acttccttta  
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 7560  
 atacacaaat tagatgcaag taaaaaaaaat cagaatttct gtagtagaaa ctacgaaaaa  
 7620  
 taaaaaggaa agtttttact ttttgggtat ttttttacga ataagaaaaa gtgagcgta  
 7680  
 atcagttcaa aaggaggtac tgctgtgtaa tgggctttgt acgttccttc tcatgtcact  
 7740  
 tacgtcacta cttcgccatc aaattgaaca agcttttaat tagatcctga aaattcacta  
 7800  
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 7860  
 aaattctttt tatctgggtt aatttctttt aaacataaca atgttaatgc tgaattgtat  
 7920  
 attaaatccc atttctaaaa accacacaat tttttctcat gtaagttgag tggaatgtgg  
 7980  
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 8028

<210> 2030

<211> 794

<212> PRT

<213> Homo sapiens

<400> 2030

Met	Arg	Val	Arg	Ile	Gly	Leu	Thr	Leu	Leu	Leu	Cys	Ala	Val	Leu	Leu
1				5				10						15	
Ser	Leu	Ala	Ser	Ala	Ser	Ser	Asp	Glu	Glu	Gly	Ser	Gln	Asp	Glu	Ser
			20					25					30		
Leu	Asp	Ser	Lys	Thr	Thr	Leu	Thr	Ser	Asp	Glu	Ser	Val	Lys	Asp	His
		35				40						45			
Thr	Thr	Ala	Gly	Arg	Val	Val	Ala	Gly	Gln	Ile	Phe	Leu	Asp	Ser	Glu
	50					55					60				
Glu	Ser	Glu	Leu	Glu	Ser	Ser	Ile	Gln	Glu	Glu	Glu	Asp	Ser	Leu	Lys
65					70					75				80	
Ser	Gln	Glu	Gly	Glu	Ser	Val	Thr	Glu	Asp	Ile	Ser	Phe	Leu	Glu	Ser

1541

```

      515              520              525
His Ala Ser Gly Thr Gly Val Met Arg Ser Cys His Thr Ala Val Glu
 530              535              540
Leu Phe Lys Asn Val Cys Glu Arg Gly Arg Trp Ser Glu Arg Leu Met
545              550              555              560
Thr Ala Tyr Asn Ser Tyr Lys Asp Gly Asp Tyr Asn Ala Ala Val Ile
      565              570              575
Gln Tyr Leu Leu Leu Ala Glu Gln Gly Tyr Glu Val Ala Gln Ser Asn
      580              585              590
Ala Ala Phe Ile Leu Asp Gln Arg Glu Ala Ser Ile Val Gly Glu Asn
      595              600              605
Glu Thr Tyr Pro Arg Ala Leu Leu His Trp Asn Arg Ala Ala Ser Gln
      610              615              620
Gly Tyr Thr Val Ala Arg Ile Lys Leu Gly Asp Tyr His Phe Tyr Gly
625              630              635              640
Phe Gly Thr Asp Val Asp Tyr Glu Thr Ala Phe Ile His Tyr Arg Leu
      645              650              655
Ala Ser Glu Gln Gln His Ser Ala Gln Ala Met Phe Asn Leu Gly Tyr
      660              665              670
Met His Glu Lys Gly Leu Gly Ile Lys Gln Asp Ile His Leu Ala Lys
      675              680              685
Arg Phe Tyr Asp Met Ala Ala Glu Ala Ser Pro Asp Ala Gln Val Pro
      690              695              700
Val Phe Leu Ala Leu Cys Lys Leu Gly Val Val Tyr Phe Leu Gln Tyr
705              710              715              720
Ile Arg Glu Thr Asn Ile Arg Asp Met Phe Thr Gln Leu Asp Met Asp
      725              730              735
Gln Leu Leu Gly Pro Glu Trp Asp Leu Tyr Leu Met Thr Ile Ile Ala
      740              745              750
Leu Leu Leu Gly Thr Val Ile Ala Tyr Arg Gln Arg Gln His Gln Asp
      755              760              765
Met Pro Ala Pro Arg Pro Pro Gly Pro Arg Pro Ala Pro Pro Gln Gln
      770              775              780
Glu Gly Pro Pro Glu Gln Gln Pro Pro Gln
785              790

```

&lt;210&gt; 2031

&lt;211&gt; 662

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2031

```

atcatcgaaa gcagcgcccg ccagcaggat tcgatttctc gccaaactgac ccagcagttc
60
atcagccaat ggcaggcggc tcacccggcg gatcagatca ccgtgcgtga cgtggcgctg
120
aaccctgtgc cgcacctgga cagcatctg ctggcggtt ggatgaaacc tgccgaacag
180
cgcagcgga tcgaacaggc ttcctggac cgctccaatc aattgaccga cgaattgctc
240
gccgcccacg tgctggtgat ggctgcaccg atgtacaact tcgctatccc cagcaccctc
300
aaagcctggc tggaccacgt gttgcgtgcc ggtgtgacct tcaagtacac cgccaccggc
360

```

cccagggat tgctgcacgg caagcgcgcg attgtgctga ccgctcgcg cggcattcat  
 420  
 accggcgcca gctccgatca ccaggaaccg tacctgcgcc aggtcatggc ctttatcggg  
 480  
 attcatgacg tcacgttcat tcatgccgaa ggggtgaact tgagcgggta cttccaggaa  
 540  
 aaaggcctta accacgccaa ggcgttgctg gcgcaacttg tggcatgaac cgagtcaacg  
 600  
 gttaatcgtc acataatcgc cgggtgttta tatcgcttca cgcaaaccct tcaagtacgc  
 660  
 gt  
 662

<210> 2032

<211> 195

<212> PRT

<213> Homo sapiens

<400> 2032

Ile	Ile	Glu	Ser	Ser	Ala	Arg	Gln	Gln	Asp	Ser	Ile	Ser	Arg	Gln	Leu
1				5					10					15	
Thr	Gln	Gln	Phe	Ile	Ser	Gln	Trp	Gln	Ala	Ala	His	Pro	Ala	Asp	Gln
			20					25					30		
Ile	Thr	Val	Arg	Asp	Val	Ala	Leu	Asn	Pro	Val	Pro	His	Leu	Asp	Thr
		35					40					45			
His	Leu	Leu	Gly	Gly	Trp	Met	Lys	Pro	Ala	Glu	Gln	Arg	Ser	Ala	Ile
	50					55					60				
Glu	Gln	Ala	Ser	Leu	Asp	Arg	Ser	Asn	Gln	Leu	Thr	Asp	Glu	Leu	Leu
65				70						75				80	
Ala	Ala	Asp	Val	Leu	Val	Met	Ala	Ala	Pro	Met	Tyr	Asn	Phe	Ala	Ile
			85						90					95	
Pro	Ser	Thr	Leu	Lys	Ala	Trp	Leu	Asp	His	Val	Leu	Arg	Ala	Gly	Val
			100					105					110		
Thr	Phe	Lys	Tyr	Thr	Ala	Thr	Gly	Pro	Gln	Gly	Leu	Leu	His	Gly	Lys
		115					120					125			
Arg	Ala	Ile	Val	Leu	Thr	Ala	Arg	Gly	Gly	Ile	His	Thr	Gly	Ala	Ser
	130					135					140				
Ser	Asp	His	Gln	Glu	Pro	Tyr	Leu	Arg	Gln	Val	Met	Ala	Phe	Ile	Gly
145				150						155				160	
Ile	His	Asp	Val	Thr	Phe	Ile	His	Ala	Glu	Gly	Val	Asn	Leu	Ser	Gly
			165						170					175	
Asp	Phe	Gln	Glu	Lys	Gly	Leu	Asn	His	Ala	Lys	Ala	Leu	Leu	Ala	Gln
			180					185					190		
Leu	Val	Ala													
		195													

<210> 2033

<211> 380

<212> DNA

<213> Homo sapiens

<400> 2033

aaattttaaa acggtcatca ttttaacaggc gaagctgtaa aacgcagtct tgaagagggga  
 60

atgaaaaaaa gtgatttgtt aaaaggatca cttcctatca aatcaatcaa cgctcatgga  
 120  
 caaaaagtca caatcaatac taaagaacct tatccagaat taaagtctga actcgcaagc  
 180  
 ccatttgctg ctatatacga cacaaaagct aaaaacaaag taactgatca acctgttggt  
 240  
 acgggtcctt atcaaattga cagttataaa cgttcgcaaa aaatcgtatt aaaacaattc  
 300  
 aaagactact ggcaaggtag gccaaaatta aaaagaatta atgtcactta tcatgaagat  
 360  
 ggtaatantc gtgttgatca  
 380

<210> 2034

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2034

Met	Lys	Lys	Ser	Asp	Leu	Leu	Lys	Gly	Ser	Leu	Pro	Ile	Lys	Ser	Ile
1				5				10					15		
Asn	Ala	His	Gly	Gln	Lys	Val	Thr	Ile	Asn	Thr	Lys	Glu	Pro	Tyr	Pro
			20					25				30			
Glu	Leu	Lys	Ser	Glu	Leu	Ala	Ser	Pro	Phe	Ala	Ala	Ile	Tyr	Asp	Thr
		35					40					45			
Lys	Ala	Lys	Asn	Lys	Val	Thr	Asp	Gln	Pro	Val	Gly	Thr	Gly	Pro	Tyr
	50					55					60				
Gln	Ile	Asp	Ser	Tyr	Lys	Arg	Ser	Gln	Lys	Ile	Val	Leu	Lys	Gln	Phe
65					70					75				80	
Lys	Asp	Tyr	Trp	Gln	Gly	Thr	Pro	Lys	Leu	Lys	Arg	Ile	Asn	Val	Thr
			85						90					95	
Tyr	His	Glu	Asp	Gly	Asn	Xaa	Arg	Val	Asp						
			100					105							

<210> 2035

<211> 495

<212> DNA

<213> Homo sapiens

<400> 2035

ngaattcctt tactgcttgc aacacaggcc caagctactc gcagccatga tacttctctg  
 60  
 cttcacttct ttcattgatg tatgtatgta tgtatgtatg tatgtatgta tgtatgtatg  
 120  
 tatgctntaa tgttccctt tcatctcgca tgtctccact tctgctgcta ttgctgttac  
 180  
 ttgtgtgttg gtgcacctaa tgggtgtccca tatttctctg atgctgtgtt catttttctt  
 240  
 gattctttct actgtctggt cttcagtttg cataatccat attgttctct ctactagttc  
 300  
 actgggtgctt ttgctgcca gctctaattt actgttatcc cctttagtga aattttttct  
 360  
 tttttctct tctcattcca gttattatac agaactattc aacttcaaga tttgtggggg  
 420

tttgttttgt tttgttttga gaccccatct caaaaaaaaa aaaaaccagc tttctcctca  
 480  
 acttggggga acctt  
 495

<210> 2036  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 2036  
 Xaa Ile Pro Leu Leu Leu Ala Thr Gln Ala Gln Ala Thr Arg Ser His  
 1 5 10 15  
 Asp Thr Ser Cys Leu His Phe Phe His Val Cys Met Tyr Val Cys Met  
 20 25 30  
 Tyr Val Cys Met Tyr Val Cys Met Tyr Ala Xaa Met Phe Pro Phe His  
 35 40 45  
 Leu Ala Cys Leu His Phe Cys Cys Tyr Cys Cys Tyr Leu Cys Val Gly  
 50 55 60  
 Ala Pro Asn Gly Val Pro Tyr Phe Ser Asp Ala Val Phe Ile Phe Leu  
 65 70 75 80  
 Asp Ser Phe Tyr Cys Leu Val Phe Ser Leu His Asn Pro Tyr Cys Ser  
 85 90 95  
 Leu Tyr

<210> 2037  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

<400> 2037  
 acgcgtgaag ggaaggggga gaccccgga gaaatggaga aatgggggag cacacagacg  
 60  
 ggaagagtga ggttgaggag cttttcccg cgtcatcttc cgtccccact ccacgccccg  
 120  
 caaatccaaa caccgcggcc tctggtggcc cgggcttcca tttcccctgg aggggcaagg  
 180  
 gcgtttcctc ttccgccccaa ccggggcgct gaggcgggg aacagcgggc ggggctttgt  
 240  
 ggtcccgggg ggtccgagtg tgtgtcaggg gctggggcgg gggatgggag cggccccctg  
 300  
 gtatccctca cggctctggt tcatgag  
 327

<210> 2038  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 2038  
 Met Glu Lys Trp Gly Arg Thr Gln Thr Gly Arg Val Arg Leu Glu Cys  
 1 5 10 15  
 Leu Ser Arg Ala His Leu Pro Ser Pro Leu His Ala Gln Gln Ile Gln



```

      20      25      30
Thr Pro Arg Pro Leu Val Ala Arg Ala Ser Ile Ser Pro Gly Gly Ala
      35      40      45
Arg Ala Phe Pro Leu Pro Pro Asn Arg Gly Ala Glu Arg Arg Glu Gln
      50      55      60
Arg Arg Gly Leu Cys Gly Pro Gly Gly Ser Glu Cys Val Ser Gly Ala
      65      70      75      80
Gly Ala Gly Asp Gly Arg Gly Pro Trp Val Ser Leu Thr Val Leu Val
      85      90      95
His Glu

```

<210> 2039  
 <211> 307  
 <212> DNA  
 <213> Homo sapiens

```

<400> 2039
accggtgac cactctgcga aagcggccgc gagcgaagcg ttcttgggtct tcttcgagat
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cgcgatgtat tgccccgaaa acagcggctt gatgccgtca ttgagaggct ctgggccaac
120
accggtacgg gcatatgcct gggcggcatt cttttggatg ttgcaagaa aggacgcatt
180
cggcgtgccg aaagccaggg atccttcacc gtagaccttg gaccgatgga ggcccccggc
240
aatcgagtcc ttcgaaattc ccccttggca tacatgtcgg ccacgtcgt cagccagagt
300
aacgcgt
307

```

<210> 2040  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

```

<400> 2040
Met Ala Asp Met Tyr Ala Lys Gly Glu Phe Arg Arg Thr Arg Leu Pro
1      5      10      15
Gly Ala Ser Ile Gly Pro Arg Ser Thr Val Lys Asp Pro Trp Leu Ser
      20      25      30
Ala Arg Arg Met Arg Pro Phe Phe Ala Thr Ser Lys Arg Met Pro Pro
      35      40      45
Arg His Met Pro Val Pro Val Leu Ala Gln Ser Leu Ser Met Thr Ala
      50      55      60
Ser Ser Arg Cys Phe Pro Gly Asn Thr Ser Arg Ser Arg Arg Arg Pro
      65      70      75      80
Arg Thr Leu Arg Ser Arg Pro Leu Ser Gln Ser Gly Ser Pro
      85      90

```

<210> 2041  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 2041

nnccggcgat gcagggattc gcccgcgatg cgctcgaacc cggcgcgggg ggcgttcctc  
 60  
 gccagcttcc tgccgttcgc cagacgcata gccgaggcgg ggggtgcgcaa ttcgctcgcc  
 120  
 cagctggctg ccaagctgac cctgcccggc atgcccgaca tctaccaggg ctgcgagatg  
 180  
 tgggacctca gcctggtcga ccgggacaat cgccgccccg tcgactacga gacacgcgac  
 240  
 gcggccctgg ccggctgggt cgcgaccccc ccggaggaaac gcgccgcggc gctgcgcacc  
 300  
 ctgtgacgg attggcgag cggcgcggtc aagctggccg tgacgcgt  
 348

&lt;210&gt; 2042

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2042

Xaa	Arg	Arg	Cys	Arg	Asp	Ser	Pro	Ala	Met	Arg	Ser	Asn	Pro	Ala	Arg
1			5					10					15		
Gly	Ala	Phe	Leu	Ala	Ser	Phe	Leu	Pro	Phe	Ala	Arg	Arg	Ile	Ala	Glu
		20						25					30		
Ala	Gly	Val	Arg	Asn	Ser	Leu	Ala	Gln	Leu	Val	Ala	Lys	Leu	Thr	Leu
		35				40						45			
Pro	Gly	Met	Pro	Asp	Ile	Tyr	Gln	Gly	Cys	Glu	Met	Trp	Asp	Leu	Ser
	50					55					60				
Leu	Val	Asp	Arg	Asp	Asn	Arg	Arg	Pro	Val	Asp	Tyr	Glu	Thr	Arg	Asp
65					70					75				80	
Ala	Ala	Leu	Ala	Gly	Trp	Val	Ala	Thr	Pro	Pro	Glu	Glu	Arg	Ala	Ala
			85					90						95	
Ala	Leu	Arg	Thr	Leu	Leu	Thr	Asp	Trp	Arg	Ser	Gly	Ala	Val	Lys	Leu
			100					105						110	
Ala	Val	Thr	Arg												
			115												

&lt;210&gt; 2043

&lt;211&gt; 712

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2043

gatctgacgg tctcgactaa gcctgaccat tccgaggatca ccgacgccga ccttgccgtc  
 60  
 gaagattcgg tgccgagagc cctgtctcga atgcgctccc gggatgccgt ccacggcgag  
 120  
 gaacgtgccg ataccgggga tggaccccg cgggtggatca ttgatccgat cgacggcact  
 180  
 gcgaattttc tgctggtgggt ccagtggtgg gccacctca ttgccctcag cgtcgaggag  
 240  
 cagattgtcg catctgtggt ctctgtcct gccctcaagc gacgtggtg ggcagcccg  
 300

ggctcaggag catggtcggg caaatccctg gcctcagcga caccgatcca cgtctcgaat  
 360  
 gtgcgcaatc ttgccgacgc attcttgtcc tactcttcgc tgcacggatg ggtcgagagc  
 420  
 ggacgagggc acgggttcgg tgaactcatg cggtcggtgt ggcggaacccg agccttcggc  
 480  
 gatttctggt cttacatgat ggtggcagaa ggtgtcgtcg atgtggcatg cgagccggaa  
 540  
 ctcagcctgc acgacatggc cgccctcgac gctatcgta ccgaggcggg cggttaagttc  
 600  
 accggtctcg atggcaaaga cggcccgtagg tctgggaatg ctctggcgtc gaatggtttc  
 660  
 cttcatgacc aggccttagc catggtccag cctcaggagt gagcaccgat cg  
 712

<210> 2044

<211> 233

<212> PRT

<213> Homo sapiens

<400> 2044

Asp	Leu	Thr	Val	Ser	Thr	Lys	Pro	Asp	His	Ser	Glu	Val	Thr	Asp	Ala
1				5				10						15	
Asp	Leu	Ala	Val	Glu	Asp	Ser	Val	Arg	Arg	Ala	Leu	Ser	Arg	Met	Arg
			20					25					30		
Ser	Arg	Asp	Ala	Val	His	Gly	Glu	Glu	Arg	Ala	Asp	Thr	Gly	Asp	Gly
		35					40					45			
Pro	Arg	Arg	Trp	Ile	Ile	Asp	Pro	Ile	Asp	Gly	Thr	Ala	Asn	Phe	Leu
	50					55					60				
Arg	Gly	Val	Pro	Val	Trp	Ala	Thr	Leu	Ile	Ala	Leu	Ser	Val	Glu	Asp
65				70				75						80	
Gln	Ile	Val	Ala	Ser	Val	Val	Ser	Ala	Pro	Ala	Leu	Lys	Arg	Arg	Trp
			85					90					95		
Trp	Ala	Ala	Arg	Gly	Ser	Gly	Ala	Trp	Ser	Gly	Lys	Ser	Leu	Ala	Ser
			100					105					110		
Ala	Thr	Pro	Ile	His	Val	Ser	Asn	Val	Arg	Asn	Leu	Ala	Asp	Ala	Phe
		115					120					125			
Leu	Ser	Tyr	Ser	Ser	Leu	His	Gly	Trp	Val	Glu	Ser	Gly	Arg	Gly	His
	130					135					140				
Gly	Phe	Gly	Glu	Leu	Met	Arg	Ser	Val	Trp	Arg	Thr	Arg	Ala	Phe	Gly
145				150						155				160	
Asp	Phe	Trp	Ser	Tyr	Met	Met	Val	Ala	Glu	Gly	Val	Val	Asp	Val	Ala
			165						170				175		
Cys	Glu	Pro	Glu	Leu	Ser	Leu	His	Asp	Met	Ala	Ala	Leu	Asp	Ala	Ile
			180					185					190		
Val	Thr	Glu	Ala	Gly	Gly	Lys	Phe	Thr	Gly	Leu	Asp	Gly	Lys	Asp	Gly
		195					200					205			
Pro	Trp	Ser	Gly	Asn	Ala	Leu	Ala	Ser	Asn	Gly	Phe	Leu	His	Asp	Gln
	210					215					220				
Ala	Leu	Ala	Met	Val	Gln	Pro	Gln	Glu							
225					230										

<210> 2045

<211> 406

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2045

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nnttgacac cggcgactat gccgccaccg cacggatcaa tcgcggaccc agggcagggg
60
atgcgccgga tgggcgacgg tgatggaccg ggcgctggac ctgggcggtc gcttcgacga
120
cantacaggc tttggccgag gcgggttga agaaaccggt caaccggtgg tttggccccg
180
catcaatgcc cagaaccaga agccttgccg attcgtccca ggccgttcaa ggccgatggc
240
gagatcgctg cgatgactgg cgacggtgac aacgacgccc cctcgctcaa ggccgccccat
300
atcggtgctg ccatggacaa acgcggcacc gacgctcgcc gcgaggcttc cgccatggtc
360
ctgctcgagg atgattttgg atcgatcgtg cagtcggtcc ggctcg
406

```

&lt;210&gt; 2046

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2046

```

Xaa Trp Thr Pro Ala Thr Met Pro Pro Pro His Gly Ser Ile Ala Asp
 1           5           10           15
Pro Gly Gln Gly Met Arg Arg Met Gly Asp Gly Asp Gly Pro Gly Ala
 20           25           30
Gly Pro Gly Arg Ser Leu Arg Arg Xaa Tyr Arg Leu Trp Pro Arg Arg
 35           40           45
Val Gly Arg Asn Arg Ser Thr Gly Gly Leu Ala Pro His Gln Cys Pro
 50           55           60
Glu Pro Glu Ala Leu Arg Ile Arg Pro Arg Pro Phe Lys Ala Asp Gly
 65           70           75           80
Glu Ile Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Pro Ser Leu
 85           90           95
Lys Ala Ala His Ile Gly Val Ala Met Asp Lys Arg Gly Thr Asp Val
100          105          110
Ala Arg Glu Ala Ser Ala Met Val Leu Leu Glu Asp Asp Phe Gly Ser
115          120          125
Ile Val Gln Ser Val Arg Leu
130          135

```

&lt;210&gt; 2047

&lt;211&gt; 796

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2047

```

aagctttgga acgagacccc tgagctctgg gttcagcccc gaggaagccc agcaacagga
60
tgaggaattt gagaagaaga ttccaagtgt ggaagacagc cttggagagg gcagcagggg
120

```

tgctggccgg ccaggagaga gaggatccgg gggcttggtc agtcctagca ctgcccacgt  
 180  
 gccggatggg gcactcgggc agagagacca gagcagctgg caaaacagtg atgctagcca  
 240  
 ggaggtggga gggcatcagg agagacagca ggcaggggct cagggccctg gcagtgtga  
 300  
 cctggaagat ggggagatgg gaaagcgagg ctgggtcggg gagtttagcc tcagtgttgg  
 360  
 cccccagcga gaggcagcat ttagcccagg gcagcaggac tggagccggg acttctgcat  
 420  
 cgaggccagt gagaggagct atcagtttgg catcattggc aacgacagag tgagtgggtgc  
 480  
 tggcttttagc ccttctagca agatggaagg tggtcacttt gtgcctcctg ggaagaccac  
 540  
 agctggctcg gtggactgga ctgaccagct gggcttcagg aacttggaag tgtccagctg  
 600  
 tgtgggttct gggggctcga gcgaggccag ggagagtgcc gtgggacaga tgggctggtc  
 660  
 aggtggcctg agcttgagag acatgaacct gaccggctgt ttggaaagtg gagggctctga  
 720  
 agagccgggg ggaatcgga ttggggagaa ggactggact tctgatgtta atgtgaagag  
 780  
 caaagatttg gctgag  
 796

&lt;210&gt; 2048

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2048

Met	Gly	Lys	Arg	Gly	Trp	Val	Gly	Glu	Phe	Ser	Leu	Ser	Val	Gly	Pro
1				5					10					15	
Gln	Arg	Glu	Ala	Ala	Phe	Ser	Pro	Gly	Gln	Gln	Asp	Trp	Ser	Arg	Asp
			20					25					30		
Phe	Cys	Ile	Glu	Ala	Ser	Glu	Arg	Ser	Tyr	Gln	Phe	Gly	Ile	Ile	Gly
		35					40					45			
Asn	Asp	Arg	Val	Ser	Gly	Ala	Gly	Phe	Ser	Pro	Ser	Ser	Lys	Met	Glu
		50					55				60				
Gly	Gly	His	Phe	Val	Pro	Pro	Gly	Lys	Thr	Thr	Ala	Gly	Ser	Val	Asp
65					70					75				80	
Trp	Thr	Asp	Gln	Leu	Gly	Leu	Arg	Asn	Leu	Glu	Val	Ser	Ser	Cys	Val
			85					90						95	
Gly	Ser	Gly	Gly	Ser	Ser	Glu	Ala	Arg	Glu	Ser	Ala	Val	Gly	Gln	Met
			100					105					110		
Gly	Trp	Ser	Gly	Gly	Leu	Ser	Leu	Arg	Asp	Met	Asn	Leu	Thr	Gly	Cys
		115					120					125			
Leu	Glu	Ser	Gly	Gly	Ser	Glu	Glu	Pro	Gly	Gly	Ile	Gly	Ile	Gly	Glu
		130				135					140				
Lys	Asp	Trp	Thr	Ser	Asp	Val	Asn	Val	Lys	Ser	Lys	Asp	Leu	Ala	Glu
145					150				155						160

&lt;210&gt; 2049

&lt;211&gt; 516

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2049

cgcgtcgctt acggtgcgct gaataccagc ctgctggcgc tggcggtcag cttcgcgtcg  
 60  
 ctgttcctcg ggatagtgtt cgggctgatg ccacgtctga tgtgcggggg gattgaactg  
 120  
 gccaacgctc ccccgccaat cgccctgggc ctgttagtag tcgccattag cggcccttca  
 180  
 gcctacggtg ccgcctgtgc ggtgatgttg gtcagttggg ctccgctggc cgccattgt  
 240  
 gcttcgttgt tggcggaagc ccgcaacgag ccctatatcc gcatgttgcc ggtattgggc  
 300  
 gtcggccgat ggcgacgct gaccactac ctgctgccgg cgctctctgc tcccctgctg  
 360  
 cgcacgcca tgttgcgtct gccgggcatt gcgctggcgc tggcggcctt gggttttttt  
 420  
 ggtcttgggc cgcagccacc cagtgcagaa tgggggctgg tgctggcgga aggcattgcct  
 480  
 tatctcgaac gggcgccctg gggagtcttg gcaccg  
 516

&lt;210&gt; 2050

&lt;211&gt; 172

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2050

Arg	Val	Ala	Tyr	Gly	Ala	Leu	Asn	Thr	Ser	Leu	Leu	Ala	Leu	Ala	Val
1				5					10					15	
Ser	Phe	Ala	Ser	Leu	Phe	Leu	Gly	Ile	Val	Phe	Gly	Leu	Met	Pro	Arg
			20					25					30		
Leu	Met	Cys	Gly	Val	Ile	Glu	Leu	Ala	Asn	Ala	Pro	Pro	Pro	Ile	Ala
		35					40					45			
Leu	Gly	Leu	Leu	Val	Val	Ala	Ile	Ser	Gly	Pro	Ser	Ala	Tyr	Gly	Ala
	50					55					60				
Ala	Cys	Ala	Val	Met	Leu	Val	Ser	Trp	Ala	Pro	Leu	Ala	Ala	His	Cys
65					70					75				80	
Ala	Ser	Leu	Leu	Ala	Glu	Ala	Arg	Thr	Gln	Pro	Tyr	Ile	Arg	Met	Leu
			85					90					95		
Pro	Val	Leu	Gly	Val	Gly	Arg	Trp	Arg	Thr	Leu	Thr	His	Tyr	Leu	Leu
		100					105						110		
Pro	Ala	Leu	Ser	Ala	Pro	Leu	Leu	Arg	His	Ala	Met	Leu	Arg	Leu	Pro
		115				120					125				
Gly	Ile	Ala	Leu	Ala	Leu	Ala	Ala	Leu	Gly	Phe	Phe	Gly	Leu	Gly	Pro
	130					135					140				
Gln	Pro	Pro	Ser	Ala	Glu	Trp	Gly	Leu	Val	Leu	Ala	Glu	Gly	Met	Pro
145					150					155				160	
Tyr	Leu	Glu	Arg	Ala	Pro	Trp	Gly	Val	Leu	Ala	Pro				
			165					170							

&lt;210&gt; 2051

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2051

gagcaaaact atcggttctac cggcaatatt ctgaaaagtg ccaaccaact tatttcgaat  
60  
aatagtgatc gtctcggtaa gaatttatgg accgacgggtg aaatggggga gccagtaggt  
120  
atttatgcag catttaatga attagatgag gcaaaatttg tggcgtctca aatccaaaat  
180  
tgggtagatg atgggtggga attagatgat tgtgctgttt tatatcgtag taatagccaa  
240  
tctcgtgtta ttgaagaagc cttgattcgt tgccaaattc cttatcgaat ttatggcggg  
300  
atgcgattct tcgaacgcca agaaattaaa gatgcgttgg catatttacg ttttaattaat  
360  
aatcgtcaag atgatgccgc atttgagcgt gtgattaata cgcctacgcg t  
411

&lt;210&gt; 2052

&lt;211&gt; 137

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2052

Glu	Gln	Asn	Tyr	Arg	Ser	Thr	Gly	Asn	Ile	Leu	Lys	Ser	Ala	Asn	Gln
1			5					10						15	
Leu	Ile	Ser	Asn	Asn	Ser	Asp	Arg	Leu	Gly	Lys	Asn	Leu	Trp	Thr	Asp
			20					25					30		
Gly	Glu	Met	Gly	Glu	Pro	Val	Gly	Ile	Tyr	Ala	Ala	Phe	Asn	Glu	Leu
		35					40					45			
Asp	Glu	Ala	Lys	Phe	Val	Ala	Ser	Gln	Ile	Gln	Asn	Trp	Val	Asp	Asp
		50				55					60				
Gly	Gly	Glu	Leu	Asp	Asp	Cys	Ala	Val	Leu	Tyr	Arg	Ser	Asn	Ser	Gln
65				70						75				80	
Ser	Arg	Val	Ile	Glu	Glu	Ala	Leu	Ile	Arg	Cys	Gln	Ile	Pro	Tyr	Arg
			85					90					95		
Ile	Tyr	Gly	Gly	Met	Arg	Phe	Phe	Glu	Arg	Gln	Glu	Ile	Lys	Asp	Ala
		100						105					110		
Leu	Ala	Tyr	Leu	Arg	Leu	Ile	Asn	Asn	Arg	Gln	Asp	Asp	Ala	Ala	Phe
		115					120					125			
Glu	Arg	Val	Ile	Asn	Thr	Pro	Thr	Arg							
		130					135								

&lt;210&gt; 2053

&lt;211&gt; 287

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2053

nccatggaag ccttcaatct tgtaagagaa agtgaacagc tgttttccat atgccaaatc  
60  
ccgctcctct gctggatcct gtgtaccagt ctgaagcaag agatgcagaa aggaaaagac  
120

ctggccctga cctgccagag cactacctct gtgtactcct ctttcgtctt taacctgttc  
 180  
 acacctgagg gtgccgaggg cccgactccg caaaccagc accagctgaa ggccctgtgc  
 240  
 tccctggctg cagagggtat gtggacagac acatttgagt tttgtga  
 287

<210> 2054

<211> 79

<212> PRT

<213> Homo sapiens

<400> 2054

Ile	Cys	Gln	Ile	Pro	Leu	Leu	Cys	Trp	Ile	Leu	Cys	Thr	Ser	Leu	Lys
1				5					10					15	
Gln	Glu	Met	Gln	Lys	Gly	Lys	Asp	Leu	Ala	Leu	Thr	Cys	Gln	Ser	Thr
			20					25					30		
Thr	Ser	Val	Tyr	Ser	Ser	Phe	Val	Phe	Asn	Leu	Phe	Thr	Pro	Glu	Gly
		35					40					45			
Ala	Glu	Gly	Pro	Thr	Pro	Gln	Thr	Gln	His	Gln	Leu	Lys	Ala	Leu	Cys
		50				55					60				
Ser	Leu	Ala	Ala	Glu	Gly	Met	Trp	Thr	Asp	Thr	Phe	Glu	Phe	Cys	
65					70					75					

<210> 2055

<211> 298

<212> DNA

<213> Homo sapiens

<400> 2055

nnacgcgttg ttatgaacaa tgacgggtgc ctctaccccg atacctgcgt ggggtactgat  
 60  
 tcccacacca ccatggaaaa tggctctggc attctgggct ggggcgtcgg tggattgaa  
 120  
 gccgaggctg ctatgcttgg ccagcccatc tccatgctta tccccgtgt tgttggcttt  
 180  
 aaacttactg gccaaacaca gccgggtgac accgctacag atgttgttct taccattact  
 240  
 gatatgcttc gccagcatgg tgtgggtgga aaattcgggg aattctatgg gggaagcg  
 298

<210> 2056

<211> 99

<212> PRT

<213> Homo sapiens

<400> 2056

Xaa	Arg	Val	Val	Met	Asn	Asn	Asp	Gly	Val	Leu	Tyr	Pro	Asp	Thr	Cys
1				5					10					15	
Val	Gly	Thr	Asp	Ser	His	Thr	Thr	Met	Glu	Asn	Gly	Leu	Gly	Ile	Leu
			20					25					30		
Gly	Trp	Gly	Val	Gly	Gly	Ile	Glu	Ala	Glu	Ala	Ala	Met	Leu	Gly	Gln
		35				40						45			
Pro	Ile	Ser	Met	Leu	Ile	Pro	Arg	Val	Val	Gly	Phe	Lys	Leu	Thr	Gly



50                      55                      60  
 Gln Thr Gln Pro Gly Val Thr Ala Thr Asp Val Val Leu Thr Ile Thr  
 65                      70                      75                      80  
 Asp Met Leu Arg Gln His Gly Val Gly Gly Lys Phe Gly Glu Phe Tyr  
                     85                      90                      95  
 Gly Gly Ser

<210> 2057  
 <211> 569  
 <212> DNA  
 <213> Homo sapiens

<400> 2057  
 acgcgtcccg acagtaccga ctataacgga ggaaactatc aggaacggta taaaatttta  
 60  
 gcagaaattc gtaaggctct tgaagacgga gatcgccaaa aagccaaacg attagctgaa  
 120  
 caaatctag ttggacccaa caacgcccg tatggtcgtt atctagcctt tggatgatc  
 180  
 ttcatggctt tcaataacca gaaaaagggg ctggatacag ttacagacta tcaccgtggt  
 240  
 ttggatatca cagaagccac tactacaact tcttacaccc aagatggaac gacctttaa  
 300  
 agagaaacct tctcaagtta ccctgatgat gttactgtta ctacttgac ccaaaaagg  
 360  
 gacaaaaaac ttgattttac agtttggaat agcttaacag aagatttact tgctaacgga  
 420  
 gactactcag cggaatattc taactacaag agtggccatg ttacgacaga ccaaatggt  
 480  
 atcctactaa aaggtacagt caaagataat ggcctccagt tcgcatccta tctaggaatt  
 540  
 aaaacggacg gaaaagttac tgttcatga  
 569

<210> 2058  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 2058  
 Met Val Phe Asn Asn Gln Lys Lys Gly Leu Asp Thr Val Thr Asp Tyr  
 1                      5                      10                      15  
 His Arg Gly Leu Asp Ile Thr Glu Ala Thr Thr Thr Ser Tyr Thr  
                     20                      25                      30  
 Gln Asp Gly Thr Thr Phe Lys Arg Glu Thr Phe Ser Ser Tyr Pro Asp  
                     35                      40                      45  
 Asp Val Thr Val Thr His Leu Thr Gln Lys Gly Asp Lys Lys Leu Asp  
                     50                      55                      60  
 Phe Thr Val Trp Asn Ser Leu Thr Glu Asp Leu Leu Ala Asn Gly Asp  
 65                      70                      75                      80  
 Tyr Ser Ala Glu Tyr Ser Asn Tyr Lys Ser Gly His Val Thr Thr Asp  
                     85                      90                      95  
 Pro Asn Gly Ile Leu Leu Lys Gly Thr Val Lys Asp Asn Gly Leu Gln

	100		105		110										
Phe	Ala	Ser	Tyr	Leu	Gly	Ile	Lys	Thr	Asp	Gly	Lys	Val	Thr	Val	His
	115				120						125				

<210> 2059  
 <211> 644  
 <212> DNA  
 <213> Homo sapiens

<400> 2059  
 gaattcgtgc caccgtgcc atacttcgcc acgcaacaga gtgccgtcag cggattgggc  
 60  
 agcaatcgac ctgtaggact cagccatgat cgactgggca tcctcgata gtcgcatgc  
 120  
 cgcaaccgcc tgcgcttcca agcctgcagc gacgtaagag gccctctcac aactgaacc  
 180  
 gatcgctcca gacaacgtgg aagcgataac ctgcgctcgc ttctgctgat tctgggcca  
 240  
 gctcgacaag aagaaccgca gaggggagc ggcctgggtca gggagcgac cttcagcgtt  
 300  
 cgtcttggtc tccgggacag caaaaagcgg ggaatcagcc aggccacgct ccgtcatgag  
 360  
 tcggccgagg tccgccggt cctctctcat ggcttcacac ggaacgcggt cacacaccac  
 420  
 cgcgatcgac gcgtgcctct cttgagcctc gttgaggaaa tcccacggca cagcgtcagc  
 480  
 gtagcgggct gctgaggtga caaagatcca cagatccggg gcctggagca actgagccgc  
 540  
 cagatcacga ttgcgggtca ccacagagtc gatgtccggg gcatcgagga tggccaaacc  
 600  
 tcgcggaatc cttgactccg cgacgagctg caaactcgac gcgt  
 644

<210> 2060  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 2060  
 Met Arg Glu Val Pro Ala Asp Leu Gly Arg Leu Met Thr Glu Arg Gly  
 1 5 10 15  
 Leu Ala Asp Ser Pro Leu Phe Ala Val Pro Glu Thr Lys Thr Asn Ala  
 20 25 30  
 Glu Gly Ala Leu Pro Asp Gln Ala Val Ala Pro Leu Arg Phe Phe Leu  
 35 40 45  
 Ser Ser Leu Ala Gln Asn Gln Gln Lys Arg Arg Glu Val Ile Ala Ser  
 50 55 60  
 Thr Leu Ser Gly Ala Ile Gly Ser Val Cys Glu Arg Ala Ser Tyr Val  
 65 70 75 80  
 Ala Ala Gly Leu Glu Ala Gln Ala Val Ala Ala Ser Arg Leu Tyr Glu  
 85 90 95  
 Asp Ala Gln Ser Ile Met Ala Glu Ser Tyr Arg Ser Ile Ala Ala Gln  
 100 105 110  
 Ser Ala Asp Gly Thr Leu Leu Arg Gly Glu Val Leu Ala Arg Trp His

1556

<210> 2063  
 <211> 419  
 <212> DNA  
 <213> Homo sapiens

<400> 2063  
 gccggcgccg tcgagcgcggt gcctttcaat atcgaggccc aagacatggg gctgctcatc  
 60  
 gcggacacca atgccccgca catgctttcc gacggccaat acgcctcccg ccggggcatc  
 120  
 atcgacgccc tccaatctgc cgccggttgc tccatccgcg agatctcgaa tgcggtggac  
 180  
 ttgcccga ccgtaaatcc cgccgaggcg gaactctatc gccgcccgt gcaccacgtg  
 240  
 gtggaagaaa ccaaccggac cctagatgcc gctaccgcgc tggcatcttc cgatctagat  
 300  
 acattccggc ggcttatgcg cgagagccac atctccctgc gcgaccttta tgaggtcacc  
 360  
 actccggagc tcgactccgt tttaccgcg gccggcgagc tgggcgctcg catgannnn  
 419

<210> 2064  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 2064.  
 Ala Gly Ala Val Glu Arg Val Pro Phe Asn Ile Glu Ala Gln Asp Met  
 1 5 10 15  
 Val Leu Leu Ile Ala Asp Thr Asn Ala Pro His Met Leu Ser Asp Gly  
 20 25 30  
 Gln Tyr Ala Ser Arg Arg Gly Ile Ile Asp Ala Val Gln Ser Ala Ala  
 35 40 45  
 Gly Cys Ser Ile Arg Glu Ile Ser Asn Ala Val Asp Phe Ala Ala Thr  
 50 55 60  
 Val Asn Pro Ala Glu Ala Glu Leu Tyr Arg Arg Val His His Val  
 65 70 75 80  
 Val Glu Glu Thr Asn Arg Thr Leu Asp Ala Ala Thr Ala Leu Ala Ser  
 85 90 95  
 Ser Asp Leu Asp Thr Phe Arg Arg Leu Met Arg Glu Ser His Ile Ser  
 100 105 110  
 Leu Arg Asp Leu Tyr Glu Val Thr Thr Pro Glu Leu Asp Ser Val Phe  
 115 120 125  
 Thr Ala Ala Gly Glu Leu Gly Ala Arg Met Xaa  
 130 135

<210> 2065  
 <211> 598  
 <212> DNA  
 <213> Homo sapiens

<400> 2065  
 gccggcgcta tggcctctct gtcgcgcgac gccgcccgatg cccttcccg cgcaaagggtg  
 60

cgcgcgaccg ttactggatc ggcgggattg ggaaccgcag aggcattggg ccttactttc  
 120  
 attcaggagg tcatagctga gacggccgcc gtccaacgtt ggaatcccga cgccgacgtg  
 180  
 cttctcgaac tcggtggtga ggatgccaaag atcacctacc ttaagccggt ccccgaacag  
 240  
 cgcataaatg gttcgtgtgc tgggtggcacc ggtgccttca tcgaccagat ggctaccctg  
 300  
 ctgcacaccg aactccccgg cctcaatgac ctgcacatccc gagccaagac catccatccg  
 360  
 atcgctcgc gctgtggtgt ttttgccaag tccgaccttc agccccctcat taacgagggga  
 420  
 gcccgccacg aggatctggc tgcctcggtc ctgcaggctg tcgccactca gtgcattgcc  
 480  
 ggcttggcat gtggtcgccc gattcgaggt aaggctcatct tccttggcgg tccgcttcac  
 540  
 tttatgccaa gtttgcgaga cgctttctcg cgcgtcctcg acggttaagg tgcgcgt  
 598

&lt;210&gt; 2066

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2066

Ala	Gly	Ala	Met	Ala	Ser	Leu	Leu	Ala	Asp	Ala	Ala	Asp	Ala	Leu	Pro
1			5					10					15		
Gly	Ala	Lys	Val	Arg	Ala	Thr	Val	Thr	Gly	Ser	Ala	Gly	Leu	Gly	Thr
			20					25					30		
Ala	Glu	Ala	Leu	Gly	Leu	Thr	Phe	Ile	Gln	Glu	Val	Ile	Ala	Glu	Thr
			35				40						45		
Ala	Ala	Val	Gln	Arg	Trp	Asn	Pro	Asp	Ala	Asp	Val	Leu	Leu	Glu	Leu
			50			55					60				
Gly	Gly	Glu	Asp	Ala	Lys	Ile	Thr	Tyr	Leu	Lys	Pro	Val	Pro	Glu	Gln
65					70					75				80	
Arg	Met	Asn	Gly	Ser	Cys	Ala	Gly	Gly	Thr	Gly	Ala	Phe	Ile	Asp	Gln
					85				90					95	
Met	Ala	Thr	Leu	Leu	His	Thr	Asp	Thr	Pro	Gly	Leu	Asn	Asp	Leu	Ala
			100					105					110		
Ser	Arg	Ala	Lys	Thr	Ile	His	Pro	Ile	Ala	Ser	Arg	Cys	Gly	Val	Phe
			115				120						125		
Ala	Lys	Ser	Asp	Leu	Gln	Pro	Leu	Ile	Asn	Glu	Gly	Ala	Arg	His	Glu
			130			135					140				
Asp	Leu	Ala	Ala	Ser	Val	Leu	Gln	Ala	Val	Ala	Thr	Gln	Cys	Ile	Ala
145					150				155					160	
Gly	Leu	Ala	Cys	Gly	Arg	Pro	Ile	Arg	Gly	Lys	Val	Ile	Phe	Leu	Gly
					165				170					175	
Gly	Pro	Leu	His	Phe	Met	Pro	Ser	Leu	Arg	Asp	Ala	Phe	Ser	Arg	Val
			180					185					190		
Leu	Asp	Gly	Lys	Val	Asp	Ala									
			195												

&lt;210&gt; 2067

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2067

ttccagcaga tgctgcaaac ctggacccgc agcggcacgc tgcaggaggc cgtggccaac  
 60  
 aagatcgccg aatggctgga tgccgacctg caacagtggg acatttcccg cgatgcaccg  
 120  
 tacttcggtt tcgagatccc gggcgagcca ggcaagtatt tctacgtgtg gctggacgcg  
 180  
 ccgatcggct acatggccag tttcaagaac ctgtgcgacc gcacgccgga gctggacttc  
 240  
 gatgctttct gggccaagga ctccaccgcc gagctgtacc atttcacgga caaggacatc  
 300  
 gtcaacttcc acgccctgtt ctggccggcg atgctcgaag gctcgggcta ccgtaaaccg  
 360  
 accggt  
 366

&lt;210&gt; 2068

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2068

Phe	Gln	Gln	Met	Leu	Gln	Thr	Trp	Thr	Arg	Ser	Gly	Thr	Leu	Gln	Glu
1				5				10					15		
Ala	Val	Ala	Asn	Lys	Ile	Ala	Glu	Trp	Leu	Asp	Ala	Asp	Leu	Gln	Gln
			20					25					30		
Trp	Asp	Ile	Ser	Arg	Asp	Ala	Pro	Tyr	Phe	Gly	Phe	Glu	Ile	Pro	Gly
		35				40						45			
Glu	Pro	Gly	Lys	Tyr	Phe	Tyr	Val	Trp	Leu	Asp	Ala	Pro	Ile	Gly	Tyr
		50				55					60				
Met	Ala	Ser	Phe	Lys	Asn	Leu	Cys	Asp	Arg	Thr	Pro	Glu	Leu	Asp	Phe
65				70					75					80	
Asp	Ala	Phe	Trp	Ala	Lys	Asp	Ser	Thr	Ala	Glu	Leu	Tyr	His	Phe	Ile
			85					90					95		
Gly	Lys	Asp	Ile	Val	Asn	Phe	His	Ala	Leu	Phe	Trp	Pro	Ala	Met	Leu
			100					105					110		
Glu	Gly	Ser	Gly	Tyr	Arg	Lys	Pro	Thr	Gly						
		115				120									

&lt;210&gt; 2069

&lt;211&gt; 280

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2069

cctagagagg atggtggaga ctgtgcgtgt gcagggtgtt ccggaacctt ccctgggatg  
 60  
 catggggcct cgccgcaggc catctctcca gacctgggct caccctgccc ctgtgctgtt  
 120  
 gcctttggct ggaattccac ccagccttc ttgcctcaag aacgcccttc cccttcaga  
 180

tctcatgggc acaggccccg tcttcctaaa cggggtcaga gccccagta atcatgacaa  
 240  
 agaccctctc ctcgatcaag ctttgggtcaa gctcctaccc  
 280

<210> 2070  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 2070  
 Met Val Glu Thr Val Arg Val Gln Gly Val Pro Glu Pro Ser Leu Gly  
 1 5 10 15  
 Cys Met Gly Pro Arg Arg Arg Pro Ser Leu Gln Thr Trp Ala His Pro  
 20 25 30  
 Ala Pro Val Leu Leu Pro Leu Ala Gly Ile Pro Pro Gln Pro Ser Cys  
 35 40 45  
 Leu Lys Asn Ala Leu Pro Pro Ser Asp Leu Met Gly Thr Gly Pro Val  
 50 55 60  
 Phe Leu Asn Gly Val Arg Ala Pro Ser Asn His Asp Lys Asp Pro Leu  
 65 70 75 80  
 Leu Asp Gln Ala Leu Val Lys Leu Leu Pro  
 85 90

<210> 2071  
 <211> 399  
 <212> DNA  
 <213> Homo sapiens

<400> 2071  
 acgcgtgtcc agcagactta gaaagcaggt tcctcttgct atacagcacg ttaacatagc  
 60  
 tgacgaggcc tgggtgtctt catcagtact gtgatgactc tttcaccttt gacttcagat  
 120  
 gctggcgctt tttacttttt gtgccaaact ctacacatga aacacttttg gaataactac  
 180  
 agacatgact ttctttatct ggggaaaagg agggcattaa accagattag gggctgggag  
 240  
 gggagggtgt caggggatga gctgctcctg aggaagaggc agagatcaag cttcactcag  
 300  
 cagctggatt ctcacctagt ttatagactg aaatcctgca aggtgggttac aacagtgaac  
 360  
 aatatgttca tacataaaga ctctaccctc aggtgatca  
 399

<210> 2072  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 2072  
 Met Thr Leu Ser Pro Leu Thr Ser Asp Ala Gly Ala Phe Tyr Phe Leu  
 1 5 10 15  
 Cys Gln Thr Leu His Met Lys His Phe Trp Asn Asn Tyr Arg His Asp

```

      20      25      30
Phe Leu Tyr Leu Gly Lys Arg Arg Ala Leu Asn Gln Ile Arg Gly Trp
      35      40      45
Glu Gly Arg Leu Ser Gly Asp Glu Leu Leu Leu Arg Lys Arg Gln Arg
      50      55      60
Ser Ser Phe Thr Gln Gln Leu Asp Ser His Leu Val Tyr Arg Leu Lys
65      70      75      80
Ser Cys Lys Val Val Thr Thr Val Asn Asn Met Phe Ile His Lys Asp
      85      90      95
Ser Thr Leu Arg
      100

```

<210> 2073  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

```

<400> 2073
ggatccactt ctgtgccttt ccagcttcta gaggctgcct gcgttccttg gctcgtggcc
60
ccttcctcca ccttcaagcc agcagcggag gcctgagtcc ttctcatgcc atctctctgt
120
tctctctcct gcctcctcct ccacactgaa ggaccctctgt gatcacactg gccccccac
180
cggatgaccc aggataatcc atctccctgt ttgaaggctcg gctgattagc aaccttcatt
240
ccatctgcct ccttcattcc ccctggccat gtaatgggat tcacagcttc tggggattag
300
gacatggaca tcttgtggcg ggggcataat tctgtcgac
339

```

<210> 2074  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

```

<400> 2074
Met Lys Glu Ala Asp Gly Met Lys Val Ala Asn Gln Pro Thr Phe Lys
1      5      10      15
Gln Gly Asp Gly Leu Ser Trp Val Ile Arg Trp Gly Gly Gln Cys Asp
      20      25      30
His Arg Gly Pro Ser Val Trp Arg Arg Arg Gln Glu Arg Glu Gln Arg
      35      40      45
Asp Gly Met Arg Arg Thr Gln Ala Ser Ala Ala Gly Leu Lys Val Glu
      50      55      60
Glu Gly Ala Thr Ser Gln Gly Thr Gln Ala Ala Ser Arg Ser Trp Lys
65      70      75      80
Gly Thr Glu Val Asp
      85

```

<210> 2075  
 <211> 481  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 2075

ntggccaggt tgacctcaaa ggtgtacatt gttttatgtg gcgacaatgg actgtcagaa  
 60  
 accaaggagc tctcctgtcc agagaagtcc ctgtttgaaa ggaattccag acacaccttt  
 120  
 atcctgagcg ctcttgccca actgggcctg ctgaggaaga tccgcctctg gcacgacagc  
 180  
 cgtgggcctt cccagggctg gttcatcagc cacgtgatgg tgaaggagct gcacacggga  
 240  
 cagggctggt tcttccttgc ccagtgtctg ctgtctgccg gcaggcatga tggtcgctg  
 300  
 gagcgggagc tcacctgtct gcaaggggga ctcggttctt ggaagctttt ctattgcaag  
 360  
 ttcacagagt acctggagga tttccatgtc tggctgtcgg tgtacagcag gccctcctcc  
 420  
 agccgctacc tgcacacgcc gcgccccacc gtgtccttct cctgtctgtg cgtctacggc  
 480  
 t  
 481

&lt;210&gt; 2076

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2076

Xaa	Ala	Arg	Leu	Thr	Ser	Lys	Val	Tyr	Ile	Val	Leu	Cys	Gly	Asp	Asn
1				5					10					15	
Gly	Leu	Ser	Glu	Thr	Lys	Glu	Leu	Ser	Cys	Pro	Glu	Lys	Ser	Leu	Phe
		20					25					30			
Glu	Arg	Asn	Ser	Arg	His	Thr	Phe	Ile	Leu	Ser	Ala	Pro	Ala	Gln	Leu
	35					40					45				
Gly	Leu	Leu	Arg	Lys	Ile	Arg	Leu	Trp	His	Asp	Ser	Arg	Gly	Pro	Ser
	50				55					60					
Pro	Gly	Trp	Phe	Ile	Ser	His	Val	Met	Val	Lys	Glu	Leu	His	Thr	Gly
65				70					75				80		
Gln	Gly	Trp	Phe	Phe	Pro	Ala	Gln	Cys	Trp	Leu	Ser	Ala	Gly	Arg	His
		85					90					95			
Asp	Gly	Arg	Val	Glu	Arg	Glu	Leu	Thr	Cys	Leu	Gln	Gly	Gly	Leu	Gly
		100					105					110			
Phe	Trp	Lys	Leu	Phe	Tyr	Cys	Lys	Phe	Thr	Glu	Tyr	Leu	Glu	Asp	Phe
	115						120				125				
His	Val	Trp	Leu	Ser	Val	Tyr	Ser	Arg	Pro	Ser	Ser	Ser	Arg	Tyr	Leu
	130					135					140				
His	Thr	Pro	Arg	Pro	Thr	Val	Ser	Phe	Ser	Leu	Leu	Cys	Val	Tyr	Ala
145					150					155					160

&lt;210&gt; 2077

&lt;211&gt; 1410

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2077

ncagagtgtt ttgagctatc tggatatcca aatgatgtga atactttcag aaaccaatgg  
60  
caaattgaac ccaactgttt gcgaattcgg caccagtaaa gatctttttt ttttttttgt  
120  
tttttttttt tttttttttt ttttgctttc taaagtggct ttaatatcac acaagcggct  
180  
ctttggctcta cagtgagaga aaacagaggg agccaggaaa ggctccccgc tggcctctgg  
240  
agtccaggag ccttaggaag gctgaaaaca gccctgacca gcaggcttag ttgtcctgag  
300  
aagagccagt gaggccacct ggtccagttc accagggtttc ccagggaagc acaggcatct  
360  
ctgggtcccc gagcacagtg ccagggaaga ccccccaat ccccatctga acaggccgag  
420  
ggcagcatgg gaaaggctca gactgcaggt tcatcccgca ggatggtaag gacacgtgct  
480  
cctccctcgc aagagcaggc ttgtgcacag ccggcacag ggccagccag ggcggccccct  
540  
gcggctgtgc agcgcttacc agggggagga gttcagccat caggaccttt tccaagtgga  
600  
tctgctggtc cagcacagcc actcgcagct tgagggccgc cagggtctgc agctcctggg  
660  
tgctggagta gacaagcagc tgggnnggct ccatgcaggc tccgctctac cccacagga  
720  
cggcgaggct ccggggggcc tnnccccaca gacatggtct tggtggtgt tccgccaccg  
780  
ctgcacgcag ctctgcagc ctgtgcagac actggccac catggcctgc agccctcca  
840  
gcgtgagcag gcagcgttac tctgcatcc agtccatggg ggctgctgag agctcctccc  
900  
tcatgcgcag tctcagcagc gagcaggcct tccgcaggcg cccgcctcc gcctccacct  
960  
ccacagcact gagcctgggc tggggcccgc ctgaagctgt ctgcatgttc tggaggaact  
1020  
gggttttggc agcggcgcca tccgtggaat cactggtctg tgtggaactg agctgggccc  
1080  
acaggctcga gttctgggaa gctgctttcc tgaatgccgc aggcagccgc agcaggtgcc  
1140  
ccttctcctt gagtgtaag gcttctgggg cctgaggagc agcggatggg gccatttgc  
1200  
ggtcctgag gcccgccca ggctggggg ttcgggctcc catcccaaca cgggtcccat  
1260  
ccccactga cagcagccgg cgctcagggt ggcccttggc aggcaccgtg gtctggcgga  
1320  
ggcccttggg gggctctcgtg tctgaagcat ggccaccagc ttggcctggg gaatgcggtg  
1380  
gggcggaggc tgctgtgcca gaagaggtga  
1410

&lt;210&gt; 2078

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2078

Gly His Leu Val Gln Phe Thr Arg Phe Pro Arg Glu Ala Gln Ala Ser  
 1 5 10 15  
 Leu Gly Pro Arg Ala Gln Cys Gln Gly Arg His Pro Gln Ser Pro Ser  
 20 25 30  
 Glu Gln Ala Glu Gly Ser Met Gly Lys Ala Gln Thr Ala Gly Ser Ser  
 35 40 45  
 Arg Arg Met Val Arg Thr Arg Ala Pro Pro Ser Gln Glu Gln Ala Cys  
 50 55 60  
 Ala Gln Pro Gly Thr Gly Pro Ala Arg Ala Ala Pro Ala Ala Val Gln  
 65 70 75 80  
 Arg Leu Pro Gly Gly Gly Val Gln Pro Ser Gly Pro Phe Pro Ser Gly  
 85 90 95  
 Ser Ala Gly Pro Ala Gln Pro Leu Ala Ala  
 100 105

&lt;210&gt; 2079

&lt;211&gt; 565

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2079

atttacctcg caaccgaccc tgatcgtgaa ggtgaaagca tcagctggca catccagcag  
 60  
 gtactggcgg tcaaatccta caaacgcatt accttcaacg agatcactct caagcgcgtt  
 120  
 gaagaggcac tggccaatcc tcgacaaaatc gatctgaaca gagttgcctc acaggaatgc  
 180  
 cggcgtgtgc ttgaccgctt ggtgggggtac ctggtgaccc aagagttgcg gcgcctgatg  
 240  
 ggcaaaccta cttccgctgg ccgcgttcaa tcacccgcg tgtttcttgt ggtcttgccg  
 300  
 gaacgcgaga tccgcaactt tcaggtgatc aatcactttg gcgtgcgtct gttctttgcc  
 360  
 gatgtaagtc ggggcaccac ttggtatgcc gagtggcaac cggtaccgga tttcgcaagc  
 420  
 aagcatttcc cctatgttca ggatagcaac ctggctcagc acgtcgccgg cactcgaaat  
 480  
 gtggctcgtg agtcctgcga ggatcgcaag gccgagcgtc atcctctctgc accattcattc  
 540  
 tcattcactc ttcaacaggc cgcca  
 565

&lt;210&gt; 2080

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2080

Ile Tyr Leu Ala Thr Asp Pro Asp Arg Glu Gly Glu Ser Ile Ser Trp  
 1 5 10 15  
 His Ile Gln Gln Val Leu Ala Val Lys Ser Tyr Lys Arg Ile Thr Phe  
 20 25 30  
 Asn Glu Ile Thr Leu Lys Arg Val Glu Glu Ala Leu Ala Asn Pro Arg

```

      35          40          45
Gln Ile Asp Leu Asn Arg Val Ala Ser Gln Glu Cys Arg Arg Val Leu
      50          55          60
Asp Arg Leu Val Gly Tyr Leu Val Thr Gln Glu Leu Arg Arg Leu Met
65          70          75          80
Gly Lys Pro Thr Ser Ala Gly Arg Val Gln Ser Pro Ala Val Phe Leu
      85          90          95
Val Val Leu Arg Glu Arg Glu Ile Arg Asn Phe Gln Val Ile Asn His
      100         105         110
Phe Gly Val Arg Leu Phe Phe Ala Asp Val Ser Arg Gly Thr Thr Trp
      115         120         125
Tyr Ala Glu Trp Gln Pro Val Pro Asp Phe Ala Ser Lys His Phe Pro
      130         135         140
Tyr Val Gln Asp Ser Asn Leu Ala Gln His Val Ala Gly Thr Arg Asn
145         150         155         160
Val Val Val Glu Ser Cys Glu Asp Arg Lys Ala Glu Arg His Pro Pro
      165         170         175
Ala Pro Phe Ile Ser Ser Thr Leu Gln Gln Ala Ala
      180         185

```

&lt;210&gt; 2081

&lt;211&gt; 319

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2081

```

aagcttatgg aaaaacgggg atacggagag gagtatataa atcgctataa aatgatgaca
60
aggttccatc atcaacgggt tccactagta attttggtgt gtggaactgc ctgtactgga
120
aaatcaacaa tcgctacaca acttgctcag aggcctcaatt tgccaatgt tttgcagacg
180
gacatggtgt atgagctgct gcggacatca acagatgcgc cacttacttc agttcctgtg
240
tgggctcgcg attttaattc acctgaagag cttatcactg aattctgcag agaatgcaga
300
gttgtagcga agggtttgg
319

```

&lt;210&gt; 2082

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2082

```

Lys Leu Met Glu Lys Arg Gly Tyr Gly Glu Glu Tyr Ile Asn Arg Tyr
1      5      10      15
Lys Met Met Thr Arg Phe His His Gln Arg Val Pro Leu Val Ile Leu
20     25     30
Val Cys Gly Thr Ala Cys Thr Gly Lys Ser Thr Ile Ala Thr Gln Leu
35     40     45
Ala Gln Arg Leu Asn Leu Pro Asn Val Leu Gln Thr Asp Met Val Tyr
50     55     60
Glu Leu Leu Arg Thr Ser Thr Asp Ala Pro Leu Thr Ser Val Pro Val

```

```
<210> 2085
<211> 478
<212> DNA
<213> Homo sapiens
```

<400> 2085  
 nnggatccca aagaccgcga tattgccatg gtgttccaaa actatgccct ctaccgcac  
 60  
 atgactgtcg ccgacaacat gggttttgcc ctcaaactgg cgaaagtgga taagaaagaa  
 120  
 atccggcgtc gcgtggagga agccgccgaa ctctcgacc tcaccgacta tctggaccgc  
 180  
 aaacccaagg cactctccgg tggccagcgg cagcgcgctg ccatggggcg cgctattgtt  
 240  
 cgttcccccc gcgtcttctt gatggacgag cctctttcta acctggatgc gcgtctgcgt  
 300  
 gtccgcaccc gcgccagat tgcggaactg cagcgccgcc tgggcaccac caccgtttat  
 360  
 gtcacccatg accaggtgga ggctatgacg atgggggatc gtgtggctgt tctctgtgcc  
 420  
 gggaaactgc agcaggtgga tactccacgt aatcttttcg accacccgc taacgcgt  
 478

<210> 2086

<211> 159

<212> PRT

<213> Homo sapiens

<400> 2086

Xaa	Asp	Pro	Lys	Asp	Arg	Asp	Ile	Ala	Met	Val	Phe	Gln	Asn	Tyr	Ala
1				5					10					15	
Leu	Tyr	Pro	His	Met	Thr	Val	Ala	Asp	Asn	Met	Gly	Phe	Ala	Leu	Lys
			20					25				30			
Leu	Ala	Lys	Val	Asp	Lys	Lys	Glu	Ile	Arg	Arg	Arg	Val	Glu	Glu	Ala
		35				40					45				
Ala	Glu	Leu	Leu	Asp	Leu	Thr	Asp	Tyr	Leu	Asp	Arg	Lys	Pro	Lys	Ala
	50					55				60					
Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Val	Ala	Met	Gly	Arg	Ala	Ile	Val
65				70				75						80	
Arg	Ser	Pro	Arg	Val	Phe	Leu	Met	Asp	Glu	Pro	Leu	Ser	Asn	Leu	Asp
			85					90					95		
Ala	Arg	Leu	Arg	Val	Arg	Thr	Arg	Ala	Gln	Ile	Ala	Glu	Leu	Gln	Arg
		100						105				110			
Arg	Leu	Gly	Thr	Thr	Thr	Val	Tyr	Val	Thr	His	Asp	Gln	Val	Glu	Ala
	115					120					125				
Met	Thr	Met	Gly	Asp	Arg	Val	Ala	Val	Leu	Cys	Ala	Gly	Lys	Leu	Gln
	130					135					140				
Gln	Val	Asp	Thr	Pro	Arg	Asn	Leu	Phe	Asp	His	Pro	Ala	Asn	Ala	
145					150					155					

<210> 2087

<211> 731

<212> DNA

<213> Homo sapiens

<400> 2087

gataattctc tacacggcat gagctgggga cgtacccccc ttgccaacgt cacctcacgg  
 60

tcgtaccgtg gtgattagca gctagccgag gcgctagccg ccatataaga ttcccaaatt  
 120  
 aaaagaaaaa gcattgcgtc ggccaagaat tgctgtcgct gctgcaacgg ctactgcgct  
 180  
 ggtcggatca atcgagcaa tcacccctc ccccgagcag aagctaactc caataggcca  
 240  
 cgctcggtag ctcaagccgc tatcgccacg gatggaaagg ggataatcaa caaggactgc  
 300  
 cgtgatgcag tcatcaacga tgcaaagctg cgtgccgcga ttgccggtgc gttggttaag  
 360  
 gctggattta gttccgccga cgcggtggct ctagcgccgc gtattgccag agaaatggca  
 420  
 aaagagggcg tcctcctcat caaccaccac aagctaaagg ctctcatcgg agcccagggtg  
 480  
 ggtctgctca ctgatgcgaa gatccagcgt gctgccgctg cagtggacct cggcatcaaa  
 540  
 gccactctag ctgcgacaat cattcccaac gcgctgcatt cagcggcatt caaggatgcg  
 600  
 gtggtcgcaa atcttgctgc cgccggtctg acaagaagtt ggcaaaggct acggctgtcg  
 660  
 ccattgccgc aactgcgctc aatcccgctc tcggggccgat cgcaaagact gaggccatta  
 720  
 aggtgagat c  
 731

&lt;210&gt; 2088

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2088

Met	Ala	Lys	Glu	Gly	Val	Leu	Leu	Ile	Asn	His	His	Lys	Leu	Lys	Ala
1				5					10				15		
Leu	Ile	Gly	Ala	Gln	Val	Gly	Leu	Leu	Thr	Asp	Ala	Lys	Ile	Gln	Arg
		20					25					30			
Ala	Ala	Ala	Ala	Val	Asp	Leu	Gly	Ile	Lys	Ala	Thr	Leu	Ala	Ala	Thr
		35					40					45			
Ile	Ile	Pro	Asn	Ala	Leu	His	Ser	Ala	Ala	Phe	Lys	Asp	Ala	Val	Val
	50					55					60				
Ala	Asn	Leu	Val	Ala	Ala	Gly	Leu	Thr	Arg	Ser	Trp	Gln	Arg	Leu	Arg
65					70					75				80	
Leu	Ser	Pro	Leu	Pro	Gln	Leu	Arg	Ser	Ile	Pro	Leu	Ser	Gly	Arg	Ser
			85					90						95	
Gln	Arg	Leu	Arg	Pro	Leu	Arg	Leu	Arg							
			100					105							

&lt;210&gt; 2089

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2089

accgggtgtgg accaggctca gctgcgcgac gccatgtttt cctaccttcc ccaccacaag  
 60

ctcggggaat tcgacatcga tctgttgctg gaccatcgcg attcccgctca gcccatcatc  
 120  
 ttcgacaccg accacttcga ggggtacgag cgccccgcc tcgtgctgca cgaagtcacc  
 180  
 gatcaacttg gccaaagcgtt ccttgatttg gaaggcccag agccggctct cggctgggaa  
 240  
 tcgttggtgg cgtctctcac gagtcttgct gactctatgg ggatccgtct gaccggcatt  
 300  
 accgattcga tcccg  
 315

<210> 2090

<211> 105

<212> PRT

<213> Homo sapiens

<400> 2090

Thr	Gly	Val	Asp	Gln	Ala	Gln	Leu	Arg	Asp	Ala	Met	Phe	Ser	Tyr	Leu
1				5					10					15	
Pro	His	His	Lys	Leu	Gly	Glu	Phe	Asp	Ile	Asp	Leu	Leu	Leu	Asp	His
			20					25					30		
Arg	Asp	Ser	Arg	Gln	Pro	Ile	Ile	Phe	Asp	Thr	Asp	His	Phe	Glu	Gly
		35				40					45				
Tyr	Glu	Arg	Pro	Arg	Leu	Val	Leu	His	Glu	Val	Thr	Asp	Gln	Leu	Gly
	50				55				60						
Gln	Ala	Phe	Leu	Val	Leu	Glu	Gly	Pro	Glu	Pro	Ala	Leu	Gly	Trp	Glu
65				70					75					80	
Ser	Leu	Val	Ala	Ser	Leu	Thr	Ser	Leu	Val	Asp	Ser	Met	Gly	Ile	Arg
			85					90						95	
Leu	Thr	Gly	Ile	Thr	Asp	Ser	Ile	Pro							
			100					105							

<210> 2091

<211> 322

<212> DNA

<213> Homo sapiens

<400> 2091

actcttgctc attgtctctg tctctgcgtt tttctctctg tctctctgtg tctctgtctc  
 60  
 tgtgtccctg tccagttctg tnnctgtgtg tgcgcgcac tctctctgtg tctctgtgng  
 120  
 agtctctgtc tcttttgtct ctgtctctct ctgtgtctct gccattttg gtctctgtct  
 180  
 tctttctctct gtgtgtctct ccatttctgt ctctcttctct ctgtctctct ccatttctgt  
 240  
 ctctgtctct tttctctctg tgtgtctctt ttgtctctct gtttctctgc gtgtctctgt  
 300  
 ccatttctgt cccttcaagc gt  
 322

<210> 2092

<211> 107

<212> PRT



<213> Homo sapiens

<400> 2092

```

Thr Leu Val His Cys Leu Cys Leu Cys Val Phe Leu Ser Val Ser Leu
 1             5             10             15
Cys Leu Cys Leu Cys Val Pro Val Gln Phe Cys Xaa Cys Val Cys Ala
 20             25             30
His Leu Ser Leu Cys Leu Cys Xaa Ser Leu Cys Leu Phe Cys Leu Cys
 35             40             45
Leu Ser Leu Cys Leu Cys Pro Phe Trp Ser Leu Leu Ser Phe Leu Cys
 50             55             60
Val Ser Leu His Phe Cys Leu Ser Ser Ser Val Ser Leu His Phe Cys
 65             70             75             80
Leu Cys Ser Phe Ser Leu Cys Val Ser Leu Leu Ser Leu Cys Phe Ser
 85             90             95
Ala Cys Leu Cys Pro Phe Leu Ser Leu His Ala
 100             105

```

<210> 2093

<211> 324

<212> DNA

<213> Homo sapiens

<400> 2093

```

gccggcggtca tgcaaacgat caaggtggcg caatttcgcc tctgccatag tcgaaaaatg
 60
tttgtggtgg cctacccgcg agagaccag gagatggtgc tcgatgcgca taaccgcgcc
 120
tttgcgttct ttggcggcgt accgcagcgg gttatctacg acaaccttaa aaccgcagt
 180
gatgcgatct tggtcggcaa ggatcgaatc ttcaaccggc gcttcctggc gttggcta
 240
cattacctgt ttgaacctgt agcctgtacg cctgctgctg gctgggagaa gggccaagtt
 300
gagaatcaag ttgcgaacat acgc
 324

```

<210> 2094

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2094

```

Ala Gly Val Met Gln Thr Ile Lys Val Ala Gln Phe Arg Leu Cys His
 1             5             10             15
Ser Arg Lys Met Phe Val Val Ala Tyr Pro Arg Glu Thr Gln Glu Met
 20             25             30
Val Leu Asp Ala His Asn Arg Ala Phe Ala Phe Phe Gly Gly Val Pro
 35             40             45
Gln Arg Val Ile Tyr Asp Asn Leu Lys Thr Ala Val Asp Ala Ile Leu
 50             55             60
Val Gly Lys Asp Arg Ile Phe Asn Arg Arg Phe Leu Ala Leu Ala Asn
 65             70             75             80
His Tyr Leu Phe Glu Pro Val Ala Cys Thr Pro Ala Ala Gly Trp Glu

```

85 90 95  
 Lys Gly Gln Val Glu Asn Gln Val Arg Asn Ile Arg  
 100 105

<210> 2095  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<400> 2095  
 cccgtcacag accaggaaga agcagacaat atgatcgctt ctttcgacac ttatgttcgc  
 60  
 accctgcccc ccgccgcaa tcttctgctt aaacaattcc atattgtgga tgttgccccg  
 120  
 cgcgtggtgg gcgtgggttc agtgggcacc cactccctgg tactgctact gtccggcccc  
 180  
 aatgatgaac ctcttgtgct gcaagtgaag gaagccctcc ccagtgtcct caccacccat  
 240  
 gggaaactgc cggatgcttt ttcggaactg tccgctgggg actcctccgg gctcctcccc  
 300  
 gataatcttg ataagcatat taaagccggc aatggctacc ggggtggtggc gtgccagcag  
 360  
 attctgcagg cccactcgga tccgctgctg ggggtggacgc gt  
 402

<210> 2096  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 2096  
 Pro Val Thr Asp Gln Glu Glu Ala Asp Asn Met Ile Ala Ser Phe Asp  
 1 5 10 15  
 Thr Tyr Val Arg Thr Leu Pro Pro Ala Ala Asn Leu Leu Leu Lys Gln  
 20 25 30  
 Phe His Ile Val Asp Val Ala Arg Arg Val Val Gly Val Gly Ser Val  
 35 40 45  
 Gly Thr His Ser Leu Val Leu Leu Ser Gly Pro Asn Asp Glu Pro  
 50 55 60  
 Leu Val Leu Gln Val Lys Glu Ala Leu Pro Ser Val Leu Thr Thr His  
 65 70 75 80  
 Gly Lys Leu Pro Asp Ala Phe Ser Glu Leu Ser Ala Gly Asp Ser Ser  
 85 90 95  
 Gly Leu Leu Pro Asp Asn Leu Asp Lys His Ile Lys Ala Gly Asn Gly  
 100 105 110  
 Tyr Arg Val Val Ala Cys Gln Gln Ile Leu Gln Ala His Ser Asp Pro  
 115 120 125  
 Leu Leu Gly Trp Thr Arg  
 130

<210> 2097  
 <211> 641  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 2097

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 120  
 gccatgagca aggaggaggc cgaccaggta ctgggcgtgc agctggggct gtctgtccgc  
 180  
 caccgcctc cagcctcac ttcaggctcc ctcccagcca ggctgtggcc tggccctcac  
 240  
 tgtcgctgct ccacatgctg tcaactcgtct cctccccagt cctgcctcat cctcacnccg  
 300  
 ccgtccctct gcgtgtcact ctctgctgt cctcactggt tcaggagccc ccagcctctc  
 360  
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 420  
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 480  
 ctccagctgg cccttagttt gagccgagaa gagcatgata aggtcagagc agcctccctg  
 540  
 tccctgcccc tgccaggggc tccccctaga ccagccccgt cgccccctcc taagtcaccc  
 600  
 cccaccatcc tgctggggcc gaagcccaca ggctcacgcg t  
 641

&lt;210&gt; 2098

&lt;211&gt; 213

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2098

Xaa Phe Leu Thr Arg Pro Pro Ala Ser Ser Ala Ala Val Gly Ser Gly  
 1 5 10 15  
 Pro Pro Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu  
 20 25 30  
 Glu Leu Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp  
 35 40 45  
 Gln Val Leu Gly Val Gln Leu Gly Leu Ser Val Arg His Pro Pro Pro  
 50 55 60  
 Arg Leu Thr Ser Gly Ser Leu Pro Ala Arg Arg Gly Pro Gly Pro His  
 65 70 75 80  
 Cys Arg Cys Ser Thr Cys Cys His Ser Ser Pro Pro Gln Ser Cys Leu  
 85 90 95  
 Ile Leu Thr Pro Pro Ser Leu Cys Val Ser Leu Ser Ala Cys Pro His  
 100 105 110  
 Trp Phe Arg Asp Pro Gln Pro Leu Phe Ile Arg Leu Tyr Leu Thr Leu  
 115 120 125  
 Ala Leu Pro Leu Thr Leu Pro Leu Ala Pro Pro Val Met Pro Leu Thr  
 130 135 140  
 Leu Ser Leu Pro Gln Pro Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln  
 145 150 155 160  
 Leu Gln Leu Ala Leu Ser Leu Ser Arg Glu Glu His Asp Lys Val Arg  
 165 170 175  
 Ala Ala Ser Leu Ser Leu Pro Leu Pro Gly Ala Pro Leu Arg Pro Ala

180 185 190  
 Pro Ser Pro Leu Pro Lys Ser Pro Pro Thr Ile Leu Leu Gly Pro Lys  
 195 200 205  
 Pro Thr Gly Ser Arg  
 210

<210> 2099  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens

<400> 2099  
 acgcgtgtgc cctgtcccct gccagacatg gacagcacct gcccacaggg gtgctcagt  
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 gaggcagtgc ccagggtgc tgtgcccctg cgtgtaccct gtcctctgcc agacgcggac  
 120  
 agcacctgcc cacggggtgc tcagtggagg cagtgccag ggctgctgtg cccacgtgtg  
 180  
 tgccctcaga catccctccc cagacacttg ctgcatgacc caggaggtgg caggcagtgg  
 240  
 cagtattctg ttcaggtgag ctcagaggtg gcaggtgcct ggctgcggcc ctgcctcact  
 300  
 ccgacagcct ctgcctccag tccactggct catccacat ggctga  
 347

<210> 2100  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 2100  
 Met Asp Ser Thr Cys Pro Gln Gly Cys Ser Val Glu Ala Val Pro Arg  
 1 5 10 15  
 Ala Ala Val Pro Met Arg Val Pro Cys Pro Leu Pro Asp Ala Asp Ser  
 20 25 30  
 Thr Cys Pro Arg Gly Ala Gln Trp Arg Gln Cys Pro Gly Leu Leu Cys  
 35 40 45  
 Pro Arg Val Cys Pro Gln Thr Ser Leu Pro Arg His Leu Leu His Asp  
 50 55 60  
 Pro Gly Gly Gly Arg Gln Trp Gln Tyr Ser Val Gln Val Ser Ser Glu  
 65 70 75 80  
 Val Ala Gly Ala Trp Leu Arg Pro Cys Leu Thr Pro Thr Ala Ser Ala  
 85 90 95  
 Ser Ser Pro Leu Ala His Pro Thr Trp Pro  
 100 105

<210> 2101  
 <211> 549  
 <212> DNA  
 <213> Homo sapiens

<400> 2101  
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 60

acgttttcgat ggggcgtgac gaattgcccc tgccgacggc gacctctctg gctctgtgtg  
 120  
 ggttgaacca cgacaagaat gagttgctgg ccagccttct catccacctt gacgagctat  
 180  
 taacagtgtg gttggagacc ggaacggtgc gggatcagta tgtggcccg tgtgacacca  
 240  
 ttggtactcc ggtccgtctg accttcgacc cagaaatcgt ggggtggtggt gagggggcca  
 300  
 ttgagggcat cgggtgtcgac gttgacgttg atggcgctat cgtggtggaa acttctgacg  
 360  
 ggcgtcgcag tttcaacgct gctgacgttc atcatttgcg aaccaggtga gttccgctac  
 420  
 ggcgtcctga gcgttccac catctagact gctgactatg acgaccaca ttttggccct  
 480  
 tgggtggtggc ggtttctcga tgtcgaaccg cggtgagcct accgctctcg accgtcacat  
 540  
 ccctgacct  
 549

&lt;210&gt; 2102

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2102

Met	Gly	Arg	Asp	Glu	Leu	Pro	Leu	Pro	Thr	Ala	Thr	Ser	Leu	Ala	Leu
1				5					10					15	
Cys	Gly	Leu	Asn	His	Asp	Lys	Asn	Glu	Leu	Leu	Ala	Ser	Leu	Leu	Ile
			20					25					30		
His	Leu	Asp	Glu	Leu	Leu	Thr	Val	Trp	Leu	Glu	Thr	Gly	Thr	Val	Arg
			35				40					45			
Asp	Gln	Tyr	Val	Ala	Arg	Cys	Asp	Thr	Ile	Gly	Thr	Pro	Val	Arg	Leu
	50					55				60					
Thr	Phe	Asp	Pro	Glu	Ile	Val	Gly	Gly	Gly	Glu	Gly	Ala	Ile	Glu	Gly
65				70						75				80	
Ile	Gly	Val	Asp	Val	Asp	Val	Asp	Gly	Ala	Ile	Val	Val	Glu	Thr	Ser
			85					90					95		
Asp	Gly	Arg	Arg	Ser	Phe	Asn	Ala	Ala	Asp	Val	His	His	Leu	Arg	Thr
			100					105						110	
Arg															

&lt;210&gt; 2103

&lt;211&gt; 459

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2103

nnacgcgtga cttatacacc gggacgcaat gcgacggcaa cggcagagca cactatcgcc  
 60  
 atgattatgg cggcagtgcg acagatcccc gccaccatg agttactcgc ttcagggggtt  
 120  
 tgggaggggg acgcatatcg gtacgaccag gttggtatgg aaatcaaagg gaatgacgtc  
 180

ggatcgtcg gatgcggagc ggtcgggtgc cgggttgccg ctgtgatggc ggccatgggt  
 240  
 gcgaccgtgc gtgtcttcga cccgtgggcc actcctgatt cttttccagc tggcgtgatg  
 300  
 gcatgtgatg atctcgatga ggttctgagg ctccagccgca tcctcactct ccacgctcgt  
 360  
 gccaacgagg acaaccgtca catgattggc gttgaacaat tagctgagat gcctgatggc  
 420  
 tccgtcctcg tcaactgtgc ccgtggctcg ctggtcgac  
 459

<210> 2104

<211> 153

<212> PRT

<213> Homo sapiens

<400> 2104

Xaa	Arg	Val	Thr	Tyr	Thr	Pro	Gly	Arg	Asn	Ala	Thr	Ala	Thr	Ala	Glu
1			5					10					15		
His	Thr	Ile	Ala	Met	Ile	Met	Ala	Ala	Val	Arg	Gln	Ile	Pro	Ala	His
		20					25					30			
His	Glu	Leu	Leu	Ala	Ser	Gly	Val	Trp	Glu	Gly	Asp	Ala	Tyr	Arg	Tyr
	35					40					45				
Asp	Gln	Val	Gly	Met	Glu	Ile	Lys	Gly	Asn	Asp	Val	Gly	Ile	Val	Gly
	50					55				60					
Cys	Gly	Ala	Val	Gly	Cys	Arg	Val	Ala	Ala	Val	Met	Ala	Ala	Met	Gly
65					70					75				80	
Ala	Thr	Val	Arg	Val	Phe	Asp	Pro	Trp	Ala	Thr	Pro	Asp	Ser	Phe	Pro
			85					90					95		
Ala	Gly	Val	Met	Ala	Cys	Asp	Asp	Leu	Asp	Glu	Val	Leu	Arg	Leu	Ser
			100					105					110		
Arg	Ile	Leu	Thr	Leu	His	Ala	Arg	Ala	Asn	Glu	Asp	Asn	Arg	His	Met
		115					120					125			
Ile	Gly	Val	Glu	Gln	Leu	Ala	Glu	Met	Pro	Asp	Gly	Ser	Val	Leu	Val
	130					135					140				
Asn	Cys	Ala	Arg	Gly	Ser	Leu	Val	Asp							
145						150									

<210> 2105

<211> 4057

<212> DNA

<213> Homo sapiens

<400> 2105

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 120  
 cccctatatg gctccagtcg gttttggggg gggcagctaa gtgggggagg gggaacacaa  
 180  
 aagtttgggc aaaacattaa cctgacaaag cttgattccg gaaaaaatc cctcaagagc  
 240  
 gcaaggccag cttagccaac tggcagctga gtggaaaggt tcagtcctct cgggcagctc  
 300

cgggtggcacc tagaggggag aggggtgcagg ctttgaagcc agaaagacat ggatgcaagt  
360  
cttactttgc ttcttgctgt taccagttgg cctgacctta ggaaatgtta tttaatctct  
420  
ctccagttgt ttccccctgga gaaagccctg tcagcctgag gatccaagac gcgtacgtaa  
480  
agtgtctgat ttcagccagt gtcccttctt gtcccttctt ggggtgtgtg tcggttgccc  
540  
tgagcgaccg gccatgggac tctgtcgtga taaccaagct tcaggggtgtg ggaagaggac  
600  
agtcaagtgt tccttggggc atcactcggg aacatcatgg gcataaaca aagtactcag  
660  
tcttcaaggt cataaagtaa ccagagtgtta ttccttttgt tttcagatct cttacctcag  
720  
ctagaagctc cgagttctct tactcccagc agtgaactca gcagcccagg ccaaagttag  
780  
ctcactaaca tggatcttgc tgcactcttc tctgacacac ctgccaatgc tagtggttct  
840  
gcaggtgggt cggatgaggg tctgaactcc ggaatcctga ctattgacgt cacttctgtg  
900  
agtcctcttc tgggagggaa cctccctgct aataatagct ccctagggcc gatggaaccc  
960  
ctggctctgg tggccacag tgatattccc ccaagcctgg acagccctct ggttctcggg  
1020  
acagcagcca cggttctgca gcagggcagc ttcagtgtgg atgacgtgca gactgtgagt  
1080  
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1140  
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1260  
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1380  
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1680  
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1740  
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1800  
accaaactct tttttaaata tagaattaac aagaaaaaaa aaaggggtggg gtttatgagc  
1860  
cttagttctt ggaggattat aagagtactt cccagtttt gaggctggac agttaatata  
1920

ctttatatca attatacatt taatataatt taatttaaaa taatttaaag attcttagga  
1980  
gatagtctga ctttcctgac ctagatggga atgatcagat agggattttt tttgtggcac  
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2280  
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2340  
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2400  
aagctccctg gtgcagctgc agctgtgggt ggaggtagag aagccagcaa gacctgggc  
2460  
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2520  
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2580  
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2640  
cagctgatgt cctctgagta ctgtctgact cctcaggca agttcctgaa ttcagtacca  
2700  
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2760  
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2820  
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2880  
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3180  
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3360  
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3480  
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3540



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 3660  
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 3720  
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 3780  
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 3840  
 ggaaactgct aaatcttttt ctaaaaacta acagtggatt tttaaaatat attgtttttt  
 3900  
 gtgtatttca tttgtccttt gtatttatct aaaaggggtg atatgatttt atatcttgct  
 3960  
 ctctattcct aatagtatta tgacttctta tttaaaataa ataacaattg ccggttttct  
 4020  
 gttaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa  
 4057

&lt;210&gt; 2106

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2106

Ser Asn Gln Ser Val Phe Leu Leu Phe Ser Asp Leu Leu Pro Gln Leu  
 1 5 10 15  
 Glu Ala Pro Ser Ser Leu Thr Pro Ser Ser Glu Leu Ser Ser Pro Gly  
 20 25 30  
 Gln Ser Glu Leu Thr Asn Met Asp Leu Ala Ala Leu Phe Ser Asp Thr  
 35 40 45  
 Pro Ala Asn Ala Ser Gly Ser Ala Gly Gly Ser Asp Glu Ala Leu Asn  
 50 55 60  
 Ser Gly Ile Leu Thr Ile Asp Val Thr Ser Val Ser Ser Ser Leu Gly  
 65 70 75 80  
 Gly Asn Leu Pro Ala Asn Asn Ser Ser Leu Gly Pro Met Glu Pro Leu  
 85 90 95  
 Val Leu Val Ala His Ser Asp Ile Pro Pro Ser Leu Asp Ser Pro Leu  
 100 105 110  
 Val Leu Gly Thr Ala Ala Thr Val Leu Gln Gln Gly Ser Phe Ser Val  
 115 120 125  
 Asp Asp Val Gln Thr Val Ser Ala Gly Ala Leu Gly Cys Leu Val Ala  
 130 135 140  
 Leu Pro Met Lys Asn Leu Ser Asp Asp Pro Leu Ala Leu Thr Ser Asn  
 145 150 155 160  
 Ser Asn Leu Ala Ala His Ile Thr Thr Pro Thr Ser Ser Ser Thr Pro  
 165 170 175  
 Arg Glu Asn Ala Ser Val Pro Glu Leu Leu Ala Pro Ile Lys Val Glu  
 180 185 190  
 Pro Asp Ser Pro Ser Arg Pro Gly Ala Val Gly Gln Gln Glu Gly Ser  
 195 200 205  
 His Gly Leu Pro Gln Ser Thr Leu Pro Ser Pro Ala Glu Gln His Gly  
 210 215 220  
 Ala Gln Asp Thr Glu Leu Ser Ala Gly Thr Gly Asn Phe Tyr Leu Val

225 230 235 240

<210> 2107  
<211> 305  
<212> DNA  
<213> Homo sapiens

<400> 2107  
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agtcctggct tggtctcgt tccagatctt aatgattctt tgagtccagt ctcaggggag  
120  
gcctcaggcc tgggtgtctga aaacaccccc agacctgatg acagcagagc tatcgctcca  
180  
gcctccctcc aaatcaccag ttcttgttct ggtgaacccc tggacctgga ttccaaggat  
240  
gtctcaaggc ctgactcaca ggggcgcctc tgtccagcct caaaccccat tctggcccn  
300  
ccnccn  
305

<210> 2108  
<211> 92  
<212> PRT  
<213> Homo sapiens

<400> 2108  
Met Ala Gln Val Pro Met Leu Asn Leu Leu Pro Ser Pro Gly Leu Ala  
1 5 10 15  
Leu Val Pro Asp Leu Asn Asp Ser Leu Ser Pro Val Ser Gly Glu Ala  
20 25 30  
Ser Gly Leu Val Ser Glu Asn Thr Pro Arg Pro Asp Asp Ser Arg Ala  
35 40 45  
Ile Ala Pro Ala Ser Leu Gln Ile Thr Ser Ser Cys Ser Gly Glu Pro  
50 55 60  
Leu Asp Leu Asp Ser Lys Asp Val Ser Arg Pro Asp Ser Gln Gly Arg  
65 70 75 80  
Leu Cys Pro Ala Ser Asn Pro Ile Leu Ala Xaa Pro  
85 90

<210> 2109  
<211> 700  
<212> DNA  
<213> Homo sapiens

<400> 2109  
naccggtcac ccacgcagac catggcagcc gccgacggtt cgctcttcga caacccagg  
60  
acgttctcca gacgtccccc agcccaggcg agtcggcaag caaaggctac gaaaagaaaa  
120  
taccaagcgt ccagtgaggc tccccagcg aaacggagga acgaaacttc atttctccca  
180  
gccaaagaaa ctagtgttaa agaaactcag aggactttta aggggaacgc acaaaaaaatg  
240

ttttctccaa agaagcattc ggtagcaca agtgatagaa accaggagga gagacagtgc  
 300  
 attaaagactt catcactgtt taaaaacaac cctgacattc cagaactcca cagacctgtg  
 360  
 gtaaagcagg tgcaagaaaa agtgtttact tcagctgctt ttcattgagct gggcctccac  
 420  
 ccacatttaa tttccacaat aaatacgggc ttaaaaatgt ctagtatgac cagtgttcag  
 480  
 aagcaaagta ttcctgtgtt gctggaaggc agagatgctc tcgtgagatc ccagacgggc  
 540  
 tcaggtaaaa ttcttgcceta ttgcatccct gtgggtccagt cccctcaagc aatggagtca  
 600  
 aaaatacagc gcagtgatgg cccctatgcc ctggtgctcg tgccaacgag agaggtaagc  
 660  
 aggcctccctt ttgggacaag ttttaagcac atgctttcat  
 700

<210> 2110

<211> 233

<212> PRT

<213> Homo sapiens

<400> 2110

Xaa	Ala	Ser	Pro	Thr	Gln	Thr	Met	Ala	Ala	Ala	Asp	Gly	Ser	Leu	Phe
1				5				10						15	
Asp	Asn	Pro	Arg	Thr	Phe	Ser	Arg	Arg	Pro	Pro	Ala	Gln	Ala	Ser	Arg
			20					25						30	
Gln	Ala	Lys	Ala	Thr	Lys	Arg	Lys	Tyr	Gln	Ala	Ser	Ser	Glu	Ala	Pro
		35					40					45			
Pro	Ala	Lys	Arg	Arg	Asn	Glu	Thr	Ser	Phe	Leu	Pro	Ala	Lys	Lys	Thr
		50				55					60				
Ser	Val	Lys	Glu	Thr	Gln	Arg	Thr	Phe	Lys	Gly	Asn	Ala	Gln	Lys	Met
65					70					75				80	
Phe	Ser	Pro	Lys	Lys	His	Ser	Val	Ser	Thr	Ser	Asp	Arg	Asn	Gln	Glu
				85					90					95	
Glu	Arg	Gln	Cys	Ile	Lys	Thr	Ser	Ser	Leu	Phe	Lys	Asn	Asn	Pro	Asp
			100					105					110		
Ile	Pro	Glu	Leu	His	Arg	Pro	Val	Val	Lys	Gln	Val	Gln	Glu	Lys	Val
		115					120					125			
Phe	Thr	Ser	Ala	Ala	Phe	His	Glu	Leu	Gly	Leu	His	Pro	His	Leu	Ile
		130				135					140				
Ser	Thr	Ile	Asn	Thr	Val	Leu	Lys	Met	Ser	Ser	Met	Thr	Ser	Val	Gln
145				150						155				160	
Lys	Gln	Ser	Ile	Pro	Val	Leu	Leu	Glu	Gly	Arg	Asp	Ala	Leu	Val	Arg
			165						170					175	
Ser	Gln	Thr	Gly	Ser	Gly	Lys	Ile	Leu	Ala	Tyr	Cys	Ile	Pro	Val	Val
		180					185						190		
Gln	Ser	Leu	Gln	Ala	Met	Glu	Ser	Lys	Ile	Gln	Arg	Ser	Asp	Gly	Pro
		195					200						205		
Tyr	Ala	Leu	Val	Leu	Val	Pro	Thr	Arg	Glu	Val	Ser	Arg	Leu	Pro	Phe
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225					230										

<210> 2111  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<400> 2111  
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 gaaggcctgg ttgagcgtgt gcgcagtgtt cttgagcgtc tgcgtgcccc agagcgcgca  
 240  
 atcatgcagc tctgcgtacg tgatgcacgc atgccgcgtg ccgacttctt gcgccagttt  
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 339

<210> 2112  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 2112  
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 20 25 30  
 Gly Arg Gly Asn Lys Leu Ala Ile Ala Glu Leu Val Ala Leu Ala Glu  
 35 40 45  
 Leu Phe Met Pro Ile Lys Leu Val Pro Lys Gln Phe Glu Gly Leu Val  
 50 55 60  
 Glu Arg Val Arg Ser Ala Leu Glu Arg Leu Arg Ala Gln Glu Arg Ala  
 65 70 75 80  
 Ile Met Gln Leu Cys Val Arg Asp Ala Arg Met Pro Arg Ala Asp Phe  
 85 90 95  
 Leu Arg Gln Phe Pro Gly Asn Glu Val Asp Glu Ser Trp Thr Asp Ala  
 100 105 110  
 Leu

<210> 2113  
 <211> 2329  
 <212> DNA  
 <213> Homo sapiens

<400> 2113  
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 120  
 aaagggaagt tgacattaga tagcagtttt aacatcgcca gccagcttc ccaggcctgg  
 180

attttgcact tctgtcaaaa actgagaaac caaacattct tttaccagac tgatgaacag  
240  
gacttcacca gctgcttcat tgagacattc aaacagtgga tggaaaacca ggactgtgat  
300  
gagcctgccc tgtacccatg ctgcagccac tggagcttcc cctacaagca agagattttt  
360  
gaactgtgca tcaagagagc tatcatggag ctggaaagga gtacagggta ccatttggat  
420  
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480  
ttccagagta cctacctctt cacactggct tatgaaaaga tgcatacagt ttataaagag  
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tttgtcagca atctggagtt ctatgacctc caggatagcc tctccgatgg caccctcatt  
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900  
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1200  
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1260  
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1320  
aagaccatt atgaagagac ccacatctgc tctgaatttt tcaacagcca agcaaagaat  
1380  
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1440  
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1560  
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1620  
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1680  
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1740  
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1800

gaaaaaattg gcaagaccaa tgtacacagt cttcagagga gcatagaaga gcatcttcca  
 1860  
 aagatggcag agccatcgtc atttgtctgc agaagcactg gatcggtact caaaacgtgt  
 1920  
 tgcgaccccg agaataaaca aagggaactc tgtaaaaata gagacgtgag caatctggag  
 1980  
 agcagtggag ggactgaaaa caaggcagga gggaaagtgg agctgagctt gtcacagacg  
 2040  
 gatgcaagtg tgaactcaga acatttcaat cagaatgaac caaaagtcct atttaatcat  
 2100  
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 2160  
 gtgagagtga agtgcaattc tgtggactgt caaatgccaa acatggaagc caatgtgcct  
 2220  
 gctgtattaa cacactcgga actttctggt gaaagtttgt taataaaaaac actataataa  
 2280  
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 2329

<210> 2114

<211> 758

<212> PRT

<213> Homo sapiens

<400> 2114

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Leu	His	Met	Pro	Ile	Thr	Val	Ile	Trp	Gly	Val	Ser	Pro	Glu	Asp	Asn
		20						25					30		
Gly	Asn	Pro	Leu	Asn	Pro	Lys	Ser	Lys	Gly	Lys	Leu	Thr	Leu	Asp	Ser
		35				40					45				
Ser	Phe	Asn	Ile	Ala	Ser	Pro	Ala	Ser	Gln	Ala	Trp	Ile	Leu	His	Phe
	50					55				60					
Cys	Gln	Lys	Leu	Arg	Asn	Gln	Thr	Phe	Phe	Tyr	Gln	Thr	Asp	Glu	Gln
65					70					75				80	
Asp	Phe	Thr	Ser	Cys	Phe	Ile	Glu	Thr	Phe	Lys	Gln	Trp	Met	Glu	Asn
			85					90					95		
Gln	Asp	Cys	Asp	Glu	Pro	Ala	Leu	Tyr	Pro	Cys	Cys	Ser	His	Trp	Ser
			100					105					110		
Phe	Pro	Tyr	Lys	Gln	Glu	Ile	Phe	Glu	Leu	Cys	Ile	Lys	Arg	Ala	Ile
			115				120						125		
Met	Glu	Leu	Glu	Arg	Ser	Thr	Gly	Tyr	His	Leu	Asp	Ser	Lys	Thr	Pro
			130				135					140			
Gly	Pro	Arg	Phe	Asp	Ile	Asn	Asp	Thr	Ile	Arg	Ala	Val	Val	Leu	Glu
145					150					155				160	
Phe	Gln	Ser	Thr	Tyr	Leu	Phe	Thr	Leu	Ala	Tyr	Glu	Lys	Met	His	Gln
			165					170					175		
Phe	Tyr	Lys	Glu	Val	Asp	Ser	Trp	Ile	Ser	Ser	Glu	Leu	Ser	Ser	Ala
			180					185					190		
Pro	Glu	Gly	Leu	Ser	Asn	Gly	Trp	Phe	Val	Ser	Asn	Leu	Glu	Phe	Tyr
			195				200						205		
Asp	Leu	Gln	Asp	Ser	Leu	Ser	Asp	Gly	Thr	Leu	Ile	Ala	Met	Gly	Leu
		210					215					220			
Ser	Val	Ala	Val	Ala	Phe	Ser	Val	Met	Leu	Leu	Thr	Thr	Trp	Asn	Ile

225                      230                      235                      240  
 Ile Ile Ser Leu Tyr Ala Ile Ile Ser Ile Ala Gly Thr Ile Phe Val  
                                  245                      250                      255  
 Thr Val Gly Ser Leu Val Leu Leu Gly Trp Glu Leu Asn Val Leu Glu  
                                  260                      265                      270  
 Ser Val Thr Ile Ser Val Ala Val Gly Leu Ser Val Asp Phe Ala Val  
                                  275                      280                      285  
 His Tyr Gly Val Ala Tyr Arg Leu Ala Pro Asp Pro Asp Arg Glu Gly  
                                  290                      295                      300  
 Lys Val Ile Phe Ser Leu Ser Arg Val Gly Ser Ala Met Ala Met Ala  
 305                                   310                      315                      320  
 Ala Leu Thr Thr Phe Val Ala Gly Ala Met Met Ile Pro Ser Thr Val  
                                  325                      330                      335  
 Leu Ala Tyr Thr Gln Leu Gly Thr Phe Met Met Leu Ile Met Cys Ile  
                                  340                      345                      350  
 Ser Trp Ala Phe Ala Thr Phe Phe Phe Gln Cys Met Cys Arg Cys Leu  
                                  355                      360                      365  
 Gly Pro Gln Gly Thr Cys Gly Gln Ile Pro Leu Pro Lys Lys Leu Gln  
                                  370                      375                      380  
 Cys Ser Ala Phe Ser His Ala Leu Ser Thr Ser Pro Ser Asp Lys Gly  
 385                                   390                      395                      400  
 Gln Ser Lys Thr His Thr Ile Asn Ala Tyr His Leu Asp Pro Arg Gly  
                                  405                      410                      415  
 Pro Lys Ser Glu Leu Glu His Glu Phe Tyr Glu Leu Glu Pro Leu Ala  
                                  420                      425                      430  
 Ser His Ser Cys Thr Ala Pro Glu Lys Thr Thr Tyr Glu Glu Thr His  
                                  435                      440                      445  
 Ile Cys Ser Glu Phe Phe Asn Ser Gln Ala Lys Asn Leu Gly Met Pro  
                                  450                      455                      460  
 Val His Ala Ala Tyr Asn Ser Glu Leu Ser Lys Ser Thr Glu Ser Asp  
 465                                   470                      475                      480  
 Thr Gly Ser Ala Leu Leu Gln Pro Pro Leu Glu Gln His Thr Val Cys  
                                  485                      490                      495  
 His Phe Phe Ser Leu Asn Gln Arg Cys Ser Cys Pro Asp Ala Tyr Lys  
                                  500                      505                      510  
 His Leu Asn Tyr Gly Pro His Ser Cys Gln Gln Met Gly Asp Cys Leu  
                                  515                      520                      525  
 Cys His Gln Cys Ser Pro Thr Thr Ser Ser Phe Val Gln Ile Gln Asn  
                                  530                      535                      540  
 Gly Val Ala Pro Leu Lys Ala Thr His Gln Ala Val Glu Gly Phe Val  
 545                                   550                      555                      560  
 His Pro Ile Thr His Ile His His Cys Pro Cys Leu Gln Gly Arg Val  
                                  565                      570                      575  
 Lys Pro Ala Gly Met Gln Asn Ser Leu Pro Arg Asn Phe Phe Leu His  
                                  580                      585                      590  
 Pro Val Gln His Ile Gln Ala Gln Glu Lys Ile Gly Lys Thr Asn Val  
                                  595                      600                      605  
 His Ser Leu Gln Arg Ser Ile Glu Glu His Leu Pro Lys Met Ala Glu  
                                  610                      615                      620  
 Pro Ser Ser Phe Val Cys Arg Ser Thr Gly Ser Leu Leu Lys Thr Cys  
 625                                   630                      635                      640  
 Cys Asp Pro Glu Asn Lys Gln Arg Glu Leu Cys Lys Asn Arg Asp Val  
                                  645                      650                      655  
 Ser Asn Leu Glu Ser Ser Gly Gly Thr Glu Asn Lys Ala Gly Gly Lys

<400> 2116																
Met	Gly	Thr	Cys	Phe	Pro	Ala	Pro	Glu	Ser	Pro	Pro	Ser	Pro	His	Ile	
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Gly	Asn	Pro	Val	Gly	Ser	Arg	Ser	Ser	Glu	Pro	Arg	Arg	Ala	Glu	Ala	
			20					25					30			
Gly	Gly	Pro	Pro	Ala	Pro	Ala	Ala	His	Arg	Leu	Gly	Met	Glu	Met	Pro	
		35					40					45				
Ser	Pro	Gly	Ser	Ser	Arg	Gln	Arg	Thr	Arg	Glu	Met	Thr	Thr	Glu	Arg	
	50					55				60						
His	Thr	Pro	Ala	Pro	Ser	His	Ser	Ser	Pro	Gln	Ile	Ser	Pro	Ser	Asp	
65					70					75					80	
Ala	Ala	Val	Arg	Phe	Asn	Val	Ser	Phe	Leu	Phe	Arg	Ala	Gly	Gly	Cys	



85 90 95  
 Gly Leu Gly Gly Leu Gln Gly Pro Lys Thr Ser Arg Trp Ala Gln Glu  
 100 105 110  
 Gly Asp Arg His Pro Pro Phe Gln Ile Leu Glu Tyr Pro Glu Ala Pro  
 115 120 125  
 Ser Gly Arg Glu Gly Gly Val Ser Gly Glu Pro Ala Pro Arg Pro Glu  
 130 135 140  
 Thr Arg  
 145

&lt;210&gt; 2117

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2117

nnacgcgttg gggagacgac ggtgaccttc ccagcaagct catcgagga tgaacaatc  
 60  
 cgcgccagcg ttaagacctt ctgcggggct gtcaccgccg atctggagaa gtgtggaccg  
 120  
 atcaggtgac actcgcggta gactgaatag atgcctgagt ctgaagacac tgtgtggctg  
 180  
 acccaagagg ccttcgataa gctcaccag gagctggagt acctcaaagg cgaaggccgc  
 240  
 accgtcattg ccaacaagat tgccgacgcc cgttcggaag gcgaccttc tgagaacggc  
 300  
 ggctaccatg ccgcccgtga ggagcagggg caggccgagg cccgcatccg tcaactcgag  
 360

&lt;210&gt; 2118

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2118

Met Pro Glu Ser Glu Asp Thr Val Trp Leu Thr Gln Glu Ala Phe Asp  
 1 5 10 15  
 Lys Leu Thr Gln Glu Leu Glu Tyr Leu Lys Gly Glu Gly Arg Thr Val  
 20 25 30  
 Ile Ala Asn Lys Ile Ala Asp Ala Arg Ser Glu Gly Asp Leu Ser Glu  
 35 40 45  
 Asn Gly Gly Tyr His Ala Ala Arg Glu Glu Gln Gly Gln Ala Glu Ala  
 50 55 60  
 Arg Ile Arg Gln Leu Glu  
 65 70

&lt;210&gt; 2119

&lt;211&gt; 465

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2119

nacgcgtgaa gggcgctgtg cggcctctca ctggcgagc ctgcactgcc gctgccgcct  
 60

cgccccgccc ttgccttggc gttgtctctg gcactgtggc ggactgacca cggccccggg  
 120  
 atgggctgca agggagacgc gagcggagtt tgctataaaa tgggagttct ggttgtaact  
 180  
 actgttctgt ggctgttctc ctcagtaaag gccgactcaa aagccattac aacctctctt  
 240  
 acaacaaaat ggttttccac tccattgttg ttagaagcca gtgagttttt agcagaagac  
 300  
 agtcaagaga aattttggaa tttttagaaa gccagtcaaa atattggatc atcagatcat  
 360  
 gacggtagcg attattccta ctatcatgca atattggagg ctgcatttca gtttctgtca  
 420  
 cccctccagc agaatttgtt taaattttgt ctgtcccttc acgcg  
 465

<210> 2120

<211> 115

<212> PRT

<213> Homo sapiens

<400> 2120

Met	Gly	Cys	Lys	Gly	Asp	Ala	Ser	Gly	Val	Cys	Tyr	Lys	Met	Gly	Val
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Leu	Val	Val	Leu	Thr	Val	Leu	Trp	Leu	Phe	Ser	Ser	Val	Lys	Ala	Asp
			20					25					30		
Ser	Lys	Ala	Ile	Thr	Thr	Ser	Leu	Thr	Thr	Lys	Trp	Phe	Ser	Thr	Pro
			35				40					45			
Leu	Leu	Leu	Glu	Ala	Ser	Glu	Phe	Leu	Ala	Glu	Asp	Ser	Gln	Glu	Lys
			50				55				60				
Phe	Trp	Asn	Phe	Val	Glu	Ala	Ser	Gln	Asn	Ile	Gly	Ser	Ser	Asp	His
65					70				75					80	
Asp	Gly	Thr	Asp	Tyr	Ser	Tyr	Tyr	His	Ala	Ile	Leu	Glu	Ala	Ala	Phe
				85				90						95	
Gln	Phe	Leu	Ser	Pro	Leu	Gln	Gln	Asn	Leu	Phe	Lys	Phe	Cys	Leu	Ser
			100					105					110		
Leu	His	Ala													
															115

<210> 2121

<211> 336

<212> DNA

<213> Homo sapiens

<400> 2121

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 tgtggctctc cttatgaaac taatggccct aaaacctttt acatttttgt agtcagaagt  
 120  
 ggaggttctt ttgttacaaa atacaacaag acaaactgtc agttttatgt agataatctc  
 180  
 tactattcaa ctgactatga gtttctgggc tcttttcaca atggagtgtc cgagggagat  
 240  
 tcagttataa gaaatgagtc aacaaatttt aatgctaaag ccctgattat attcctggtg  
 300

tttctgatta ttgtgacatc aatagccttg cttgtt  
336

<210> 2122

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2122

Pro	Asp	Lys	Val	Asn	Gly	Met	Lys	Thr	Ser	Arg	Pro	Thr	Asp	Asn	Ser
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Ile	Asn	Val	Thr	Cys	Gly	Pro	Pro	Tyr	Glu	Thr	Asn	Gly	Pro	Lys	Thr
		20						25					30		
Phe	Tyr	Ile	Leu	Val	Val	Arg	Ser	Gly	Gly	Ser	Phe	Val	Thr	Lys	Tyr
	35					40					45				
Asn	Lys	Thr	Asn	Cys	Gln	Phe	Tyr	Val	Asp	Asn	Leu	Tyr	Tyr	Ser	Thr
	50				55						60				
Asp	Tyr	Glu	Phe	Leu	Val	Ser	Phe	His	Asn	Gly	Val	Tyr	Glu	Gly	Asp
65				70					75					80	
Ser	Val	Ile	Arg	Asn	Glu	Ser	Thr	Asn	Phe	Asn	Ala	Lys	Ala	Leu	Ile
			85					90					95		
Ile	Phe	Leu	Val	Phe	Leu	Ile	Ile	Val	Thr	Ser	Ile	Ala	Leu	Leu	Val
		100						105					110		

<210> 2123

<211> 426

<212> DNA

<213> Homo sapiens

<400> 2123

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cagcaactga ccgacgaact ggaagcgatg ctctgcgcgc ccacagggtta tgacgcgatc  
120  
tccttgacgc cgaacgctgg ctcccagggc gagtacgcgc gtctgctggc gatccgcgct  
180  
taccaccaga gccgtggcga tgagcgctgc gacatctgcc tgattccgtc ctctgcccac  
240  
ggcaccaacc cggcaaccgc caacatggcc ggcatgcgcg tggtcgtgac cgcttgcgac  
300  
gcccgcggca acgtcgacat cgaagacctg cgcgccaagg ctatcgagca ccgcgaacac  
360  
ctcgcggcgc tgatgatcac ctaccgctcg acccagggcg tgttcgaaga aggcacccgc  
420  
gagatc  
426

<210> 2124

<211> 142

<212> PRT

<213> Homo sapiens

<400> 2124

Asn Trp Ala Glu Phe Gly Asn Leu His Pro Phe Ala Pro Ala Glu Gln

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Ser Ala Gly Tyr Gln Gln Leu Thr Asp Glu Leu Glu Ala Met Leu Cys
      20           25           30
Ala Ala Thr Gly Tyr Asp Ala Ile Ser Leu Gln Pro Asn Ala Gly Ser
      35           40           45
Gln Gly Glu Tyr Ala Gly Leu Leu Ala Ile Arg Ala Tyr His Gln Ser
      50           55           60
Arg Gly Asp Glu Arg Arg Asp Ile Cys Leu Ile Pro Ser Ser Ala His
      65           70           75           80
Gly Thr Asn Pro Ala Thr Ala Asn Met Ala Gly Met Arg Val Val Val
      85           90           95
Thr Ala Cys Asp Ala Arg Gly Asn Val Asp Ile Glu Asp Leu Arg Ala
      100          105          110
Lys Ala Ile Glu His Arg Glu His Leu Ala Ala Leu Met Ile Thr Tyr
      115          120          125
Pro Ser Thr His Gly Val Phe Glu Glu Gly Ile Arg Glu Ile
      130          135          140

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&lt;210&gt; 2125

&lt;211&gt; 285

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2125

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60
acagtcaagc ccaatatggt tatgttacct attcaaaaca caagagggtc aagattggtt
120
ctaaaggcgg ctgaagacgc ggcaccaccg gctgtcaccg ttgaagcggc caaggaagag
180
aagccgaagc caccaccaat tggacctaaag agaggagcca aggtgagaat tcttaggaag
240
gagtcatact ggttcaaagg agtgggatca gttgtgactg ttgat
285

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&lt;210&gt; 2126

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2126

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Xaa Met Ala Ser Ala Ala Ser Ser Phe Val Val Thr Pro Asn Val Thr
      1           5           10           15
Ser Asn Thr Thr Thr Val Lys Pro Asn Met Val Met Leu Pro Ile Gln
      20           25           30
Asn Thr Arg Gly Ser Arg Leu Val Leu Lys Ala Ala Glu Asp Ala Ala
      35           40           45
Pro Pro Ala Val Thr Val Glu Ala Ala Lys Glu Glu Lys Pro Lys Pro
      50           55           60
Pro Pro Ile Gly Pro Lys Arg Gly Ala Lys Val Arg Ile Leu Arg Lys
      65           70           75           80
Glu Ser Tyr Trp Phe Lys Gly Val Gly Ser Val Val Thr Val Asp
      85           90           95

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<210> 2127  
 <211> 454  
 <212> DNA  
 <213> Homo sapiens

<400> 2127  
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 gcgacgcata ttccagggca cttgtcacca gtcatgccat tgggtaccat gaacccatgc  
 120  
 atgcagtact gcatgatgca acaggggctt gccagcttga tggcgtgtcc gtccttgatg  
 180  
 ctgcagcaac tgttggcctt accgcttcag acgatgccag tgatgatgcc acagatgatg  
 240  
 acgcctaaca tgatgtcacc attgatgatg ccgagcatga tgtcaccaat ggtcttgccg  
 300  
 agcatgatgt cgaaatgat gatgccacaa tgtcactgcg acgccgtctc gcagattatg  
 360  
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 420  
 ttacagcaac cctttgttgg tgctgcattc taga  
 454

<210> 2128  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 2128  
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 20 25 30  
 Pro Leu Gly Thr Met Asn Pro Cys Met Gln Tyr Cys Met Met Gln Gln  
 35 40 45  
 Gly Leu Ala Ser Leu Met Ala Cys Pro Ser Leu Met Leu Gln Gln Leu  
 50 55 60  
 Leu Ala Leu Pro Leu Gln Thr Met Pro Val Met Met Pro Gln Met Met  
 65 70 75 80  
 Thr Pro Asn Met Met Ser Pro Leu Met Met Pro Ser Met Met Ser Pro  
 85 90 95  
 Met Val Leu Pro Ser Met Met Ser Gln Met Met Met Pro Gln Cys His  
 100 105 110  
 Cys Asp Ala Val Ser Gln Ile Met Leu Gln Gln Gln Leu Pro Phe Met  
 115 120 125  
 Phe Asn Pro Met Ala Met Thr Ile Pro Pro Met Phe Leu Gln Gln Pro  
 130 135 140  
 Phe Val Gly Ala Ala Phe  
 145 150

<210> 2129  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 2129  
 acgcgtgact tgggaacaa acccatatcc atcacccct tcggtgttga tacgaaata  
 60  
 ctacacccct ttgacaagcg gcgtgatgag aacggcggtg acgggggtgt gcgcacgagg  
 120  
 actatcaagg ctctccactc caaatatggg atcgggtgaac tcatccgtgc cttcagtcgg  
 180  
 gtccatgatg aacggcctaa taccgtcctt cgtatctggg gcggcgggcc agacgagaat  
 240  
 cccctcaagg tcttggtcgc ccgtcttgtc ccggacgggt cggtaggagt tcgcgggtgcc  
 300  
 attgatcatt ctgaggtcag aaatgccttg ggtagtttgg acatctttgc cgcc  
 354

<210> 2130  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 2130  
 Thr Arg Asp Leu Val Asn Lys Pro Ile Ser Ile Thr Pro Phe Gly Val  
 1 5 10 15  
 Asp Thr Glu Ile Leu Thr Pro Phe Asp Lys Arg Arg Asp Ala Asn Gly  
 20 25 30  
 Gly Asp Gly Val Val Arg Ile Gly Thr Ile Lys Ala Leu His Ser Lys  
 35 40 45  
 Tyr Gly Ile Gly Glu Leu Ile Arg Ala Phe Ser Arg Val His Asp Glu  
 50 55 60  
 Arg Pro Asn Thr Val Leu Arg Ile Trp Gly Gly Gly Pro Asp Glu Asn  
 65 70 75 80  
 Pro Leu Lys Val Leu Ala Arg Arg Leu Val Pro Asp Gly Ser Val Glu  
 85 90 95  
 Phe Arg Gly Ala Ile Asp His Ser Glu Val Arg Asn Ala Leu Gly Ser  
 100 105 110  
 Leu Asp Ile Phe Ala Ala  
 115

<210> 2131  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 2131  
 gcacgcggc cattggttat gtgtgcctat tccattggtt atgtggaagg ttgggatcag  
 60  
 ccagacagtc attatgatgg tttgttacag ctgggcgagt ggggctttcg aatcaatgac  
 120  
 ctgatgaaga cggtagaggg cgccgcaggg tgcattgagt attatgaaat gctcaacgaa  
 180  
 caacgccccg acttgtctta tgacatagac ggtattgttt ataaagttga tcagattgac  
 240  
 ctgcaagaag agcttggttt tattgtcgt gcgccacgct gggcaattgc tcgaaaattt  
 300

cctgctcaag aagaagttac gcgt  
324

<210> 2132  
<211> 108  
<212> PRT  
<213> Homo sapiens

<400> 2132  
Ala Ser Arg Pro Leu Val Met Cys Ala Tyr Ser Ile Gly Tyr Val Glu  
1 5 10 15  
Gly Trp Asp Gln Pro Asp Ser His Tyr Asp Gly Leu Leu Gln Leu Gly  
20 25 30  
Glu Trp Gly Phe Arg Ile Asn Asp Leu Met Lys Thr Val Glu Gly Ala  
35 40 45  
Ala Gly Cys Ile Glu Tyr Tyr Glu Met Leu Asn Glu Gln Arg Pro Asp  
50 55 60  
Leu Ser Tyr Asp Ile Asp Gly Ile Val Tyr Lys Val Asp Gln Ile Asp  
65 70 75 80  
Leu Gln Glu Glu Leu Gly Phe Ile Ala Arg Ala Pro Arg Trp Ala Ile  
85 90 95  
Ala Arg Lys Phe Pro Ala Gln Glu Glu Val Thr Arg  
100 105

<210> 2133  
<211> 292  
<212> DNA  
<213> Homo sapiens

<400> 2133  
ggtacctgca atatggtatt gcatgacatg aataaatttt tccttactct gaactcacta  
60  
gtggctgtct ttagaggacc cggcgaactt ttcttgcttt ttcccacttg ctccatcaca  
120  
tacatcacat caccaacacc catcacatac atacacagtc atgaacggcc atcaggccac  
180  
accagattac atcgctgtgg atccaaccct gcattttcct gcccttcctt tactgagagt  
240  
gtcacctcta cccggaaagg tcttcaacct ccaagtttcc cagtaattta tt  
292

<210> 2134  
<211> 93  
<212> PRT  
<213> Homo sapiens

<400> 2134  
Met Val Leu His Asp Met Asn Lys Phe Phe Leu Thr Leu Asn Ser Leu  
1 5 10 15  
Val Ala Val Phe Arg Gly Pro Gly Glu Leu Phe Leu Leu Phe Pro Thr  
20 25 30  
Cys Ser Ile Thr Tyr Ile Thr Ser Pro Thr Pro Ile Thr Tyr Ile His  
35 40 45  
Ser His Glu Arg Pro Ser Gly His Thr Arg Leu His Arg Cys Gly Ser

50                      55                      60  
 Asn Pro Ala Phe Ser Cys Pro Ser Phe Thr Ala Ser Val Thr Ser Thr  
 65                      70                      75                      80  
 Arg Lys Gly Leu Gln Pro Pro Ser Phe Pro Val Ile Tyr  
                     85                      90

&lt;210&gt; 2135

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2135

acgcgttcca ttggtgtgtc gaatttcaag accgagcatc tggacgccat cgagggggcc  
 60  
 actccgagcg tcgaccaaatt cgagatgcat ccctcgttca accagggcgac cttccgcgca  
 120  
 gagctggcgc agcgcggcat taaccgggag gcctggagcc cgctggggcca gtcgaaggac  
 180  
 ctcgacaatc ccgtcctcac cgatatttcc aaggcgactg gaaagacgcc tgcccaggtg  
 240  
 gtcattcgct ggcacctgca gatcggcaac gtggtattcc ccaagtcggt gacaccatca  
 300  
 cgaattgccg agaactttga tgtgttcgat ttcgagctgt ctgacgagca gatcgccgca  
 360  
 attgatggcc tggatcacgg caacaggtc ggtggtgacc cttctaccgc cgacttctga  
 420  
 ttctgcaaca ataaccggt  
 439

&lt;210&gt; 2136

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2136

Thr Arg Ser Ile Gly Val Ser Asn Phe Lys Thr Glu His Leu Asp Ala  
 1                      5                      10                      15  
 Ile Glu Gly Ala Thr Pro Ser Val Asp Gln Ile Glu Met His Pro Ser  
                     20                      25                      30  
 Phe Asn Gln Ala Thr Phe Arg Ala Glu Leu Ala Glu Arg Gly Ile Asn  
                     35                      40                      45  
 Pro Glu Ala Trp Ser Pro Leu Gly Gln Ser Lys Asp Leu Asp Asn Pro  
                     50                      55                      60  
 Val Leu Thr Asp Ile Ser Lys Ala Thr Gly Lys Thr Pro Ala Gln Val  
 65                      70                      75                      80  
 Val Ile Arg Trp His Leu Gln Ile Gly Asn Val Val Phe Pro Lys Ser  
                     85                      90                      95  
 Val Thr Pro Ser Arg Ile Ala Glu Asn Phe Asp Val Phe Asp Phe Glu  
                     100                      105                      110  
 Leu Ser Asp Glu Gln Ile Ala Ala Ile Asp Gly Leu Asp His Gly Asn  
                     115                      120                      125  
 Arg Leu Gly Gly Asp Pro Ser Thr Ala Asp Phe  
                     130                      135



<210> 2137  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 2137  
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 60  
 tccgggacag agatggctgg cggagcctgg ggccgcctgg cctgttactt ggagttcctg  
 120  
 aagaaggagg agctgaagga gttccagctt ctgctcgcca ataaagcgca ctccaggagc  
 180  
 tcttccgggtg agacaccgc tcagccagag aagacgagtg gcatggaggt ggcctcgta  
 240  
 ctgggtggctc agtatgggga gcagcgggcc tgggacctag ccctccatac ctgggagcag  
 300  
 atggggctga ggtaactgtg cgcccaagcc  
 330

<210> 2138  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 2138  
 Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu  
 1 5 10 15  
 Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala  
 20 25 30  
 His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr  
 35 40 45  
 Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln  
 50 55 60  
 Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg  
 65 70 75 80  
 Ser Leu Cys Ala Gln Ala  
 85

<210> 2139  
 <211> 433  
 <212> DNA  
 <213> Homo sapiens

<400> 2139  
 gagcagttga gcgcccagaa caccgggatac aacagcaacc tgtcggacat ggccggccag  
 60  
 gtgaacaagc tggcgagtac catcgcccag tacaacgatac agatttccaa agtcaccacc  
 120  
 gccgccgggtg ccccgaaacga cctgctggac cagcgcagcg aggcgggtgcg ccagttgtcc  
 180  
 gagctggctg ggaccaggt ggtccagcgc ggttcgagtt atgacgtcta tatcggcagc  
 240  
 ggtcagcgcc tgggtgatggg caacagcacc aacaccctgt ccgcagtgcc gagcaaggac  
 300

gacccgagcc agtcggcctt gcagctggat cgcggcacca gcaccgtcga tatcacctcc  
 360  
 acggtgaccg gtggcgagat cgggtggtctg ctgcgctatc gcagcgatgt gctcgaccgc  
 420  
 tcgatcaacg cgt  
 433

<210> 2140

<211> 144

<212> PRT

<213> Homo sapiens

<400> 2140

Glu	Gln	Leu	Ser	Ala	Gln	Asn	Thr	Gly	Ile	Asn	Ser	Asn	Leu	Ser	Asp
1				5				10					15		
Met	Ala	Gly	Gln	Val	Asn	Lys	Leu	Ala	Ser	Thr	Ile	Ala	Gln	Tyr	Asn
		20					25					30			
Asp	Gln	Ile	Ser	Lys	Val	Thr	Thr	Ala	Ala	Gly	Ala	Pro	Asn	Asp	Leu
	35					40					45				
Leu	Asp	Gln	Arg	Ser	Glu	Ala	Val	Arg	Gln	Leu	Ser	Glu	Leu	Val	Gly
	50				55				60						
Thr	Gln	Val	Val	Gln	Arg	Gly	Ser	Ser	Tyr	Asp	Val	Tyr	Ile	Gly	Ser
65				70				75					80		
Gly	Gln	Arg	Leu	Val	Met	Gly	Asn	Ser	Thr	Asn	Thr	Leu	Ser	Ala	Val
		85					90					95			
Pro	Ser	Lys	Asp	Asp	Pro	Ser	Gln	Ser	Ala	Leu	Gln	Leu	Asp	Arg	Gly
	100					105					110				
Thr	Ser	Thr	Val	Asp	Ile	Thr	Ser	Thr	Val	Thr	Gly	Gly	Glu	Ile	Gly
	115					120					125				
Gly	Leu	Leu	Arg	Tyr	Arg	Ser	Asp	Val	Leu	Asp	Pro	Ser	Ile	Asn	Ala
	130					135					140				

<210> 2141

<211> 426

<212> DNA

<213> Homo sapiens

<400> 2141

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 gtttatcctt atctttcttt ccgcttgatc aatgatattg tggataaagg cgaagtgtta  
 120  
 ggtgacccaa ttgcttgatc tggttaaata cgtaaaggta ttaacaaagg cttgatgaaa  
 180  
 atcctgtcta aaatgggtat ttcaacgatt gcctcttata gtggtgcgca attgtttgaa  
 240  
 gcggttggtc tggatactaa agtggctgac ctttggttca aaggcggttc aagtcgtatc  
 300  
 aaagggtgctc gttttgaaga tttccagcgt gatcaagcaa cgattgccaa taatgcttgg  
 360  
 aagttacgta aacctattca acagggcggg tatcttaaata acgtacatga ctctgagtat  
 420  
 cacgcg  
 426

<210> 2142  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 2142  
 Xaa Tyr Pro Cys Ser Asp Pro His Gln Phe Ala Val Leu Leu Gly Phe  
 1 5 10 15  
 Gly Ala Thr Ala Val Tyr Pro Tyr Leu Ser Phe Arg Leu Ile Asn Asp  
 20 25 30  
 Met Val Asp Lys Gly Glu Val Leu Gly Asp Pro Ile Ala Cys His Val  
 35 40 45  
 Lys Tyr Arg Lys Gly Ile Asn Lys Gly Leu Met Lys Ile Leu Ser Lys  
 50 55 60  
 Met Gly Ile Ser Thr Ile Ala Ser Tyr Arg Gly Ala Gln Leu Phe Glu  
 65 70 75 80  
 Ala Val Gly Leu Asp Thr Lys Val Val Asp Leu Cys Phe Lys Gly Val  
 85 90 95  
 Ala Ser Arg Ile Lys Gly Ala Arg Phe Glu Asp Phe Gln Arg Asp Gln  
 100 105 110  
 Ala Thr Ile Ala Asn Asn Ala Trp Lys Leu Arg Lys Pro Ile Gln Gln  
 115 120 125  
 Gly Gly Tyr Leu Lys Tyr Val His Asp Ser Glu Tyr His Ala  
 130 135 140

<210> 2143  
 <211> 1008  
 <212> DNA  
 <213> Homo sapiens

<400> 2143  
 gccggcttga caagcatgtt caccggtgac gctgtcgtga tcgtcgaggt gagccaattg  
 60  
 tgtcatattg tacgcagtat gtcttttcaa cgattcttgg cgggggtggc agccatcttg  
 120  
 cttctcctgc ctactgcgtg cgctgatgat gcgcaggcgc ccgttgctga taacctcggg  
 180  
 acggtcctca gcccctccaa ctccctcatt cgcgagccgg cgaattcgtc agtcaacggg  
 240  
 acgctcaaga gcacatatga gtacctcggg ctcatcgacg gtcacgatct acccgacgac  
 300  
 gatggctacg ctcatgatca tctggtcgcg gctttgcgcc cgtatttggt gaatgggtga  
 360  
 gacagtcggc aggcccacgt caccacaactc atggcggcgt catccctgaa aacctcaac  
 420  
 gcgttgctccg acaaggagag atcagaggte gacaaacgta cccgcctgcc gaagggtgc  
 480  
 atcacgagaa agacggtgat gacggatctg cccatcgca cgatgaggcg ggagatcggc  
 540  
 ctgtccaacg acgggttggt cctcacaccg tggaaggta agacgacttc ttccgaggag  
 600  
 gctcgggtggg cgatgcaggc gctggccagt gccgacctat tcagcaatgc taaggacgcc  
 660

gagaaatggg ggtgggagtc gatctcggac gggattttgc gccatctcga gacctacagt  
 720  
 ggcccagta cgactatcgc gatggccttg tcggcggcga ataccgtctc tacattgtct  
 780  
 cgttcccagt tgcaacgcat cggcgacagt ctgcgggatg cgccatatcc gaggaaggac  
 840  
 cttggtccgg cgctcattcg caatggaaag ccggtcaagg acaagtgcag tatcgaatcg  
 900  
 gcgtacctgt tgaggtattc cgggaattgg gcgtggtgac atgacgggtt cttggcaagg  
 960  
 tgtgaccaag acattcccct cgggcgatcc cgcgctggg ggggtgcac  
 1008

<210> 2144

<211> 307

<212> PRT

<213> Homo sapiens

<400> 2144

Met	Phe	Thr	Gly	Asp	Ala	Val	Val	Ile	Val	Glu	Val	Ser	Gln	Leu	Cys
1				5					10					15	
His	Ile	Val	Arg	Ser	Met	Ser	Phe	Gln	Arg	Phe	Leu	Ala	Gly	Val	Ala
			20					25					30		
Ala	Ile	Leu	Leu	Leu	Leu	Pro	Thr	Ala	Cys	Ala	Asp	Asp	Ala	Gln	Ala
		35				40					45				
Pro	Val	Val	Asp	Asn	Leu	Gly	Thr	Val	Leu	Ser	Pro	Ser	Asn	Ser	Leu
	50				55					60					
Ile	Arg	Glu	Pro	Ala	Asn	Ser	Ser	Val	Asn	Gly	Thr	Leu	Lys	Ser	Thr
65				70					75					80	
Tyr	Glu	Tyr	Leu	Arg	Leu	Ile	Asp	Gly	His	Asp	Leu	Pro	Asp	Asp	Asp
			85					90					95		
Gly	Tyr	Ala	His	Asp	His	Leu	Val	Ala	Ala	Leu	Arg	Pro	Tyr	Leu	Val
			100					105					110		
Asn	Gly	Gly	Asp	Ser	Arg	Gln	Ala	His	Val	Thr	Gln	Leu	Met	Ala	Ala
		115					120					125			
Ser	Ser	Leu	Lys	Thr	Leu	Asn	Ala	Leu	Ser	Asp	Lys	Glu	Arg	Ser	Glu
	130					135					140				
Val	Asp	Lys	Arg	Thr	Arg	Leu	Pro	Lys	Gly	Cys	Ile	Thr	Arg	Lys	Thr
145				150					155					160	
Val	Met	Thr	Asp	Leu	Pro	Ile	Ala	Thr	Met	Arg	Arg	Glu	Ile	Gly	Leu
			165					170					175		
Ser	Asn	Asp	Gly	Leu	Cys	Leu	Thr	Pro	Trp	Lys	Val	Lys	Thr	Thr	Ser
		180						185					190		
Ser	Glu	Glu	Ala	Arg	Trp	Ala	Met	Gln	Ala	Leu	Ala	Ser	Ala	Asp	Leu
	195					200						205			
Phe	Ser	Asn	Ala	Lys	Asp	Ala	Glu	Lys	Trp	Gly	Trp	Glu	Ser	Ile	Ser
	210					215					220				
Asp	Gly	Tyr	Leu	Arg	His	Leu	Glu	Thr	Tyr	Ser	Gly	Pro	Ser	Thr	Thr
225				230					235					240	
Ile	Ala	Met	Ala	Leu	Ser	Ala	Ala	Asn	Thr	Val	Ser	Thr	Leu	Ser	Arg
			245					250					255		
Ser	Gln	Leu	Gln	Arg	Ile	Gly	Asp	Ser	Leu	Ala	Asp	Ala	Pro	Tyr	Pro
			260					265					270		
Arg	Lys	Asp	Leu	Gly	Pro	Ala	Leu	Ile	Arg	Asn	Gly	Lys	Pro	Val	Lys

275                      280                      285  
 Asp Lys Cys Ser Ile Glu Ser Ala Tyr Leu Leu Arg Tyr Ser Gly Asn  
 290                      295                      300  
 Trp Ala Trp  
 305

<210> 2145  
 <211> 389  
 <212> DNA  
 <213> Homo sapiens

<400> 2145  
 tctagaatcg tgtataacat tctacacaat aagctaagcc tactcttgta gagtgcgatc  
 60  
 atgacaaccc ttgaacaatc attatctcaa attcccgcac ttctgattat tcatgaacat  
 120  
 ttatttagct cggcccagcc ttctgctgaa caactaaaat tgattaaaga gtttggttgt  
 180  
 agcacagtca ttaaccttgc ttttaactaat gcttcaaadc atcttgagaa tgaagaccgt  
 240  
 atttggttag accttggttt aaattatatt catattccaa ttgattggga gatgccttct  
 300  
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 360  
 tggatacatt gcgcacaaaa taaacgcgt  
 389

<210> 2146  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 2146  
 Met Thr Thr Leu Glu Gln Ser Leu Ser Gln Ile Pro Ala Phe Ser Ile  
 1                      5                      10                      15  
 Ile His Glu His Leu Phe Ser Ser Ala Gln Pro Ser Ala Glu Gln Leu  
 20                      25                      30  
 Lys Leu Ile Lys Glu Phe Gly Cys Ser Thr Val Ile Asn Leu Ala Leu  
 35                      40                      45  
 Thr Asn Ala Ser Asn His Leu Glu Asn Glu Asp Arg Ile Cys Leu Asp  
 50                      55                      60  
 Leu Gly Leu Asn Tyr Ile His Ile Pro Ile Asp Trp Glu Met Pro Ser  
 65                      70                      75                      80  
 Ala Glu Gln Cys Leu Leu Val Leu Asp Leu Ile Asp His Leu Val Gln  
 85                      90                      95  
 Asn Glu Ile Val Trp Ile His Cys Ala Lys Asn Lys Arg  
 100                      105

<210> 2147  
 <211> 235  
 <212> DNA  
 <213> Homo sapiens

<400> 2147

ctccctgcgg gctgcgtctc cgaggacatg tgcagtcctg acccctgttt caatgggtggg  
 60  
 acttgccctg tcacctggaa tgacttccac tgtacctgcc ctgccaatTT caccggggcct  
 120  
 acatgtgccc agcagctgtg gtgtcccggc cagccctgtc tcccacctgc cactgtgtg  
 180  
 gcggaggcca cgttccgcga gggccccccc gccgcgttca gcgggcacaa cgcgt  
 235

<210> 2148

<211> 78

<212> PRT

<213> Homo sapiens

<400> 2148

Leu	Pro	Ala	Gly	Cys	Val	Ser	Glu	Asp	Met	Cys	Ser	Pro	Asp	Pro	Cys
1				5					10					15	
Phe	Asn	Gly	Gly	Thr	Cys	Leu	Val	Thr	Trp	Asn	Asp	Phe	His	Cys	Thr
			20					25					30		
Cys	Pro	Ala	Asn	Phe	Thr	Gly	Pro	Thr	Cys	Ala	Gln	Gln	Leu	Trp	Cys
		35					40					45			
Pro	Gly	Gln	Pro	Cys	Leu	Pro	Pro	Ala	Thr	Cys	Val	Ala	Glu	Ala	Thr
	50					55					60				
Phe	Arg	Glu	Gly	Pro	Pro	Ala	Ala	Phe	Ser	Gly	His	Asn	Ala		
65					70					75					

<210> 2149

<211> 1474

<212> DNA

<213> Homo sapiens

<400> 2149

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 gtccctgtga tgggtggctgc gaatgatttg ccttgacaat agctgaaaaa ccaccatctg  
 120  
 caacacgtgg gagtaagact tctcctgctc tttgccagtg gtctgaggtg atgaaccacc  
 180  
 ctggcttggg gtgctgtgtc cagcaaacta caggggtgcc gctggtagtt atggtgaaac  
 240  
 cagacacttt tcttatccac gagattaaga ctcttctgctc taaagcgaag atccaagaca  
 300  
 tggttgctat taggcacacg gcctgcaatg agcagcagcg gacaacaatg attctgtctg  
 360  
 gtgaggatgg cagcctgcgc atttacctgg ccaacgtgga gaacacctcc tactggctgc  
 420  
 agccatccct gcagcccagc agtgtcatca gcatcatgaa gcctgttcga aagcgcaaaa  
 480  
 cagctacaat cacaaccng cactgtctagc caggtgactt tccccattga cttttttgaa  
 540  
 cacaaccagc agctgacaga tgtggagttt ggtggtaacg acctctaca ggtctataat  
 600  
 gcacaacaga taaaacaccg gctgaattcc actggcatgt atgtggccaa caccaagccc  
 660

ggaggcttca ccattgagat tagtaacaac aatagcacta tggatgatgac aggcattgcgg  
 720  
 atccagattg ggactcaagc aatagaacgg gcccgcgtcat atactgagat cttcggcaga  
 780  
 actatgcagc tcaacctgag tcgctcacgc tggtttgact tccccctcac cagagaagaa  
 840  
 gccctgcagg ctgataagaa gctgaacctc ttcattgggg cctcgggtgga tccagcaggt  
 900  
 gtcaccatga tagatgctgt aaaaatttat ggcaagacta aggagcagtt tggctggcct  
 960  
 gatgagcccc cagaagaatt cccttctgcc tctgtcagca acatctgccc ttcaaactctg  
 1020  
 aaccagagca acggcactgg agatagcgac tcagctgccc ccactacgac cagtgggaact  
 1080  
 gtcctggaga ggctggttgt gagttcttta gaagccctgg aaagctgctt tgccgttggc  
 1140  
 ccaatcatcg agaaggagag aaacaagaat gctgctcagg agctggccac ttgctgttg  
 1200  
 tccctgccag cacctgccag tgtccagcag cagtccaaga gccttctggc cagcctgcac  
 1260  
 accagccgct cggcctacca cagccacaag gtaactgttc tctcagggaa aggaaattgc  
 1320  
 agtgctgaca gggaatcaaa taagttagct cttcattgta aagcaacagc acagcaaagt  
 1380  
 aaggtagagg gaggatagca ttcagattag acctacattt tacagagttt ctcctgagaa  
 1440  
 attctcaagt gccactcaaa actgagggtta agcc  
 1474

&lt;210&gt; 2150

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2150

Ser	Leu	Phe	Glu	Ser	Ala	Lys	Gln	Leu	Gln	Ser	Gln	Pro	Xaa	Thr	Ser
1				5				10						15	
Ser	Gln	Val	Thr	Phe	Pro	Ile	Asp	Phe	Phe	Glu	His	Asn	Gln	Gln	Leu
			20					25					30		
Thr	Asp	Val	Glu	Phe	Gly	Gly	Asn	Asp	Leu	Leu	Gln	Val	Tyr	Asn	Ala
		35					40					45			
Gln	Gln	Ile	Lys	His	Arg	Leu	Asn	Ser	Thr	Gly	Met	Tyr	Val	Ala	Asn
	50					55					60				
Thr	Lys	Pro	Gly	Gly	Phe	Thr	Ile	Glu	Ile	Ser	Asn	Asn	Asn	Ser	Thr
65				70					75					80	
Met	Val	Met	Thr	Gly	Met	Arg	Ile	Gln	Ile	Gly	Thr	Gln	Ala	Ile	Glu
			85					90						95	
Arg	Ala	Pro	Ser	Tyr	Ile	Glu	Ile	Phe	Gly	Arg	Thr	Met	Gln	Leu	Asn
		100						105					110		
Leu	Ser	Arg	Ser	Arg	Trp	Phe	Asp	Phe	Pro	Phe	Thr	Arg	Glu	Glu	Ala
	115					120						125			
Leu	Gln	Ala	Asp	Lys	Lys	Leu	Asn	Leu	Phe	Ile	Gly	Ala	Ser	Val	Asp
	130					135					140				
Pro	Ala	Gly	Val	Thr	Met	Ile	Asp	Ala	Val	Lys	Ile	Tyr	Gly	Lys	Thr

```
<210> 2151
<211> 511
<212> DNA
<213> Homo sapiens
```

```
<210> 2152
<211> 170
<212> PRT
<213> Homo sapiens
```

1601



1	5	10	15
Met Asp Gln Phe His Gln Ser Leu Xaa Gly Cys Arg Arg Xaa Arg Gln			
	20	25	30
His Phe His His Phe Met Gly Trp Val His Gln Arg Ser Phe Gln Leu			
	35	40	45
Thr Gly Ile Ala Asp Pro Leu Arg Ala Leu Ala Arg Glu Leu Ala Ala			
	50	55	60
Glu Val Arg Val Leu Cys Phe Asp Glu Leu Phe Val Asn Asp Ile Gly			
65	70	75	80
Asp Ala Ile Ile Leu Gly Arg Leu Phe Gln Val Met Phe Asp Ala Gly			
	85	90	95
Val Val Val Val Cys Thr Ser Asn Leu Pro Pro Asp Gln Leu Tyr Ala			
	100	105	110
Asp Gly Phe Asn Arg Asp Arg Phe Leu Pro Ala Ile Thr Ala Ile Lys			
	115	120	125
Gln His Met Gln Val Val Ala Val Asn Gly Ala Glu Asp His Arg Leu			
	130	135	140
His Pro Gly Ala Ile Glu Gln Arg Tyr Trp Val Ala Leu Pro Glu Gln			
145	150	155	160
Gly Ser Ala Leu Ser Gln Val Phe Asp Ala			
	165	170	

&lt;210&gt; 2153

&lt;211&gt; 528

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2153

nnaccggtgc caaagagctg gggatcaacc tgccgaacac cgccggtacg cagcagggtg  
 60  
 tcagtacgtg cacggcgatt ggcggcggca attgggacca ctccgcgctg atcaagggcc  
 120  
 tggagcatat ggccaacttt tcgattcgcg atcaataagc cacaccgctc ccacctttga  
 180  
 tggcattcca agtctgaaat tgatccatct ctaataacaa aaatccccgg gagccccgtt  
 240  
 atgtcggctg atccgcaaca cctgcttcgc gagctgtttg ccacagccat cgatgccgc  
 300  
 cacccccggc atgtccttga accttatctg cccgctgacc gcacaggccg tgtgattgtg  
 360  
 attgggcccc gcaaaaccgc acccgccatg gccctcgtcg tcgagaacgg ctggcaaggc  
 420  
 gaagtcaccg gcctggtggt caccgctac ggccacggcg cgccgtgcaa aaaaatcgaa  
 480  
 gtggtcgagg ccgctcaccg ggtgccggat gccgcccggc tggcgggtg  
 528

&lt;210&gt; 2154

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2154

Met Ser Val Asp Pro Gln His Leu Leu Arg Glu Leu Phe Ala Thr Ala

```

      1             5             10             15
Ile Asp Ala Ala His Pro Arg His Val Leu Glu Pro Tyr Leu Pro Ala
      20             25             30
Asp Arg Thr Gly Arg Val Ile Val Ile Gly Pro Gly Lys Thr Ala Pro
      35             40             45
Ala Met Ala Leu Val Val Glu Asn Gly Trp Gln Gly Glu Val Thr Gly
      50             55             60
Leu Val Val Thr Arg Tyr Gly His Gly Ala Pro Cys Lys Lys Ile Glu
      65             70             75             80
Val Val Glu Ala Ala His Pro Val Pro Asp Ala Ala Gly Leu Ala Val
      85             90             95

```

<210> 2155  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

```

<400> 2155
gtgcaccgcc acggcacacc cgccatgccg cgccgctatt tcgaggccct gctgcaggag
60
ttcggccccc actgcgaggt gtcaccgtc accgattcag agggcaaccc ctcagtctcg
120
gtgctcagtt tctacttccg tgatgaagtg ctgccctact atgcggggcga cgccgtcgcg
180
gcgcgcgaac tggcggccaa tgacttcaaa tactgggagc tgatgcgacg cgctgtgcg
240
cgcggcctca aggtgtttga ctacggccgc agcaagcagg gcacgggctc ctacgcn
297

```

<210> 2156  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

```

<400> 2156
Met Pro Arg Arg Tyr Phe Glu Ala Leu Leu Gln Glu Phe Gly Pro Asp
1             5             10             15
Cys Glu Val Leu Thr Val Thr Asp Ser Glu Gly Asn Pro Leu Ser Ser
      20             25             30
Val Leu Ser Phe Tyr Phe Arg Asp Glu Val Leu Pro Tyr Tyr Ala Gly
      35             40             45
Asp Ala Val Ala Ala Arg Glu Leu Ala Ala Asn Asp Phe Lys Tyr Trp
      50             55             60
Glu Leu Met Arg Arg Ala Cys Ala Arg Gly Leu Lys Val Phe Asp Tyr
      65             70             75             80
Gly Arg Ser Lys Gln Gly Thr Gly Ser Tyr Ala
      85             90

```

<210> 2157  
 <211> 711  
 <212> DNA  
 <213> Homo sapiens

<400> 2157

naccgagata acgaggtcgt catcatctcc actgggtccc aaggtgagcc actttcgccc  
 60  
 ctagcaagga tcgccaaccg agagcaccga gacatcgagg tgggggaggg agataccgtt  
 120  
 ttgctggcat cctctctcat cccgggtaat gagaatgccg tctatcgagt gattaatggc  
 180  
 ctgacgaagc ttggcgccgc cgtggtacat aagggaacg ctttgggtcca cgtttccggc  
 240  
 catgccgcag ccggagagct gctgtacgcg tataacatcg tgcggccacg cgctgtgatg  
 300  
 ccgattcatg gtgaggtgcg tcatcttgtc gctaatagcc atctggccaa agcaaccggt  
 360  
 gtcgatgaga acaacgtggg gcttgtcgag gacggcgggg ttattgacct tgttgacgga  
 420  
 gtaccgcgag ttgttgcaa ggtcgatgcc tcgtacatcc ttgttgacgg atctgggggtg  
 480  
 ggggagctta ccgaggacac gctcactgat cgccgtatcc tcggtgagga gggattcttg  
 540  
 tcagtcgtca ccgtggtcga caccgctcg gcgtcagtgg tgtctcgccc ggcgatccag  
 600  
 gcgcgtggtt ttgccgaggg cgactcggtc ttcgcggaga tcaccgacca gatcgtcacc  
 660  
 gagctagaga aggcgatggc cgggtggtatg gacgataccc accggttgca a  
 711

&lt;210&gt; 2158

&lt;211&gt; 237

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2158

Xaa	Arg	Asp	Asn	Glu	Val	Val	Ile	Ile	Ser	Thr	Gly	Ser	Gln	Gly	Glu
1			5						10					15	
Pro	Leu	Ser	Ala	Leu	Ala	Arg	Ile	Ala	Asn	Arg	Glu	His	Arg	Asp	Ile
			20					25					30		
Glu	Val	Gly	Glu	Gly	Asp	Thr	Val	Leu	Leu	Ala	Ser	Ser	Leu	Ile	Pro
		35				40						45			
Gly	Asn	Glu	Asn	Ala	Val	Tyr	Arg	Val	Ile	Asn	Gly	Leu	Thr	Lys	Leu
	50				55					60					
Gly	Ala	Ala	Val	Val	His	Lys	Gly	Asn	Ala	Leu	Val	His	Val	Ser	Gly
65					70					75				80	
His	Ala	Ala	Ala	Gly	Glu	Leu	Leu	Tyr	Ala	Tyr	Asn	Ile	Val	Arg	Pro
			85					90						95	
Arg	Ala	Val	Met	Pro	Ile	His	Gly	Glu	Val	Arg	His	Leu	Val	Ala	Asn
			100					105						110	
Ala	Asp	Leu	Ala	Lys	Ala	Thr	Gly	Val	Asp	Glu	Asn	Asn	Val	Val	Leu
		115					120					125			
Val	Glu	Asp	Gly	Gly	Val	Ile	Asp	Leu	Val	Asp	Gly	Val	Pro	Arg	Val
	130				135						140				
Val	Gly	Lys	Val	Asp	Ala	Ser	Tyr	Ile	Leu	Val	Asp	Gly	Ser	Gly	Val
145				150						155				160	
Gly	Glu	Leu	Thr	Glu	Asp	Thr	Leu	Thr	Asp	Arg	Arg	Ile	Leu	Gly	Glu
			165					170						175	
Glu	Gly	Phe	Leu	Ser	Val	Val	Thr	Val	Val	Asp	Thr	Arg	Ser	Ala	Ser

```

                180                185                190
Val Val Ser Arg Pro Ala Ile Gln Ala Arg Gly Phe Ala Glu Gly Asp
                195                200                205
Ser Val Phe Ala Glu Ile Thr Asp Gln Ile Val Thr Glu Leu Glu Lys
                210                215                220
Ala Met Ala Gly Gly Met Asp Asp Thr His Arg Leu Gln
225                230                235

```

<210> 2159  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

```

<400> 2159
tcgcgagcac actccagcct ctggagagac gacaacgcgt gaagggggcac cagcttgagg
60
ggcagcagct ccagggggcgg cctgggaggg ctttgtgcag aagaagcctg tttccttcta
120
cctgttttga aaagtgtgtct ctgcagatgg tgggtgagag ttcgctgcca gggccactgt
180
cttcctgtcc ctgcggacac ttcttcccca ccttcctaaa gctgtggggag acctggagcc
240
gtggagcatc aatggctctt tgactcagga atcttaaaaa atcacaccct ggggctacca
300
tgggggcctt ctggttctcc tt
322

```

<210> 2160  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

```

<400> 2160
Met Val Ala Pro Gly Cys Asp Phe Leu Arg Phe Leu Ser Gln Arg Ala
1      5      10      15
Ile Asp Ala Pro Arg Leu Gln Val Ser His Ser Phe Arg Lys Val Gly
20     25     30
Lys Lys Cys Pro Gln Gly Arg Glu Asp Ser Gly Pro Gly Ser Glu Leu
35     40     45
Ser Pro Thr Ile Cys Arg Asp Asn Phe Ser Lys Gln Val Glu Gly Asn
50     55     60
Arg Leu Leu Leu His Lys Ala Leu Pro Gly Arg Pro Trp Ser Cys Cys
65     70     75     80
Pro Ala Ser Trp Cys Pro Phe Thr Arg Cys Arg Leu Ser Arg Gly Trp
85     90     95
Ser Val Leu Ala
100

```

<210> 2161  
 <211> 1070  
 <212> DNA  
 <213> Homo sapiens

<400> 2161

tcttagggga agggaaggct tatctgaaga gtagacctct ggttttgaat gagggagaca  
 60  
 gtggggatat gaggggagga aacctcaaaa agaatatgta tccatcacta tgaaaggtta  
 120  
 ggctatacag gggaagcctc caaagggaaa tctggaaaaa tgttctgaga gggacattaa  
 180  
 ggatgtactc agaaattaag aaaacatatt aggacttgcc aaaagtgaga gaagcaactg  
 240  
 aggagactta tatgcaaaaa tcgcaaagaa ggagagaaca aaagatggag gttggatgct  
 300  
 aaatagggaa agagaacgcg tgaatgaggt agggggcaga acatgcagtg cagaaaaaca  
 360  
 acagatatgg aagggcatta aagagggcta aatgggaata ttaggaaatg agagttggga  
 420  
 atttgtcaga gttgtgtatt aacaaggaga gggtaaggta agaaggtggc aaagtaagag  
 480  
 ccagggcata aggttttgct gtccaggaag ctttgttgga aaaatgttag aagtaatggg  
 540  
 tttggtcagt atggtgagag gtgagagagg ctaaattggga tgggcataaa gggcaggcca  
 600  
 gtggcaagaa tcctatgaaa gtgtaggcag atctgagagc acagacaaat acagtggaga  
 660  
 atgtggcaca gggcagaggg cagtgggctg agcagcgagt gcccattggg aggggagtat  
 720  
 ccagaagaac ccattgagtc cctaagaatg acacacaggt gacagctgaa agaaggaggg  
 780  
 acacagaaga tatagcagca tgattctctg gggcaaaatg aggaagaaag gaatggaaga  
 840  
 agaaagttaa gggttcctgc tgatgtgagg ggatgactgg aggaaaggca ggtattgact  
 900  
 gggggggtaaa ggaaccattc ttgatcaag gttatgatgg aataagaagg aagagagagc  
 960  
 tggctagctg agtaaaggac catcgataaa aacagacaaa agttaagact agatggagtg  
 1020  
 gcaactaggc agatcagatg tatttttaaa aggggaaact gctaagatct  
 1070

&lt;210&gt; 2162

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2162

Met Val Leu Tyr Ser Ala Ser Gln Leu Ser Leu Pro Ser Tyr Ser Ile  
 1 5 10 15  
 Ile Thr Leu Ile Gln Glu Trp Phe Leu Tyr Pro Pro Val Asn Thr Cys  
 20 25 30  
 Leu Ser Ser Ser His Pro Leu Thr Ser Ala Gly Thr Leu His Phe Leu  
 35 40 45  
 Leu Pro Phe Leu Ser Ser Ser Phe Cys Pro Arg Glu Ser Cys Cys Tyr  
 50 55 60  
 Ile Phe Cys Val Pro Pro Ser Phe Ser Cys His Leu Cys Val Ile Leu  
 65 70 75 80  
 Arg Asp Ser Met Gly Ser Ser Gly Tyr Ser Pro Pro His Gly His Ser

```
<210> 2163
<211> 657
<212> DNA
<213> Homo sapiens
```

```

<400> 2163
tattttaaate tttataaaaa aggtaggagg atcaggactt cgacccccctt aaaacgcggg
60
ggcctccctc caatccacct ccacttctta caccaccccc gctctccccc ccccccttt
120
tggttccggg ttggaagggt gggtgaaatg ggaaccgaat accaatttca cccgggaacc
180
agtaatgccc atgataaccg ccaagttggg accgaagttg ggatccataa gtacggggcg
240
ccagtgggggt ggaattgggt taagccccct cccagccttt ctccgaccgc gtgctccgtc
300
agacatgccca agaggctctc tctccaggag agccacctgt gaaaccacc cggcattgctc
360
ctcccaccac tgtgcacaga cgagtgcctg ggctccagag agggagggag ctgaaggcct
420
cagacaggag tccgtcccggt ccagtcccat catcccaaga aacatccggc ccgactccct
480
gcagctccat ggctcaacaa ggtgcggatg cctgctggac ctggctgctt tccatccaac
540
tttgatccct tccccaagag gaagagtgtt acctagggac aagtgtggtg cgcacaggca
600
tcgagcctgg tctcttgctc aggcggcttg cgcagattcc tagaggaatc tgcagcg
657

```

```
<210> 2164
<211> 152
<212> PRT
<213> Homo sapiens
```

<400> 2164																
Met	Pro	Met	Ile	Thr	Ala	Lys	Leu	Gly	Pro	Lys	Leu	Gly	Ser	Ile	Ser	
1				5					10					15		
Thr	Gly	Gly	Gln	Trp	Gly	Gly	Ile	Gly	Leu	Ser	Pro	Leu	Pro	Ala	Phe	
			20					25					30			
Leu	Arg	Pro	Arg	Ala	Pro	Ser	Asp	Met	Pro	Arg	Gly	Ser	Leu	Ser	Arg	
		35				40						45				
Arg	Ala	Thr	Cys	Glu	Thr	His	Pro	Ala	Cys	Ser	Ser	His	His	Cys	Ala	
	50					55					60					
Gln	Thr	Ser	Ala	Trp	Ala	Pro	Glu	Arg	Glu	Gly	Ala	Glu	Gly	Leu	Arg	

65		70		75		80									
Gln	Glu	Ser	Val	Pro	Ser	Ser	Pro	Ile	Ile	Pro	Arg	Asn	Ile	Arg	Pro
			85				90						95		
Asp	Ser	Leu	Gln	Leu	His	Gly	Ser	Thr	Arg	Cys	Gly	Cys	Leu	Leu	Asp
		100					105					110			
Leu	Ala	Ala	Phe	His	Pro	Thr	Leu	Ile	Pro	Ser	Pro	Arg	Gly	Arg	Val
		115				120						125			
Leu	Pro	Arg	Asp	Lys	Cys	Gly	Ala	His	Arg	His	Ala	Ala	Trp	Ser	Leu
		130			135						140				
Ala	Gln	Ala	Ala	Cys	Ala	Asp	Ser								
145					150										

&lt;210&gt; 2165

&lt;211&gt; 962

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2165

```

nctttctcat cgacagcgac gcacaaccgg cgacatcacc ggtgacgggt caaggtggca
60
gccccgagggc cgcgcgtgaa cttattgtgt cgtcttatgg aagaaaagtc actcggaagt
120
accgtaaatc accccagcgc ctcaccccc gaatctgttc gccatctgct gtcgccccctg
180
cgcttaaggc atcacccac tagactgacc gaagtctcgc cgagggaggc tagggaggct
240
taggtggcca ggaatgacat cgggacgacg tctacgcgtc gaataggcag cggacgtacg
300
tcgagtaccg gccgtacggt ggtgtcttct gaccgcacac gcagagctat cgctaaaaga
360
ttgatggccc gcacctcagc tatgacgacg gccactctag aggaaatggg tcgtcgacac
420
tcctggttcc gtgatctgtc agccgaagaa agatcgtgga tctcgatcgt ggctcgctca
480
ggtattgacg gcttcgtcca gtggtttgct gacgatgacg ccgagcccta ctccccacc
540
gacgtcttcg acgtggcgcc ccggtccatg acccgcaaga tctccttgca ccagacagtc
600
gagctcgccc gcaccacgat tgacgtcgtt gaggcacaaa ttgagaccga aatgccacgc
660
ggtgatcgcc aagtgtctgc cactgccatc gttcactact cccgcgaggt ggccttcgcc
720
gccgccgagg tttacgcgcg agccgccgaa cgtcgcggtg cctgggatga acgtctggaa
780
tcctctgctg ttgatgccgt cgtgcgagcc gacgccgatg aacagctcat ctgcgagct
840
tctactctcg gctggcgccc gggcatcaac ctctgcgtcg ttgtcgggcg ggccccgacg
900
accgagcatg aactccacgt gctgcgacgt gatggagaac gcatgcagat gacggtgcta
960
gc
962

```

&lt;210&gt; 2166

<211> 239  
 <212> PRT  
 <213> Homo sapiens

<400> 2166  
 Val Ala Arg Asn Asp Ile Gly Thr Thr Ser Thr Arg Arg Ile Gly Ser  
 1 5 10 15  
 Gly Arg Thr Ser Ser Thr Gly Arg Thr Val Val Ser Ser Asp Arg Thr  
 20 25 30  
 Arg Arg Ala Ile Ala Lys Arg Leu Met Ala Arg Thr Ser Ala Met Thr  
 35 40 45  
 Thr Ala Thr Leu Glu Glu Met Gly Arg Arg His Ser Trp Phe Arg Asp  
 50 55 60  
 Leu Ser Ala Glu Glu Arg Ser Trp Ile Ser Ile Val Ala Arg Ser Gly  
 65 70 75 80  
 Ile Asp Gly Phe Val Gln Trp Phe Ala Asp Asp Asp Ala Glu Pro Tyr  
 85 90 95  
 Ser Pro Thr Asp Val Phe Asp Val Ala Pro Arg Ser Met Thr Arg Lys  
 100 105 110  
 Ile Ser Leu His Gln Thr Val Glu Leu Val Arg Thr Thr Ile Asp Val  
 115 120 125  
 Val Glu Ala Gln Ile Glu Thr Glu Met Pro Arg Gly Asp Arg Gln Val  
 130 135 140  
 Leu Arg Thr Ala Ile Val His Tyr Ser Arg Glu Val Ala Phe Ala Ala  
 145 150 155 160  
 Ala Glu Val Tyr Ala Arg Ala Ala Glu Arg Gly Thr Trp Asp Glu  
 165 170 175  
 Arg Leu Glu Ser Leu Val Val Asp Ala Val Val Arg Ala Asp Ala Asp  
 180 185 190  
 Glu Gln Leu Ile Ser Arg Ala Ser Thr Leu Gly Trp Arg Pro Gly Ile  
 195 200 205  
 Asn Leu Cys Val Val Val Gly Arg Ala Pro Thr Thr Glu His Glu Leu  
 210 215 220  
 His Val Leu Arg Arg Asp Gly Glu Arg Met Gln Met Thr Val Leu  
 225 230 235

<210> 2167  
 <211> 325  
 <212> DNA  
 <213> Homo sapiens

<400> 2167  
 accggtgcag tttgtgaggg gttggtgacg cccgatcggg aggttcacgc cgtcacggcg  
 60  
 catccacatt atcccgactg gaagatctcg ccagggttacg gacagtgggc gcgtagcgaa  
 120  
 cagatcgaca gtgtgactgt gacgcgagtc agacacttcg tcccgcggcg tcccacggcg  
 180  
 attcttcgag cgggtgtctga ggtgacgttc gggttgcgtc tctgcgccgt ccgttggcga  
 240  
 agcaccgcgg cgattgtggc tgtgtcgccg gccttgctct cgacgcggtc gcgcgggctg  
 300  
 tgcgtgatc tcccacagca taccc  
 325



<210> 2168  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 2168  
 Thr Gly Ala Val Cys Glu Gly Leu Val Thr Pro Asp Arg Glu Val His  
 1 5 10 15  
 Ala Val Thr Ala His Pro His Tyr Pro Asp Trp Lys Ile Ser Pro Gly  
 20 25 30  
 Tyr Gly Gln Trp Ser Arg Ser Glu Gln Ile Asp Ser Val Thr Val Thr  
 35 40 45  
 Arg Val Arg His Phe Val Pro Arg Arg Pro Thr Ala Ile Leu Arg Ala  
 50 55 60  
 Val Ser Glu Val Thr Phe Gly Leu Arg Leu Cys Ala Val Arg Trp Arg  
 65 70 75 80  
 Ser Thr Ala Ala Ile Val Ala Val Ser Pro Ala Leu Leu Ser Thr Arg  
 85 90 95  
 Ser Arg Gly Ser Cys Ala Asp Leu Pro Gln His Thr  
 100 105

<210> 2169  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<400> 2169  
 gaggacgcct acgtgctcat caccagggc aagatctcgg cgatcgccga cgtcctgccg  
 60  
 atcctggaga aggtcgtaaa ggccggcaag ccgctgctcg tcatcgccga ggacatcgac  
 120  
 ggggaggccc tgtccaccct cgctcgtaat aagatcccg gtagcttcag ctcggtggca  
 180  
 gtcaaggcgc ccggtctcgg tgaccgccgc aaggcaatgc tgcaggacat cgccaccctc  
 240  
 accggtggtc aggtcgctcg tcccgagggt gggctcaagc tcgaccaggt gggcctcgag  
 300  
 gttcagggc  
 309

<210> 2170  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 2170  
 Glu Asp Ala Tyr Val Leu Ile Thr Gln Gly Lys Ile Ser Ala Ile Ala  
 1 5 10 15  
 Asp Val Leu Pro Ile Leu Glu Lys Val Val Lys Ala Gly Lys Pro Leu  
 20 25 30  
 Leu Val Ile Ala Glu Asp Ile Asp Gly Glu Ala Leu Ser Thr Leu Val  
 35 40 45  
 Val Asn Lys Ile Arg Gly Thr Phe Ser Ser Val Ala Val Lys Ala Pro

```

      50              55              60
Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln Asp Ile Ala Thr Leu
65              70              75              80
Thr Gly Gly Gln Val Val Ala Pro Glu Val Gly Leu Lys Leu Asp Gln
      85              90              95
Val Gly Leu Glu Val Gln Gly
      100

```

&lt;210&gt; 2171

&lt;211&gt; 518

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2171

```

cgcgtaatgt gtattaaggt ccttggtggc tcgcatcgcc gttatgcagc aatcgggtgat
60
atcatcaaag tttcagtga ggaagcaatt cctcgcgga aaattaaaaa aggtaatggt
120
cattcagctg tggtagtgcg taccagaaaa ggtgtacgtc gtcccgatgg ttctgttatt
180
cgttttgatc gcaacgcagc ggttatcttg aatgcaaaca accagccagt cggtacacgt
240
atctttggcc ctgtaaccgc tgagcttcga aatgaaaatt tcatgaagat tgtttcactg
300
gcgccagaag tactgtaagg aaccgaaaat ggcagcaaaa ataaaacgtg acgatgaagt
360
aattgttatt gccggtaaag ataaaggtaa aactgggaaa gtttctcaag ttttaactaa
420
cggtaaagta attattgaag gtgtaaattgt tcaaaagaaa caccaaaaac caaacctca
480
agcgggcgtg gaaggcggaa tcattgaaca gaatgcat
518

```

&lt;210&gt; 2172

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2172

```

Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr Ala
1              5              10              15
Ala Ile Gly Asp Ile Ile Lys Val Ser Val Lys Glu Ala Ile Pro Arg
      20              25              30
Gly Lys Ile Lys Lys Gly Asn Val His Ser Ala Val Val Val Arg Thr
      35              40              45
Arg Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp Arg
      50              55              60
Asn Ala Ala Val Ile Leu Asn Ala Asn Asn Gln Pro Val Gly Thr Arg
65              70              75              80
Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Asn Glu Asn Phe Met Lys
      85              90              95
Ile Val Ser Leu Ala Pro Glu Val Leu
      100              105

```

<210> 2173  
 <211> 475  
 <212> DNA  
 <213> Homo sapiens

<400> 2173  
 nntggggaag aaatgccggt gcatgcactt tgtgcagcat taggtgcagg ggtgatgcag  
 60  
 cgggcgcggtg cctttttgcgg cgggggtttcg agcattcattc tggatgcagc attttcgcag  
 120  
 gcattttcttg tatcctcgtc atgcgtttct ccccatgcac acacattatc gcctttgcac  
 180  
 ccgcagggac gcatggaata cctcgtgaaa tggaagggat ggtcgcagaa gtacagcaca  
 240  
 tggaaccgg aggaaaacat cctggatgct cgcttgctcg cagcctttga ggaaagggaa  
 300  
 agagagatgg agctctatgg ccccaaaaag cgtggaccca agcccaaaac cttcctcctc  
 360  
 aaagcgagg ccaaggcaaa ggccaaaact tacgagtttc gaagtgactc agccaggggc  
 420  
 atccggatcc cctaccctgg ccgctcgccc caggacctgg cctccacttc ccggg  
 475

<210> 2174  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<400> 2174  
 Xaa Gly Glu Glu Met Pro Val His Ala Leu Cys Ala Ala Leu Gly Ala  
 1 5 10 15  
 Gly Val Met Gln Arg Ala Arg Ala Phe Cys Gly Gly Val Ser Ser Ile  
 20 25 30  
 His Leu Val His Ala Phe Ser His Ala Phe Leu Val Ser Ser Ser Cys  
 35 40 45  
 Val Ser Pro His Ala His Thr Leu Ser Pro Leu His Pro Gln Gly Arg  
 50 55 60  
 Met Glu Tyr Leu Val Lys Trp Lys Gly Trp Ser Gln Lys Tyr Ser Thr  
 65 70 75 80  
 Trp Glu Pro Glu Glu Asn Ile Leu Asp Ala Arg Leu Leu Ala Ala Phe  
 85 90 95  
 Glu Glu Arg Glu Arg Glu Met Glu Leu Tyr Gly Pro Lys Lys Arg Gly  
 100 105 110  
 Pro Lys Pro Lys Thr Phe Leu Leu Lys Ala Gln Ala Lys Ala Lys Ala  
 115 120 125  
 Lys Thr Tyr Glu Phe Arg Ser Asp Ser Ala Arg Gly Ile Arg Ile Pro  
 130 135 140  
 Tyr Pro Gly Arg Ser Pro Gln Asp Leu Ala Ser Thr Ser Arg  
 145 150 155

<210> 2175  
 <211> 462  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 2175

cgcgacaccc tctttggtgg ggccttcct tctccgaatt cgcgaaacct ccagactctg  
60  
gccaggagg ttgtcgagcg tggagccgat atcggcattg ccactgatgg tgacgcagac  
120  
cgcttcggta tcattgatga ccaggggcat ttcttgcata ccaaccagat cctcgtattg  
180  
ctgtacacct accttctgga ggacaaggga tggcaggtgc cctgcgtgcg taacctcgcg  
240  
acgacccacc tgcttgaccg tgtcgccgag gccacgggc agacctgtta cgaggtaccg  
300  
gtcggattta agtgggtgtc gtccaagatg gccgagacca acgccgtcat cgggtggtgag  
360  
tcctccggtg gtttgaccgt ccaggggcat attgcaggca aggatggtgt ctatgctggc  
420  
accctgctgg tggaaatgat cgccaagcgg ggtaagaagc tt  
462

&lt;210&gt; 2176

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2176

Arg	Asp	Thr	Leu	Phe	Gly	Gly	Arg	Leu	Pro	Ser	Pro	Asn	Ser	Arg	Thr
1				5					10					15	
Leu	Gln	Thr	Leu	Ala	Gln	Glu	Val	Val	Glu	Arg	Gly	Ala	Asp	Ile	Gly
			20					25					30		
Ile	Ala	Thr	Asp	Gly	Asp	Ala	Asp	Arg	Leu	Gly	Ile	Ile	Asp	Asp	Gln
		35					40					45			
Gly	His	Phe	Leu	His	Pro	Asn	Gln	Ile	Leu	Val	Leu	Leu	Tyr	Thr	Tyr
		50				55					60				
Leu	Leu	Glu	Asp	Lys	Gly	Trp	Gln	Val	Pro	Cys	Val	Arg	Asn	Leu	Ala
65					70					75				80	
Thr	Thr	His	Leu	Leu	Asp	Arg	Val	Ala	Glu	Ala	His	Gly	Gln	Thr	Cys
			85					90					95		
Tyr	Glu	Val	Pro	Val	Gly	Phe	Lys	Trp	Val	Ser	Ser	Lys	Met	Ala	Glu
			100					105					110		
Thr	Asn	Ala	Val	Ile	Gly	Gly	Glu	Ser	Ser	Gly	Gly	Leu	Thr	Val	Gln
		115					120					125			
Gly	His	Ile	Ala	Gly	Lys	Asp	Gly	Val	Tyr	Ala	Gly	Thr	Leu	Leu	Val
	130					135					140				
Glu	Met	Ile	Ala	Lys	Arg	Gly	Lys	Lys	Leu						
145						150									

&lt;210&gt; 2177

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2177

ctcgaagaac atgacggcga cgacgtgact atctccaccc gtgtgcctcg tgacggcggg  
60

accttggaact cgattgtcgg cgtgctggcc ggggcatcct ggtatcagcg ggagatccac  
 120  
 gacttttttg gtgtgaggtt tgtcggccct ggggcagatg atcgtgccct ccttgccac  
 180  
 gatgcaccga aaccgcccct gcgcaaggaa gctgtgttg cgcagcgagc tgacaccgtg  
 240  
 tggccgggtg cggctgacca ggctggctcg aagtccgcga gtcgacgtct gccggtcggc  
 300  
 gttcctgacc ctgagacgtg gcggcgatc aaagacggcg aggatattcc ggatgccgag  
 360  
 gtcacgcgg ccatgtctgg ccggcgcccg cgatcagctg cccgtcgaat ggcaagcacg  
 420  
 gcgtcaggca ggcaggcatg agacattcga ctatcaacct tgacgtcgac gcgtgcac  
 478

<210> 2178

<211> 146

<212> PRT

<213> Homo sapiens

<400> 2178

Leu	Glu	Asn	His	Asp	Gly	Asp	Asp	Val	Thr	Ile	Ser	Thr	Arg	Val	Pro
1				5				10						15	
Arg	Asp	Gly	Gly	Thr	Leu	Asp	Ser	Ile	Val	Gly	Val	Leu	Ala	Gly	Ala
		20					25						30		
Ser	Trp	Tyr	Gln	Arg	Glu	Ile	His	Asp	Phe	Phe	Gly	Val	Arg	Phe	Val
	35					40					45				
Gly	Pro	Gly	Ala	Asp	Asp	Arg	Ala	Leu	Leu	Val	His	Asp	Ala	Pro	Lys
	50				55					60					
Pro	Pro	Leu	Arg	Lys	Glu	Ala	Val	Leu	Ala	Gln	Arg	Ala	Asp	Thr	Val
65				70					75					80	
Trp	Pro	Gly	Ala	Ala	Asp	Gln	Ala	Gly	Ser	Lys	Ser	Ala	Ser	Arg	Arg
			85				90						95		
Leu	Pro	Val	Gly	Val	Pro	Asp	Pro	Glu	Thr	Trp	Arg	Arg	Ile	Lys	Asp
		100					105						110		
Gly	Glu	Asp	Ile	Pro	Asp	Ala	Glu	Val	Ile	Ala	Ala	Met	Ser	Gly	Arg
	115						120					125			
Arg	Pro	Arg	Ser	Ala	Ala	Arg	Arg	Met	Ala	Ser	Thr	Ala	Ser	Gly	Arg
	130					135						140			
Gln	Ala														
145															

<210> 2179

<211> 296

<212> DNA

<213> Homo sapiens

<400> 2179

gtgcacttcc gaggcgtcgc attaacgggg ccggcgcggt gggcgcacac  
 60  
 aagacgtcga tgctgcagga tctggacngc gaccgcgcga tggagatcga cccgctcgtc  
 120  
 tccgctgttc aggagatggg acgcctggcc aacgtgccga cgcccacgct cgatgtcgtg  
 180

ctcccactga tcaagcaacg tgaattcatg acgaagccgg atgccgtggc ggccgcgcag  
 240  
 gaacgtctgg ctaaagcggc ataaaccagc cgccgaaacc agcggcataa cgcggn  
 296

<210> 2180  
 <211> 87  
 <212> PRT  
 <213> Homo sapiens

<400> 2180  
 Val His Phe Arg Val Asp Val Glu Arg Arg Ile Asn Gly Ala Gly Ala  
   1                  5                  10                  15  
 Val Gly Ala His Lys Thr Ser Met Leu Gln Asp Leu Asp Xaa Asp Arg  
                   20                  25                  30  
 Ala Met Glu Ile Asp Pro Leu Val Ser Val Val Gln Glu Met Gly Arg  
           35                  40                  45  
 Leu Ala Asn Val Pro Thr Pro Thr Leu Asp Val Val Leu Pro Leu Ile  
       50                  55                  60  
 Lys Gln Arg Glu Phe Met Thr Lys Pro Asp Ala Val Ala Ala Ala Gln  
   65                  70                  75                  80  
 Glu Arg Leu Ala Lys Ala Ala  
                   85

<210> 2181  
 <211> 387  
 <212> DNA  
 <213> Homo sapiens

<400> 2181  
 ngcgcgcgcg gatggatcat agtctggctc gatgcatcac gtgcgcgcgc gcgcgcgcgc  
 60  
 tcgattcccc acggcatgat cgcggcactc gaccgtaccg gcaaggcgca aacgcacctc  
 120  
 acgctggcat cgccggaagc ggggtgtcgtc agcgaactga acgtgcgcga cgggtgcgatg  
 180  
 gtcgcgcgcg ggcagacgct cgcgaagatt tcgggcctct cgaagctctg gctgatcgtc  
 240  
 gagattccgg aagcgctcgc gctcgatgcg cgtccgggca tgaccgtcga cgcgacgttc  
 300  
 tcgggcgatc cgacgcagca tttcaccggg cgtatccgcg agatcctgcc gggcatcacc  
 360  
 accagtagcc gcacgcttca ggcgcgcc  
 387

<210> 2182  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<400> 2182  
 Xaa Ala Pro Gly Trp Ile Ile Val Trp Leu Asp Ala Ser Arg Ala Arg  
   1                  5                  10                  15  
 Met Arg Ala Leu Ser Ile Pro Asp Gly Met Ile Ala Ala Leu Asp Arg

```

      20      25      30
Thr Gly Lys Ala Gln Thr His Leu Thr Leu Ala Ser Pro Glu Ala Gly
      35      40      45
Val Val Ser Glu Leu Asn Val Arg Asp Gly Ala Met Val Ala Pro Gly
      50      55      60
Gln Thr Leu Ala Lys Ile Ser Gly Leu Ser Lys Leu Trp Leu Ile Val
65      70      75      80
Glu Ile Pro Glu Ala Leu Ala Leu Asp Ala Arg Pro Gly Met Thr Val
      85      90      95
Asp Ala Thr Phe Ser Gly Asp Pro Thr Gln His Phe Thr Gly Arg Ile
      100      105      110
Arg Glu Ile Leu Pro Gly Ile Thr Thr Ser Ser Arg Thr Leu Gln Ala
      115      120      125
Arg

```

<210> 2183  
 <211> 310  
 <212> DNA  
 <213> Homo sapiens

```

<400> 2183
aagcttgaaa aacaaatttg tgcacagtct gataacccaa aaatgactga tggattggct
60
ctgcattttc caagcagggg ggggtcgggc atggagaatg aaacattctg agaaaagact
120
taaagtgtga aacttttggg tcaagagggt attctaggag atacaagaaa tatctcctgg
180
gggcatacaa agggaataac actgtaatct tgagtgatgt atggttccat tgcccagagga
240
ataggggatga aaaccataaa ctcccttggg tgggtattaa cttatcantc aaagttacca
300
tanataatgg
310

```

<210> 2184  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

```

<400> 2184
Met Val Thr Leu Xaa Asp Lys Leu Ile Pro Thr Gln Arg Ser Leu Trp
1      5      10      15
Phe Ser Ser Leu Phe Leu Gly Gln Trp Asn His Thr Ser Leu Lys Ile
      20      25      30
Thr Val Leu Phe Pro Leu Asp Ala Pro Arg Arg Tyr Phe Leu Tyr Leu
      35      40      45
Leu Glu Tyr Pro Leu Glu Pro Lys Val Ser Thr Phe Lys Ser Phe Leu
      50      55      60
Arg Met Phe His Ser Pro Cys Pro Thr Pro Pro Cys Leu Glu Asn Ala
65      70      75      80
Glu Pro Ile His Gln Ser Phe Leu Gly Tyr Gln Thr Val His Lys Phe
      85      90      95
Val Phe Gln Ala

```

100

&lt;210&gt; 2185

&lt;211&gt; 723

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2185

```

ngaatatcca tgcagcagct cgtcgacaat ttgacgggtg ccatccctga cgatcttgac
60
tctcttgtga ccctgcccgg agtcggtcgt aagaccgcca atgttgtttt aggtaatgcc
120
ttcggcatcc ccggaatcac cccggacacc cacgtcatgc gggatatctcg acgtctgggc
180
tggaccgatg cgactacccc cgccaagggtg gaaaccgacc tggctgagct ttttgacccg
240
tctgaatggg tgatgttggtg tcaccgcctc atctggcacg ggcgggcgcg ctgtcactcg
300
cggcgtcctg cctgcgggggt atgcccgggt gccgagtggg gcccgctcctt cggggaaggc
360
ccaacggatc ccgaggaggc cgccacgtta gtccgggagc cgctcgatg agggggatga
420
acgttttcgg cgcggtgatg gccgccttga tgtttgctgg ctgcggggga gatgcgggca
480
tagctcatca gcgtgaaaat gccggaatac cggggtgctc gcatttgccg tcggggccga
540
ttgcgaaaag ttccgggccg gccacagagg gccggcccat gcccgatcac ggcttgcaat
600
gccttggtga ggggccgacg atctccatgt ctcgggcgac atcgaggggc gtgaccgtcg
660
tgacgatctg ggcgtcgtgg tgcgaccat gtcgtagtga ggctccgctc attgcgaacg
720
cgt
723

```

&lt;210&gt; 2186

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2186

```

Xaa Ile Ser Met Gln Gln Leu Val Asp Asn Phe Asp Gly Ala Ile Pro
1           5           10           15
Asp Asp Leu Asp Ser Leu Val Thr Leu Pro Gly Val Gly Arg Lys Thr
20           25           30
Ala Asn Val Val Leu Gly Asn Ala Phe Gly Ile Pro Gly Ile Thr Pro
35           40           45
Asp Thr His Val Met Arg Val Ser Arg Arg Leu Gly Trp Thr Asp Ala
50           55           60
Thr Thr Pro Ala Lys Val Glu Thr Asp Leu Ala Glu Leu Phe Asp Pro
65           70           75           80
Ser Glu Trp Val Met Leu Cys His Arg Leu Ile Trp His Gly Arg Arg
85           90           95
Arg Cys His Ser Arg Arg Pro Ala Cys Gly Val Cys Pro Val Ala Glu

```



100 105 110  
 Trp Cys Pro Ser Phe Gly Glu Gly Pro Thr Asp Pro Glu Glu Ala Ala  
 115 120 125  
 Thr Leu Val Arg Glu Pro Arg Arg  
 130 135

<210> 2187  
 <211> 342  
 <212> DNA  
 <213> Homo sapiens

<400> 2187  
 nnacgcgtga aggatgcgcc ccggtcgacc ggccatccgt cttgcctcgc aggcattccag  
 60  
 ccgcccatat gctgcaaccg caacaccgct ttgccgtcgc atggcatctc cactccggat  
 120  
 cgcattgatc caccaggggt atcggcgcca aagaagttgc cggggcaaaa tcccggcgag  
 180  
 gaaagcccga tggagtggaa gacgtgtctc aacgacaccc gcttcggagg ggtcgccagg  
 240  
 ctcgatggga cgcgcggacg gtcggagttc cagaaggacc acgaccggat catcttctcc  
 300  
 gaagccttcc gcaagctggg ccgcaagacc caggtgcacc cg  
 342

<210> 2188  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<400> 2188  
 Met Glu Trp Lys Thr Leu Leu Asn Asp Thr Arg Phe Gly Gly Val Ala  
 1 5 10 15  
 Ser Leu Asp Gly Thr Arg Gly Arg Ser Glu Phe Gln Lys Asp His Asp  
 20 25 30  
 Arg Ile Ile Phe Ser Glu Ala Phe Arg Lys Leu Gly Arg Lys Thr Gln  
 35 40 45  
 Val His Pro  
 50

<210> 2189  
 <211> 1412  
 <212> DNA  
 <213> Homo sapiens

<400> 2189  
 ntcgcttcat ggtgcgcaat tacgacaacg ccaagtctca gaatgccgag gcttacaccg  
 60  
 cgtttctcca cgcgatgcta gatgccgggg tcaacctgcc gccatcgtgc tttgaggcct  
 120  
 ggttcctctc ggacgtcac gacgacgaag ctttcgaggt tttccgcgcc gcctgccga  
 180  
 gggctgccca ggcggtgcc caggtgatca gtgcctgaca cggggtgac ttcgcaggtc  
 240

atcgaggcaa tctgtgcctg gtctgacgcc aacggacgcg atctgccgtg gcgccgaccc  
 300  
 ggcacctccg cgtggggcgt gcttgtagc gaggtcatga gccaacagac cccgatgtcc  
 360  
 cgggtgatcg ggccgtggca cgagtggatg aaccgctggc ccaccctga tgatttggcg  
 420  
 gagggaggact ctggggaagc ggttgccgcg tgggggcgcc tgggttaccg gcgtcgggccc  
 480  
 ttacgcctgc attcctgtgc cgtcacgac gccaccgagc acgacggggg tgtgcccac  
 540  
 agtgacgacg agctcgtcgc cctcccggtt attggcgact acaccgcgag cgcagtcgtc  
 600  
 tcttttgcgt ttggcgggcg cgccacagtg cttgacacca atgtacgtcg cctcatcgct  
 660  
 agagcagagt ctgggatcgc aaactgtcca acctcgggtga cgagggctga gcgggtagtc  
 720  
 gccgacgcgt tggttcccga cgaagacgac cgagcggcca agtggggcgtt ggcgtcgatg  
 780  
 gaattggggg cactgggtatg cacggcgcgg tctccgcagt gtgaggtctg cccgatccgg  
 840  
 gatggctgca ggtgggtgat cgacggtagg ccggacaatg ccccgggccc tcgaggacag  
 900  
 ccatggaagg gcacggatcg ccagtgccgc ggcgtgatta tggacgtggt gcgcaacagc  
 960  
 cctcacgggg tgaagggtcca gatggtcttt tccgcctggc ccgagctcga tcaggcatca  
 1020  
 aggtgccttg aatccttact cgatgacggt ttagtgcacc gacgaggtaa ccttattagc  
 1080  
 ctgtgacctg agaaattctt ggccccgacc acccaaacag accgagtcca gcagtgatgc  
 1140  
 cgctgggtta tccttagagg cggtcctcaa attggatcag ccaaaccacg tcaccgatca  
 1200  
 agacaccatg agcacaacac ccaaacagcc gcgcacggcg acagctgccc gacgccgaca  
 1260  
 cattgtcgac catctgcgtt ctttggggca ctcggagtcc atcggagatc ttaccaact  
 1320  
 gttcgggtgc tctacatcga cgattcgccg cgatgtcgat gccctctcgg atgaatccaa  
 1380  
 gatctggaag atttccgggg gagacgtcat ga  
 1412

&lt;210&gt; 2190

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2190

Ser	Val	Pro	Asp	Thr	Gly	Leu	Thr	Ser	Gln	Val	Ile	Glu	Ala	Ile	Cys
1				5				10						15	
Ala	Trp	Phe	Asp	Ala	Asn	Gly	Arg	Asp	Leu	Pro	Trp	Arg	Arg	Pro	Gly
			20				25					30			
Thr	Ser	Ala	Trp	Gly	Val	Leu	Val	Ser	Glu	Val	Met	Ser	Gln	Gln	Thr
		35				40					45				
Pro	Met	Ser	Arg	Val	Ile	Gly	Pro	Trp	His	Glu	Trp	Met	Asn	Arg	Trp

```

      50              55              60
Pro Thr Pro Asp Asp Leu Ala Glu Glu Asp Ser Gly Glu Ala Val Ala
65              70              75              80
Ala Trp Gly Arg Leu Gly Tyr Pro Arg Arg Ala Leu Arg Leu His Ser
      85              90              95
Cys Ala Val Thr Ile Ala Thr Glu His Asp Gly Gly Val Pro Asn Ser
      100             105             110
Asp Asp Glu Leu Val Ala Leu Pro Gly Ile Gly Asp Tyr Thr Ala Ser
      115             120             125
Ala Val Val Ser Phe Ala Phe Gly Gly Arg Ala Thr Val Leu Asp Thr
      130             135             140
Asn Val Arg Arg Leu Ile Ala Arg Ala Glu Ser Gly Ile Ala Asn Cys
145             150             155             160
Pro Thr Ser Val Thr Arg Ala Glu Arg Val Val Ala Asp Ala Leu Val
      165             170             175
Pro Asp Glu Asp Val Arg Ala Ala Lys Trp Ala Val Ala Ser Met Glu
      180             185             190
Leu Gly Ala Leu Val Cys Thr Ala Arg Ser Pro Gln Cys Glu Val Cys
      195             200             205
Pro Ile Arg Asp Gly Cys Arg Trp Val Ile Asp Gly Arg Pro Asp Asn
      210             215             220
Ala Pro Ala Arg Arg Gly Gln Pro Trp Lys Gly Thr Asp Arg Gln Cys
225             230             235             240
Arg Gly Val Ile Met Asp Val Val Arg Asn Ser Pro His Gly Val Lys
      245             250             255
Val Gln Met Ala Leu Ser Ala Trp Pro Glu Leu Asp Gln Ala Ser Arg
      260             265             270
Cys Leu Glu Ser Leu Leu Asp Asp Gly Leu Val His Arg Arg Gly Asn
      275             280             285
Leu Ile Ser Leu
      290

```

&lt;210&gt; 2191

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2191

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nnacgcgtcg agaattctcta ctccctgcccc aacaacgtcc ggcttcgtca ggctcacgat
60
gactcccttg acgacgacac catttcctggg ggtagccac attggtgctg cctcatggac
120
tacattgaat cccgttcaat cctgaacggc gttcaggacg tctccagtct cggaaggacc
180
agagtattgc tgaatctagc cgacatgacc gaacgcggcc tgagggggga gtccattacc
240
cgcgaggagg ccctcgagat tcttcgcagc agtgatgatg agctcatgtc aatcatcgcc
300
gccgcgggaa aagtgcgtcg ccactttttc gataaccggg ttgcctcaa ctacctggtc
360
aacctcaagt ccggcctgtg tcccgaagac tgctcctatt gctcgcagcg tctgggatcg
420
cgtgccgaga tcacgaaata ctctggggc gatccgcaga aggtacacga cgccgtcgag
480

```

gctgggattg ccggtggtgc ac  
502

<210> 2192  
<211> 104  
<212> PRT  
<213> Homo sapiens

<400> 2192  
Leu Asn Leu Ala Asp Met Thr Glu Arg Gly Leu Arg Gly Glu Ser Ile  
1 5 10 15  
Thr Arg Glu Glu Ala Leu Glu Ile Leu Arg Ser Ser Asp Asp Glu Leu  
20 25 30  
Met Ser Ile Ile Ala Ala Ala Gly Lys Val Arg Arg His Phe Phe Asp  
35 40 45  
Asn Arg Val Arg Leu Asn Tyr Leu Val Asn Leu Lys Ser Gly Leu Cys  
50 55 60  
Pro Glu Asp Cys Ser Tyr Cys Ser Gln Arg Leu Gly Ser Arg Ala Glu  
65 70 75 80  
Ile Thr Lys Tyr Ser Trp Ala Asp Pro Gln Lys Val His Asp Ala Val  
85 90 95  
Glu Ala Gly Ile Ala Gly Gly Ala  
100

<210> 2193  
<211> 321  
<212> DNA  
<213> Homo sapiens

<400> 2193  
ccatggggaa tgcagagcac ggacagtcac acagactgtc ctctctggcc ttctggaccc  
60  
aacatactcc tcttgccaac tgggtattac tggaccttac tgggccttac tggacccaac  
120  
atactcctct tgccaactgg ggatttaaaa attttaaaag cccctttatc tccctccaca  
180  
agtcatgtac tgccaacagg gacacactgt tttctttgga aaccctgctg tgtgcccaga  
240  
cagagggtccc actgccctgg gacagctccc ttgcctanag gggaaggagg gtgtgtgtgc  
300  
tgtgtgtgtt taggttgggg a  
321

<210> 2194  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 2194  
Met Gly Asn Ala Glu His Gly Gln Ser His Arg Leu Ser Ser Leu Ala  
1 5 10 15  
Phe Trp Thr Gln His Thr Pro Leu Ala Asn Trp Val Leu Leu Asp Leu  
20 25 30  
Thr Gly Pro Tyr Trp Thr Gln His Thr Pro Leu Ala Asn Trp Gly Phe

```

      35          40          45
Lys Asn Phe Lys Ser Pro Phe Ile Ser Leu His Lys Ser Cys Thr Ala
  50          55          60
Asn Arg Asp Thr Leu Phe Ser Leu Glu Thr Leu Leu Cys Ala Gln Thr
  65          70          75          80
Glu Val Pro Leu Pro Trp Asp Ser Ser Leu Ala Xaa Arg Gly Arg Arg
      85          90          95
Val Cys Val Leu Cys Val Phe Arg Leu Gly
      100          105

```

&lt;210&gt; 2195

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2195

```

nagcgtctc cctacatcaa tgcccaccgc gattgcacct ttgttgteat gtcacctggc
  60
gacggtgtgg cacaccccaa ctttggcaat atcgccacg acctggtgct gttgcacagc
  120
ctgggtgtgc gtctggtact ggtccacggt tcgcgcccgc agatcgacag ccgccttgag
  180
gcacgaggcc tggtgccgta ttaccacaag ggcattgctg tcaccgatgc atcaacgctc
  240
gaatgcgtga tcgatgctgt cgggcaactg cgcattgcca ttgaagcgcg cttgtcgatg
  300
gacatggcgt cttcgccaat gcagggttcg cgtctgcgcg tagccagcgg caacctggtc
  360
actgcgcggc cgatcggcgt gctcgacggt gtggattttc accataccgg cgaagtgcgc
  420
cgggtggacc gcaagggcat caaccgctg ctcatgagc gctcgattgt gctgctgtcg
  480
cccttgggtt actgcccac cggt
  504

```

&lt;210&gt; 2196

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2196

```

Xaa Ala Ser Pro Tyr Ile Asn Ala His Arg Asp Cys Thr Phe Val Val
  1          5          10          15
Met Leu Pro Gly Asp Gly Val Ala His Pro Asn Phe Gly Asn Ile Val
      20          25          30
His Asp Leu Val Leu Leu His Ser Leu Gly Val Arg Leu Val Leu Val
      35          40          45
His Gly Ser Arg Pro Gln Ile Asp Ser Arg Leu Glu Ala Arg Gly Leu
      50          55          60
Val Pro Tyr Tyr His Lys Gly Met Arg Val Thr Asp Ala Ser Thr Leu
      65          70          75          80
Glu Cys Val Ile Asp Ala Val Gly Gln Leu Arg Ile Ala Ile Glu Ala
      85          90          95
Arg Leu Ser Met Asp Met Ala Ser Ser Pro Met Gln Gly Ser Arg Leu

```

```

          100          105          110
Arg Val Ala Ser Gly Asn Leu Val Thr Ala Arg Pro Ile Gly Val Leu
          115          120          125
Asp Gly Val Asp Phe His His Thr Gly Glu Val Arg Arg Val Asp Arg
          130          135          140
Lys Gly Ile Asn Arg Leu Leu Asp Glu Arg Ser Ile Val Leu Leu Ser
          145          150          155          160
Pro Leu Gly Tyr Ser Pro Thr Gly
          165

```

&lt;210&gt; 2197

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2197

```

acaagtcctg cgacgattcg ctttccggag gcgggcccag gaatggtaat gaaacccgag
60
ttatggggcc ctgcgctcga cgagattgcc gcgggaaaac gtgccggagg ggctgaacag
120
ttagattccg cagtgcagca catccacggt gctactcacg ataaactgtc cgggtgctgt
180
ccgaaacgct acgatggctg ggatgtcttg gcaggcgagg acccgaatgc accgttgctg
240
cttgtgccta gcccggtggtg tgcagtgttt agtcaaaata aggcacaagc ctggtccaat
300
gaagaccaca ttgtttttgc ctgtggggcg tatgaaggta ttgatcaacg c
351

```

&lt;210&gt; 2198

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2198

```

Thr Ser Pro Ser Thr Ile Arg Phe Pro Glu Ala Gly Pro Gly Met Val
1          5          10          15
Met Lys Pro Glu Leu Trp Gly Pro Ala Leu Asp Glu Ile Ala Ala Gly
          20          25          30
Lys Arg Ala Gly Gly Ala Glu Gln Leu Asp Ser Ala Val Gln His Ile
          35          40          45
His Gly Ala Thr His Asp Lys Leu Ser Gly Ala Val Pro Lys Arg Tyr
          50          55          60
Asp Gly Arg Asp Val Leu Ala Gly Glu Asp Pro Asn Ala Pro Leu Leu
65          70          75          80
Leu Val Pro Ser Pro Ala Gly Ala Val Phe Ser Gln Asn Lys Ala Gln
          85          90          95
Ala Trp Ser Asn Glu Asp His Ile Val Phe Ala Cys Gly Arg Tyr Glu
          100          105          110
Gly Ile Asp Gln Arg
          115

```

&lt;210&gt; 2199

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2199

```

agacgccggc cgccaagatc tgcattcccta ggccacgcta agaccctggg gaagagcgca
60
ggagccccggg agaagggctg gaaggagggg actggacgtg cggagaattc cccctaaaa
120
ggcagaagcc cccgccccca cctccgagc tccgttcggg cagagcgctt gcctgcctgc
180
cgttgctggg ggcgcccacc tcgcccagcc atgccaggcc cggccaccga cgcggggaag
240
atccctttct gcgacgcaa ggaagaaatc cgtgccgggc tcgaaagctc tgagggcggc
300
ggcgggcccg agaggccagg cgcgcgcggg cagcggcaga acatcgtctg gaggaatgtc
360
gtcctgatga gcttgctcca cttggggggc gtgtactccc tgggtctcat ccccaaagcc
420
aagccactca ctctgctctg gggtaagtcc cgccggc
457

```

&lt;210&gt; 2200

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2200

```

Arg Arg Arg Pro Pro Arg Ser Ala Ser Leu Gly His Ala Lys Thr Leu
1      5      10      15
Gly Lys Ser Ala Gly Ala Arg Glu Lys Gly Trp Lys Glu Gly Thr Gly
20      25      30
Arg Ala Glu Asn Ser Pro Leu Lys Gly Arg Ser Pro Arg Pro His Pro
35      40      45
Pro Ser Ser Val Arg Ala Glu Arg Leu Pro Ala Cys Arg Cys Trp Gly
50      55      60
Arg Pro Pro Arg Pro Ala Met Pro Gly Pro Ala Thr Asp Ala Gly Lys
65      70      75      80
Ile Pro Phe Cys Asp Ala Lys Glu Glu Ile Arg Ala Gly Leu Glu Ser
85      90      95
Ser Glu Gly Gly Gly Gly Pro Glu Arg Pro Gly Ala Arg Gly Gln Arg
100     105     110
Gln Asn Ile Val Trp Arg Asn Val Val Leu Met Ser Leu Leu His Leu
115     120     125
Gly Ala Val Tyr Ser Leu Val Leu Ile Pro Lys Ala Lys Pro Leu Thr
130     135     140
Leu Leu Trp Gly Lys Ser Arg Arg
145     150

```

&lt;210&gt; 2201

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2201

agtactgcga tggacagcta tgctgtggat ggtggtcgca aattacatgt ttgtggtaac  
 60  
 aaccctgatt gcgatggta tgaagtcgaa gaaggcgaat tcaagatcaa gggttatgat  
 120  
 ggtccgacta tcccatgcga taaatgtgat ggtgagatgc agcttaaaac gggtcgtttt  
 180  
 ggtccatatt tcgcatgtac tagctgtgac aatactcgta aggtactcaa gagtgggtcaa  
 240  
 cctgctccgc cacgtgtaga cccaatcaaa atggagcatc tacgttcaac gaagcatgat  
 300  
 gattttcttcg tcttacgtga gggcgtgct ggttta  
 336

<210> 2202

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2202

Ser	Thr	Ala	Met	Asp	Ser	Tyr	Val	Val	Asp	Gly	Gly	Arg	Lys	Leu	His
1				5					10					15	
Val	Cys	Gly	Asn	Asn	Pro	Asp	Cys	Asp	Gly	Tyr	Glu	Val	Glu	Glu	Gly
		20						25					30		
Glu	Phe	Lys	Ile	Lys	Gly	Tyr	Asp	Gly	Pro	Thr	Ile	Pro	Cys	Asp	Lys
		35				40					45				
Cys	Asp	Gly	Glu	Met	Gln	Leu	Lys	Thr	Gly	Arg	Phe	Gly	Pro	Tyr	Phe
	50				55					60					
Ala	Cys	Thr	Ser	Cys	Asp	Asn	Thr	Arg	Lys	Val	Leu	Lys	Ser	Gly	Gln
65					70				75					80	
Pro	Ala	Pro	Pro	Arg	Val	Asp	Pro	Ile	Lys	Met	Glu	His	Leu	Arg	Ser
				85				90					95		
Thr	Lys	His	Asp	Asp	Phe	Phe	Val	Leu	Arg	Glu	Gly	Ala	Ala	Gly	Leu
			100					105					110		

<210> 2203

<211> 273

<212> DNA

<213> Homo sapiens

<400> 2203

ctcgagagat gcagtcaccag ccgggggtggg aagctgtgca gacagccccg gatctggggac  
 60  
 gtgatggaaa actcaacaga ctgggttcaga tcttggtccc gagcccagag gcaccgggga  
 120  
 cccccagggc tgtttctccc tggccacacc agtaccacac ttccaaatgc cctgtagggtg  
 180  
 accaccaggc cacacaggcc cgtctgaggg gccacaggct gtgcaccatg ggacgcaggc  
 240  
 ctgtccctgc ctccctccga tgtcctgatg gtg  
 273

<210> 2204

<211> 88

<212> PRT



&lt;213&gt; Homo sapiens

&lt;400&gt; 2204

```

Met Gln Ser Gln Pro Gly Trp Glu Ala Val Gln Thr Ala Pro Asp Leu
 1             5             10             15
Gly Arg Asp Gly Lys Leu Asn Arg Leu Val Gln Ile Leu Ala Arg Ser
          20             25             30
Pro Glu Ala Pro Gly Thr Pro Arg Ala Val Ser Pro Trp Pro His Gln
          35             40             45
Tyr Pro Thr Ser Lys Cys Pro Val Gly Asp His Gln Ala Thr Gln Ala
 50             55             60
Arg Leu Arg Gly His Arg Leu Cys Thr Met Gly Arg Arg Pro Val Pro
65             70             75             80
Ala Ser Leu Arg Cys Pro Asp Gly
          85

```

&lt;210&gt; 2205

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2205

```

gnnnnnggng nnnnactggt gtgcatgggt aaaatcctgc aagctactgg gttgccacag
60
catctgtccc actttgtggt ctgcaaatac agcttctggg atcaacagga gccggtgatt
120
gtcgctcctg aagtggacac ctctcctct tccgtcagca aggagccgca ctgcatgggt
180
gtctttgatc attgcaatga gttttctggt aacatcaccg aagactttat cgagcatctt
240
tccgaaggag cattggcaat tgaagtatat ggacataaaa taaacgatcc ccggaaaaac
300
cccgccctgt gggatttggg aatcatccaa gcaaagacac gtagtcttcg ggacagatgg
360
agtgaagtgc ccaggaaatt ggaattc
387

```

&lt;210&gt; 2206

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2206

```

Xaa Xaa Gly Xaa Xaa Leu Val Cys Met Val Lys Ile Leu Gln Ala Thr
 1             5             10             15
Gly Leu Pro Gln His Leu Ser His Phe Val Phe Cys Lys Tyr Ser Phe
          20             25             30
Trp Asp Gln Gln Glu Pro Val Ile Val Ala Pro Glu Val Asp Thr Ser
          35             40             45
Ser Ser Ser Val Ser Lys Glu Pro His Cys Met Val Val Phe Asp His
 50             55             60
Cys Asn Glu Phe Ser Val Asn Ile Thr Glu Asp Phe Ile Glu His Leu
65             70             75             80
Ser Glu Gly Ala Leu Ala Ile Glu Val Tyr Gly His Lys Ile Asn Asp

```

85 90 95  
 Pro Arg Lys Asn Pro Ala Leu Trp Asp Leu Gly Ile Ile Gln Ala Lys  
 100 105 110  
 Thr Arg Ser Leu Arg Asp Arg Trp Ser Glu Val Pro Arg Lys Leu Glu  
 115 120 125  
 Phe

<210> 2207  
 <211> 667  
 <212> DNA  
 <213> Homo sapiens

<400> 2207  
 atctccaacc ccgagaccct ctccaataca gccggcttcg agggctacat cgacctgggc  
 60  
 cgcgagctct ccagcctgca ctcaactgctc tgggaggccg tcagccagct ggagcagaac  
 120  
 atagtatcca aactgggacc cctgcctcgg atcctgaggg acgtccacac agcactgagc  
 180  
 accccaggta gcgggcagct ccaggggacc aatgacctgg cctccacacc gggctctggc  
 240  
 agcagcagca tctcagctgg gctgcagaag atgggtgattg agaacgatct ttccggtctg  
 300  
 atagatttca cccggttacc gtctccaacc cccgaaaaca aggacttggt ttttgtcaca  
 360  
 aggtcctccg ggggccagcc ctcaactgcc cgcagctcga gttactcgga agccaacgag  
 420  
 cctgatcttc agatggccaa cgggtggcaag agcctctcca tgggtggacct ccaggacgcc  
 480  
 cgcacgctgg atggggaggc aggtcccccg gcgggccccg acgtcctccc cacagatggg  
 540  
 caggccgctg cagctcagct ggtggccggg tggccggccc gggcaacccc agtgaacctg  
 600  
 gcagggtggt ccacgggtgcg gcgggcaggc cagacaccaa ccacaccagg cacctccgag  
 660  
 ggcgcgcg  
 667

<210> 2208  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens

<400> 2208  
 Ile Ser Asn Pro Glu Thr Leu Ser Asn Thr Ala Gly Phe Glu Gly Tyr  
 1 5 10 15  
 Ile Asp Leu Gly Arg Glu Leu Ser Ser Leu His Ser Leu Leu Trp Glu  
 20 25 30  
 Ala Val Ser Gln Leu Glu Gln Ser Ile Val Ser Lys Leu Gly Pro Leu  
 35 40 45  
 Pro Arg Ile Leu Arg Asp Val His Thr Ala Leu Ser Thr Pro Gly Ser  
 50 55 60  
 Gly Gln Leu Pro Gly Thr Asn Asp Leu Ala Ser Thr Pro Gly Ser Gly

```

65          70          75          80
Ser Ser Ser Ile Ser Ala Gly Leu Gln Lys Met Val Ile Glu Asn Asp
      85          90          95
Leu Ser Gly Leu Ile Asp Phe Thr Arg Leu Pro Ser Pro Thr Pro Glu
      100          105          110
Asn Lys Asp Leu Phe Phe Val Thr Arg Ser Ser Gly Val Gln Pro Ser
      115          120          125
Pro Ala Arg Ser Ser Ser Tyr Ser Glu Ala Asn Glu Pro Asp Leu Gln
      130          135          140
Met Ala Asn Gly Gly Lys Ser Leu Ser Met Val Asp Leu Gln Asp Ala
      145          150          155          160
Arg Thr Leu Asp Gly Glu Ala Gly Ser Pro Ala Gly Pro Asp Val Leu
      165          170          175
Pro Thr Asp Gly Gln Ala Ala Ala Ala Gln Leu Val Ala Gly Trp Pro
      180          185          190
Ala Arg Ala Thr Pro Val Asn Leu Ala Gly Leu Ala Thr Val Arg Arg
      195          200          205
Ala Gly Gln Thr Pro Thr Thr Pro Gly Thr Ser Glu Gly Ala
      210          215          220

```

&lt;210&gt; 2209

&lt;211&gt; 353

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2209

```

ngggaagttg gtactagcct cccaaagcca ctctcctgag tgacattgag agcatcctat
60
agagaaggcc atgagagaga tagcactggg acagatggtg tcagcagagg ggactccaga
120
ccacagcaga agtgaccaag ctgtagcttc cttagatggc cccaaggggtg ggaggcttca
180
cacagcagag cctgggtctg gaggcacctt ggggatgttt ttccccatta ggcccctgag
240
ctctatggaa gcacttaact gctgttccc cgcttattct gtgtttaaac caaggaaaca
300
acatgcctgg ggtctgaaat cctggattca aatcctgact gtgttggtgtg ctt
353

```

&lt;210&gt; 2210

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2210

```

Met Arg Glu Ile Ala Leu Gly Gln Met Val Ser Ala Glu Gly Thr Pro
1          5          10          15
Asp His Ser Arg Ser Asp Gln Ala Val Ala Ser Leu Asp Gly Pro Lys
      20          25          30
Gly Gly Arg Leu His Thr Ala Glu Pro Gly Ser Gly Gly Thr Leu Gly
      35          40          45
Met Phe Phe Pro Ile Arg Pro Leu Ser Ser Met Glu Ala Leu Asn Cys
      50          55          60
Leu Phe Pro Ala Tyr Ser Val Phe Lys Pro Arg Lys Gln His Ala Trp

```

65                      70                      75  
Gly Leu Lys Ser Trp Ile Gln Ile Leu Thr Val Leu Cys Ala  
                      85                      90

```
<210> 2211
<211> 493
<212> DNA
<213> Homo sapiens
```

```
<400> 2211
ctgaccacat ctccgacgat cctagacctc tgttctgcat ctcggaacac accgactgct
60
cactgtaccc tgggactgca cagagggaaa cgattaccaa acccagagac ggggaccgga
120
aggaaggagg ggaaggggat ggatccatgt actttgggggt tggagaaatg ggggacagca
180
agtctcctca acccaaatac agcccccttg ggaggtcctt gccccgtctc tgtggatagt
240
gagcccagct gcaagggcgg cctgccaggg acaaaccac caaaaggaaa gatgtttag
300
aaccaaagag aggtccctg aaagaggcgt ctcccggggc ctccaagccc gggagcgccc
360
ggcggacagg gggcagtggc caagtctgtg cggaccctga ccgcctcaga gaacgagagc
420
atgcgcaaag tcatgcccac caccaagtcc agcagaggcg ccggctggag gcgaccagag
480
ctgtcatccc ggg
493
```

```
<210> 2212
<211> 126
<212> PRT
<213> Homo sapiens
```

```

<400> 2212
Met Gly Met Thr Leu Arg Met Leu Ser Phe Ser Glu Ala Val Arg Val
 1                    5                      10                      15
Arg Thr Asp Leu Ala Thr Ala Pro Cys Pro Pro Gly Ala Pro Gly Leu
      20                      25                      30
Gly Gly Pro Gly Arg Arg Leu Phe Gln Gly Ala Ser Leu Trp Phe Tyr
      35                      40                      45
Asn Ile Phe Pro Phe Gly Gly Phe Val Pro Gly Arg Pro Pro Leu Gln
      50                      55                      60
Leu Gly Ser Leu Ser Thr Glu Thr Gly Gln Glu Pro Pro Arg Gly Ala
65                      70                      75                      80
Val Phe Gly Leu Arg Arg Leu Ala Val Pro His Phe Ser Asn Pro Lys
      85                      90
Val His Gly Ser Ile Pro Phe Pro Ser Phe Leu Pro Val Pro Val Ser
      100                      105                      110
Gly Phe Gly Asn Arg Phe Pro Leu Cys Ser Pro Arg Val Gln
      115                      120                      125

```

<210> 2213  
<211> 327

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2213

acgcgtccga ccggcagttc cggcagctgc gggaaagctg cgatgcgctc gccgagcatt  
60  
gcegggtgctt cgacacactg gggttatatcg ccctcaaagc acaggtctac gaaggttctg  
120  
acggaaggcc cggccaatcc gatcgcggcc tcggcgctgc gcatcatccg ggcgcgctg  
180  
tcgcagctct ggggcacgtc gctgctccgc aacggacggg cggaacagag tgtggtggag  
240  
atgccccggt tggtcgacgc gatcacgtca cgggacgagg aagccgccca gcgtgcactg  
300  
ctcgaccaca atcgacgcgc gttggaa  
327

&lt;210&gt; 2214

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2214

Met	Arg	Ser	Pro	Ser	Ile	Ala	Gly	Ala	Ser	Thr	His	Trp	Val	Ile	Ser
1				5					10				15		
Pro	Ser	Lys	His	Arg	Ser	Thr	Lys	Val	Leu	Thr	Glu	Gly	Pro	Ala	Asn
			20					25					30		
Pro	Ile	Ala	Ala	Ser	Ala	Leu	Arg	Ile	Ile	Arg	Ala	Arg	Val	Ser	Gln
		35					40					45			
Leu	Trp	Gly	Thr	Ser	Leu	Leu	Arg	Asn	Gly	Arg	Ala	Glu	Gln	Ser	Val
	50					55				60					
Val	Glu	Ile	Ala	Arg	Leu	Val	Asp	Ala	Ile	Thr	Ser	Arg	Asp	Glu	Glu
65				70					75					80	
Ala	Ala	Gln	Arg	Ala	Leu	Leu	Asp	His	Asn	Arg	Ser	Ala	Leu	Glu	
			85						90					95	

&lt;210&gt; 2215

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2215

ctggggatca tgccctacat cactgcgtcg atcatcctgc agctgctgac agtcgtgac  
60  
ccgaagctgg aaacccttaa gaaggagggc gcgtccggtc agaacaagat caccagctac  
120  
accggttacc tcaactctcgt gcttggcctg ttgcaggcaa cggccttcgt cacgcttgcc  
180  
acctccggcc gtctattcac cnntgcagct ntgccagtcg tctactccac ctcggtcttc  
240  
gaagtcgtcg tcatgatcct gactatgacg gccggtacga ccatcgatcat gtggatgggt  
300  
gagctcatca ccgaccgagg tatcggcaac ggtatgtcga tcatgatttt cactcagatt  
360

gcggcgcggtt tccctgactc gctgtggtct atcaaggtcg ctcgaaatgg cgccggtcag  
 420  
 gctcacgcgt  
 430

<210> 2216  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 2216  
 Leu Gly Ile Met Pro Tyr Ile Thr Ala Ser Ile Ile Leu Gln Leu Leu  
 1 5 10 15  
 Thr Val Val Ile Pro Lys Leu Glu Thr Leu Lys Lys Glu Gly Ala Ser  
 20 25 30  
 Gly Gln Asn Lys Ile Thr Gln Tyr Thr Arg Tyr Leu Thr Leu Val Leu  
 35 40 45  
 Gly Leu Leu Gln Ala Thr Ala Phe Val Thr Leu Ala Thr Ser Gly Arg  
 50 55 60  
 Leu Phe Thr Xaa Ala Ala Xaa Pro Val Val Tyr Ser Thr Ser Val Phe  
 65 70 75 80  
 Glu Val Val Val Met Ile Leu Thr Met Thr Ala Gly Thr Thr Ile Val  
 85 90 95  
 Met Trp Met Gly Glu Leu Ile Thr Asp Arg Gly Ile Gly Asn Gly Met  
 100 105 110  
 Ser Ile Met Ile Phe Thr Gln Ile Ala Ala Arg Phe Pro Asp Ser Leu  
 115 120 125  
 Trp Ser Ile Lys Val Ala Arg Asn Gly Ala Gly Gln Ala His Ala  
 130 135 140

<210> 2217  
 <211> 444  
 <212> DNA  
 <213> Homo sapiens

<400> 2217  
 accagggccg cttcgaagga cctctctcca gctatcgtga cgacgacggc gaagcgggct  
 60  
 atgacgtggc tcgatgacga cgtgggcgcc gacctgttga atcaggctga ttccatggac  
 120  
 catgccctgg aggccaccgt cccagggtcgg gtcaccacgc cggacgccca agtcattccag  
 180  
 acctgtgccg tggttgctga ccttgctcgc gtggcagtcg gccagctggg ccgaaatgac  
 240  
 gaggactcta gggaaccagt cgatgcggag agagtacagg ctcaagcgnc gatgcggggag  
 300  
 gttttcgaga ccgccgaacg catggtgggg ctggccgccg ccgacgtggt gtgggtctct  
 360  
 gagtctgaga agggataccg cagcattcac gtcgtccgc tgagtgttg cggttgcta  
 420  
 cgagagaatg tctttgctca gtcc  
 444

<210> 2218

<211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 2218  
 Thr Arg Ala Ala Ser Lys Asp Leu Ser Pro Ala Ile Val Thr Thr Thr  
 1 5 10 15  
 Ala Lys Arg Ala Met Thr Trp Leu Asp Asp Asp Val Gly Ala Asp Leu  
 20 25 30  
 Leu Asn Gln Ala Asp Ser Met Asp His Ala Leu Glu Ala Thr Val Pro  
 35 40 45  
 Gly Arg Val Thr Thr Pro Asp Ala Gln Val Ile Gln Thr Cys Ala Val  
 50 55 60  
 Leu Arg Asp Leu Ala Arg Val Ala Val Ser Gln Leu Gly Arg Asn Asp  
 65 70 75 80  
 Glu Asp Ser Arg Glu Pro Val Asp Ala Glu Arg Val Gln Ala Gln Ala  
 85 90 95  
 Xaa Met Arg Glu Val Phe Glu Thr Ala Glu Arg Met Val Gly Leu Ala  
 100 105 110  
 Ala Ala Asp Val Val Trp Val Ser Glu Ser Glu Lys Gly Tyr Arg Ser  
 115 120 125  
 Ile His Val Ala Pro Leu Ser Val Gly Gly Leu Leu Arg Glu Asn Val  
 130 135 140  
 Phe Ala Gln Ser  
 145

<210> 2219  
 <211> 688  
 <212> DNA  
 <213> Homo sapiens

<400> 2219  
 acgcgtaccg tcgttggcat gagcgtcctg ccactggaaa tttggctgtc attcagctac  
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 120  
 tggtcgatcc ttttccccgc tgggtggctg accagcgtt tggtcagtca ggggttcggt  
 180  
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 240  
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 360  
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 420  
 atcgagacga atctcggcgc tccgttcattg ttgctcattg tgaaagcttg gcgcgcgcca  
 480  
 cccgaaggaa ttcttggtc taccagtcgg cgcccgaccg cccgtggcac agcgcgagtc  
 540  
 tatatgaggg atgatcttgt ttctcgacgc cttctacagc gtccttgaga gcctctgcga  
 600  
 gcgaagggcg cgggtgtagg tctccccggg gctcgttggtg gtccctctc tcgctgacgc  
 660

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688

<210> 2220

<211> 189

<212> PRT

<213> Homo sapiens

<400> 2220

Met	Ser	Val	Leu	Pro	Leu	Glu	Ile	Trp	Leu	Ser	Phe	Ser	Tyr	Gly	Ile
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Thr	Asn	Met	Ala	Trp	Met	Trp	Leu	Trp	Phe	Asp	Glu	Pro	Gly	Asn	Arg
			20					25					30		
Trp	Glu	Trp	Ser	Ile	Leu	Phe	Pro	Ala	Gly	Trp	Leu	Thr	Ser	Ala	Leu
		35				40					45				
Val	Ser	Gln	Gly	Phe	Gly	Gly	Met	Phe	His	Ser	Val	Gln	Ile	Ala	Arg
	50				55						60				
His	Val	Ser	Ser	Tyr	His	Gly	Ile	Met	Val	Ala	Phe	Ala	Leu	Val	Gly
65				70					75					80	
Tyr	Gly	Trp	Leu	Ala	Met	His	Asn	Leu	Arg	His	Pro	Asp	Glu	Arg	Tyr
			85					90					95		
Ser	Ile	Arg	Ser	Ala	Leu	Ile	Ile	Gly	Ile	Gly	Ile	Gln	Phe	Thr	Trp
		100						105				110			
Glu	Ala	Val	Leu	Met	Ile	Ser	Gly	Ile	Arg	Pro	Leu	Thr	Trp	Arg	Pro
	115						120				125				
Leu	Val	Ile	Asp	Ser	Leu	Ile	Glu	Thr	Asn	Leu	Gly	Ala	Pro	Phe	Met
	130					135					140				
Leu	Leu	Ile	Val	Lys	Ala	Trp	Arg	Ala	Pro	Pro	Glu	Gly	Ile	Pro	Gly
145				150					155					160	
Ser	Thr	Ser	Pro	Arg	Pro	Thr	Ala	Arg	Gly	Thr	Ala	Arg	Val	Tyr	Met
			165					170					175		
Arg	Asp	Asp	Leu	Val	Ser	Arg	Arg	Leu	Leu	Gln	Arg	Pro			
			180					185							

<210> 2221

<211> 530

<212> DNA

<213> Homo sapiens

<400> 2221

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120  
ctacaacaac gcctcagtaa aaccaaacc atcaagcaag gcatgatgca agaactactc  
180  
acagggaaaa cgaggttggt atgagccaca aggtgaattt agtgcattgag ctggataagc  
240  
gtattatctc ggtaaatacg ttattgtcac agcctgagct tgctattccg gcttatcagc  
300  
ggccttataa atggtcacaa gagaacctaa atgcgctgat gaggattta cgaatttacc  
360  
gtaacaaatc ggcttatcgg ctggggacgg tggtttttca ttatcataat gaaccgtag  
420



acaacgagaa taccacaag ctggatattg tagacggta gcaacgtacc ttaaccttgt  
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 tgctgctagt caaagccatt ttagaagaac ggttgctctgc gttaacgcgt  
 530

<210> 2222  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

<400> 2222  
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 1 5 10 15  
 Ile Leu Pro Pro Lys Glu Glu Gln Thr Ala Ile Ala Asn Val Leu Ser  
 20 25 30  
 Asp Met Asp Thr Glu Leu Asp Ala Leu Gln Gln Arg Leu Ser Lys Thr  
 35 40 45  
 Lys Thr Ile Lys Gln Gly Met Met Gln Glu Leu Leu Thr Gly Lys Thr  
 50 55 60  
 Arg Leu Val  
 65

<210> 2223  
 <211> 482  
 <212> DNA  
 <213> Homo sapiens

<400> 2223  
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 120  
 tgcatttatc caacggccgg gacagggccg gcagttcaca gtccagtttg taaagcgtg  
 180  
 cgcgtcctgc gctgatatag gcctggagat gcccattggc gtgtcgggca acctcgtagt  
 240  
 tcaggccgtc gagcaccaca aggatgacgt tgtgttcat aaggggagac gctccgcaac  
 300  
 gataggcttg actcatttca cttgaggaac ggggtcaaaa ctgtgggcgc gggcaagccc  
 360  
 gctccacac aagcccgctgc ccacattgga tctccaatgt gggctacagc cttactgcat  
 420  
 attgatgatg acttcttctt gccattctg cggcagtgcc ttggaggtct tttccacgc  
 480  
 gt  
 482

<210> 2224  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 2224  
 Met Ser Gln Ala Tyr Arg Cys Gly Ala Ser Pro Leu Met Lys His Asn

1	5	10	15
Val Ile Leu Val Val Leu Asp Gly Leu Asn Tyr Glu Val Ala Arg His			
	20	25	30
Ala Met Gly His Leu Gln Ala Tyr Ile Ser Ala Gly Arg Ala Ala Leu			
	35	40	45
Tyr Lys Leu Asp Cys Glu Leu Pro Ala Leu Ser Arg Pro Leu Asp Lys			
	50	55	60
Cys Ile Phe Thr Gly Val Pro Pro Ile Asp Ser Gly Ile Val His Asn			
65	70	75	80
Asn Val Ser Arg Leu Ser Asn Gln Arg Ser Ile Phe His Tyr Ala Thr			
	85	90	95
Asp Ala Gly Leu Thr Thr Ala Ala Ala			
	100	105	

&lt;210&gt; 2225

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2225

```

naccgctctg atccacacgg gccactgacg tggcggttatg acaggagcgg ggccggtgcc
60
ggcgtcatcc tcgatctcat gggtcacgga gaggatctcg tccagtatct actcaaaggg
120
cgattcactg aggtgtccgc cgtgtccgag acgttcatcc gtcagcgtcc caagccactc
180
aaggagggca tcggccacac aggttgggtc gtctcggacg agctcggggc ggtgggcaac
240
gaggattatt gcgctgtcat cgcccgtatg gaaaacggag tgatgtgcac cctggagtcc
300
agtcgggtca gtgttggggc gcgcgcggag tacatcgtcg agatctatgg aaccgacgga
360
tcaatccggt ggaacttcga ggatctcaac catttgcagg tctgtctggg gcgaaacaat
420
cgtgccctgc agggatatgt caactgcatg gccggaccag acttcccgga gttcatgcgt
480
ttccaaccgg gagccggaac atccatgggc tttagcaca tgaaggctcg tgaggctcgc
540
aaattcgtcc gaggggtctt ggatgggcag caatatggcc catctgtcgc cgatggttgg
600
gcctcagcgg aggtcaacga tgcgacgtt gcctcctgcg ggggaccatg cctggcatga
660
cgtgaagccg gtttcgggga gaaccacgtt cgataagtga ccgcgtcatc gcgtgtctgt
720
gaccaggcct ggcggcacaa ccaggtcgcc ggc
753

```

&lt;210&gt; 2226

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2226

Xaa Ala Ser Asp Pro His Gly Pro Leu Thr Trp Arg Tyr Asp Arg Glu

```

1           5           10           15
Arg Ala Gly Ala Gly Val Ile Leu Asp Leu Met Gly His Gly Glu Asp
20           25           30
Leu Val Gln Tyr Leu Leu Lys Gly Arg Phe Thr Glu Val Ser Ala Val
35           40           45
Ser Glu Thr Phe Ile Arg Gln Arg Pro Lys Pro Leu Lys Glu Gly Ile
50           55           60
Gly His Thr Gly Trp Val Val Ser Asp Glu Leu Gly Pro Val Gly Asn
65           70           75           80
Glu Asp Tyr Cys Ala Val Ile Ala Arg Met Glu Asn Gly Val Met Cys
85           90           95
Thr Leu Glu Ser Ser Arg Val Ser Val Gly Pro Arg Ala Glu Tyr Ile
100          105          110
Val Glu Ile Tyr Gly Thr Asp Gly Ser Ile Arg Trp Asn Phe Glu Asp
115          120          125
Leu Asn His Leu Gln Val Cys Leu Gly Arg Asn Asn Arg Ala Leu Gln
130          135          140
Gly Tyr Val Asn Cys Met Ala Gly Pro Asp Phe Pro Glu Phe Met Arg
145          150          155          160
Phe Gln Pro Gly Ala Gly Thr Ser Met Gly Phe Asp Asp Met Lys Val
165          170          175
Val Glu Ala Ala Lys Phe Val Arg Gly Val Leu Asp Gly Gln Gln Tyr
180          185          190
Gly Pro Ser Val Ala Asp Gly Trp Ala Ser Ala Glu Val Asn Asp Ala
195          200          205
Ile Val Ala Ser Cys Gly Gly Pro Cys Leu Ala
210          215

```

&lt;210&gt; 2227

&lt;211&gt; 324

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2227

```

ggatccgaaa cggtgggagc ataaagcagc atggcgccacc tactgaagac ggtggtggct
60
ggctgttcat gtcctttcct tagcaacttg gggctctcta aggttctacc tgggaagaga
120
gactttgtac gaacgcttcg tactcaccag gcaactgtgggt gtaaatcccc ggtaaagcca
180
ggaattccat ataagcagtt gacagttggg gtccccaagg agattttcca aaacgagaag
240
cgagttgcat tgtctcctgc ggggggtccag gccctgggtca agcaggggctt caatgttgtc
300
gtggaatcag gcgcaggcga agct
324

```

&lt;210&gt; 2228

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2228

```

Met Ala His Leu Leu Lys Thr Val Val Ala Gly Cys Ser Cys Pro Phe

```

```

      1             5             10             15
Leu Ser Asn Leu Gly Ser Ser Lys Val Leu Pro Gly Lys Arg Asp Phe
      20             25             30
Val Arg Thr Leu Arg Thr His Gln Ala Leu Trp Cys Lys Ser Pro Val
      35             40             45
Lys Pro Gly Ile Pro Tyr Lys Gln Leu Thr Val Gly Val Pro Lys Glu
      50             55             60
Ile Phe Gln Asn Glu Lys Arg Val Ala Leu Ser Pro Ala Gly Val Gln
      65             70             75             80
Ala Leu Val Lys Gln Gly Phe Asn Val Val Val Glu Ser Gly Ala Gly
      85             90             95
Glu Ala

```

&lt;210&gt; 2229

&lt;211&gt; 320

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2229

```

acgcgtgaag gggccctgtg acgaggtcat ttctgtccat ggggggtcca gatggtgagg
60
cccacagaga gggaacgggc ggggggaggg gaggagagaa gacagactca ggcagaaccc
120
tagctcagcc ccttcctgcg tgcttgcccc tgggaggatg ccatccccag tccccctctc
180
tgggccctgc tctggggact cggcacagat ggatccagtg catcctcagc cccctgagaa
240
gctgtgctgc catcagctcc ttctctgggt acagggcacg ggaagcggct gcccagcagg
300
cctcggtccc gccaaagtgt
320

```

&lt;210&gt; 2230

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2230

```

Met Gly Gly Pro Asp Gly Glu Ala His Arg Glu Gly Thr Gly Gly Gly
      1             5             10             15
Arg Gly Gly Glu Lys Thr Asp Ser Gly Arg Thr Leu Ala Gln Pro Leu
      20             25             30
Pro Ala Cys Leu Ala Leu Gly Gly Cys His Pro Gln Ser Pro Leu Leu
      35             40             45
Gly Pro Ala Leu Gly Thr Arg His Arg Trp Ile Gln Cys Ile Leu Ser
      50             55             60
Pro Leu Arg Ser Cys Ala Ala Ile Ser Ser Phe Ser Gly Tyr Arg Ala
      65             70             75             80
Arg Glu Ala Ala Ala Gln Gln Ala Ser Val Pro Pro Ser Cys
      85             90

```

&lt;210&gt; 2231

&lt;211&gt; 671

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2231

```

gggctgtcta ccacgggctt cgggacttgg ggcagcttcc tgagctctct gagctgcagt
60
tccttcaacc acaaaatgag gagagtgcag gacctcagag gcttactgtg aggatggaga
120
aaagcccagt tcaatgcccc actgggaaat gcttcccatt aattgtggaa ttgtcgtgcc
180
catttactgt cggggtgaca ggggggggtgg gggtcagagt agagacagga gaaggaagtg
240
agcatttgtg ggataccac cacgtgccag ggactgaacc ctatctggat ctctgcagc
300
cctccaatg gcactgtgaa gccagtgttg ttttacagat gaggaaactg agatttgtgg
360
ctataacaga taaacagatg accctgaatg gggcaggtca tgtcatctgc catagataca
420
tgcatagaac aatgcaaacc agtcagtcct ctctgagtca gaccaggctg accatcaggg
480
acatgcagac actggcaggg ctgggggttg tccccatcgg tgatagcctg gtgccccat
540
ggcccctgat gcccacggct gtctggaagg ctgggtcact gctgagaaga caaggagaca
600
ttttctctca ccagctttct ttttctatt ccttcttaga cacctgagct gcggtgatca
660
cagctcttaa g
671

```

&lt;210&gt; 2232

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2232

```

Met Glu Lys Ser Pro Val Gln Cys Pro Thr Gly Lys Cys Phe Pro Leu
1           5           10          15
Ile Val Glu Leu Ser Cys Pro Phe Thr Val Gly Val Thr Gly Gly Val
20          25          30
Gly Val Arg Val Glu Thr Gly Glu Gly Ser Glu His Leu Trp Asp Thr
35          40          45
His His Val Pro Gly Thr Glu Pro Tyr Leu Asp Leu Leu Gln Pro Ser
50          55          60
Gln Trp His Cys Glu Ala Ser Val Val Leu Gln Met Arg Lys Leu Arg
65          70          75          80
Phe Val Ala Ile Thr Asp Lys Gln Met Thr Leu Asn Gly Ala Gly His
85          90          95
Val Ile Cys His Arg Tyr Met His Arg Thr Met Gln Thr Ser Gln Ser
100         105         110
Pro Leu Ser Gln Thr Arg Leu Thr Ile Arg Asp Met Gln Thr Leu Ala
115         120         125
Gly Leu Gly Leu Phe Pro Ile Gly Asp Ser Leu Val Pro Pro Trp Pro
130         135         140
Leu Met Pro Thr Ala Val Trp Lys Ala Gly Ser Leu Leu Arg Arg Gln

```

145		150		155		160									
Gly	Asp	Ile	Phe	Ser	His	Gln	Leu	Ser	Phe	Phe	Tyr	Ser	Phe	Leu	Asp
					165					170				175	
Thr															

&lt;210&gt; 2233

&lt;211&gt; 6199

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2233

```

acgctgatg atcggaatg tgaatcag ctggttctgc tgcttggtt caacacctt
60
gatttcatta aagtgttgcg gcagcacagg atgatgattt tatactgtac cttgctggcc
120
agtgcacaaa gtgaagctga aaaggaaagg attatgggaa agatggaagc tgaccagag
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240
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300
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660
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1200
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1260

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2640  
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<211> 1701

<212> PRT

<213> Homo sapiens

<400> 2234

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Pro	Lys	Tyr	Ala	Gln	Ala	Gly	Phe	Glu	Gly	Phe	Lys	Thr	Leu	Asn	Arg
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Ile	Gln	Ser	Lys	Leu	Tyr	Arg	Ala	Ala	Leu	Glu	Thr	Asp	Glu	Asn	Leu
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Leu	Leu	Cys	Ala	Pro	Thr	Gly	Ala	Gly	Lys	Thr	Asn	Val	Ala	Leu	Met
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Cys	Met	Leu	Arg	Glu	Ile	Gly	Lys	His	Ile	Asn	Met	Asp	Gly	Thr	Ile
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Asn	Val	Asp	Asp	Phe	Lys	Ile	Ile	Tyr	Ile	Ala	Pro	Met	Arg	Ser	Leu
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Val	Gln	Glu	Met	Val	Gly	Ser	Phe	Gly	Lys	Arg	Leu	Ala	Thr	Tyr	Gly
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Ile	Thr	Val	Ala	Glu	Leu	Thr	Gly	Asp	His	Gln	Leu	Cys	Lys	Glu	Glu
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Ile	Val	Leu	Asp	Glu	Ile	His	Leu	Leu	His	Asp	Asp	Arg	Gly	Pro	Val
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Leu	Glu	Ala	Leu	Val	Ala	Arg	Ala	Ile	Arg	Asn	Ile	Glu	Met	Thr	Gln
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Glu	Asp	Val	Arg	Leu	Ile	Gly	Leu	Ser	Ala	Thr	Leu	Pro	Asn	Tyr	Glu
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Asp	Val	Ala	Thr	Phe	Leu	Arg	Val	Asp	Pro	Ala	Lys	Gly	Leu	Phe	Tyr
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Phe	Asp	Asn	Ser	Phe	Arg	Pro	Val	Pro	Leu	Glu	Gln	Thr	Tyr	Val	Gly
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Val	Tyr	Glu	Lys	Ile	Met	Glu	His	Ala	Gly	Lys	Asn	Gln	Val	Leu	Val
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Phe	Val	His	Ser	Arg	Lys	Glu	Thr	Gly	Lys	Thr	Ala	Arg	Ala	Ile	Arg
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Asp	Met	Cys	Leu	Glu	Lys	Asp	Thr	Leu	Gly	Leu	Phe	Leu	Arg	Glu	Gly
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Ser	Ala	Ser	Thr	Glu	Val	Leu	Arg	Thr	Glu	Ala	Glu	Gln	Cys	Lys	Asn
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Leu	Glu	Leu	Lys	Asp	Leu	Leu	Pro	Tyr	Gly	Phe	Ala	Ile	His	His	Ala

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Gly Met Thr Arg Val Asp Arg Thr Leu Val Glu Asp Leu Phe Ala Asp
      355      360      365
Lys His Ile Gln Val Leu Val Ser Thr Ala Thr Leu Ala Trp Gly Val
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Asn Leu Pro Ala His Thr Val Ile Ile Lys Gly Thr Gln Val Tyr Ser
385      390      395      400
Pro Glu Lys Gly Arg Trp Thr Glu Leu Gly Ala Leu Asp Ile Leu Gln
      405      410      415
Met Leu Gly Arg Ala Gly Arg Pro Gln Tyr Asp Thr Lys Gly Glu Gly
      420      425      430
Ile Leu Ile Thr Ser His Gly Glu Leu Gln Tyr Tyr Leu Ser Leu Leu
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Asn Gln Gln Leu Pro Ile Glu Ser Gln Met Val Ser Lys Leu Pro Asp
450      455      460
Met Leu Asn Ala Glu Ile Val Leu Gly Asn Val Gln Asn Ala Lys Asp
465      470      475      480
Ala Val Asn Trp Leu Gly Tyr Ala Tyr Leu Tyr Ile Arg Met Leu Arg
      485      490      495
Ser Pro Thr Leu Tyr Gly Ile Ser His Asp Asp Leu Lys Gly Asp Pro
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Leu Leu Asp Gln Arg Arg Leu Asp Leu Val His Thr Ala Ala Leu Met
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Leu Asp Lys Asn Asn Leu Val Lys Tyr Asp Lys Lys Thr Gly Asn Phe
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Gln Val Thr Glu Leu Gly Arg Ile Ala Ser His Tyr Tyr Ile Thr Asn
545      550      555      560
Asp Thr Val Gln Thr Tyr Asn Gln Leu Leu Lys Pro Thr Leu Ser Glu
      565      570      575
Ile Glu Leu Phe Arg Val Phe Ser Leu Ser Ser Glu Phe Lys Asn Ile
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Thr Val Arg Glu Glu Glu Lys Leu Glu Leu Gln Lys Leu Leu Glu Arg
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Val Pro Ile Pro Val Lys Glu Ser Ile Glu Glu Pro Ser Ala Lys Ile
610      615      620
Asn Val Leu Leu Gln Ala Phe Ile Ser Gln Leu Lys Leu Glu Gly Phe
625      630      635      640
Ala Leu Met Ala Asp Met Val Tyr Val Thr Gln Ser Ala Gly Arg Leu
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Thr Asp Lys Thr Leu Asn Leu Cys Lys Met Ile Asp Lys Arg Met Trp
675      680      685
Gln Ser Met Cys Pro Leu Arg Gln Phe Arg Lys Leu Pro Glu Glu Val
690      695      700
Val Lys Lys Ile Glu Lys Lys Asn Phe Pro Phe Glu Arg Leu Tyr Asp
705      710      715      720
Leu Asn His Asn Glu Ile Gly Glu Leu Ile Arg Met Pro Lys Met Gly
      725      730      735
Lys Thr Ile His Lys Tyr Val His Leu Phe Pro Lys Leu Glu Leu Ser
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Val His Leu Gln Pro Ile Thr Arg Ser Thr Leu Lys Val Glu Leu Thr
755      760      765
Ile Thr Pro Asp Phe Gln Trp Asp Glu Lys Val His Gly Ser Ser Glu

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770	775	780
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His Glu Tyr Phe Leu Leu Lys Ala Lys Tyr Ala Gln Asp Glu His Leu		800
	805	810
Ile Thr Phe Phe Val Pro Val Phe Glu Pro Leu Pro Pro Gln Tyr Phe		815
	820	825
Ile Arg Val Val Ser Asp Arg Trp Leu Ser Cys Glu Thr Gln Leu Pro		830
	835	840
Val Ser Phe Arg His Leu Ile Leu Pro Glu Lys Tyr Pro Pro Pro Thr		845
	850	855
Glu Leu Leu Asp Leu Gln Pro Leu Pro Val Ser Ala Leu Arg Asn Ser		860
865	870	875
Ala Phe Glu Ser Leu Tyr Gln Asp Lys Phe Pro Phe Phe Asn Pro Ile		880
	885	890
Gln Thr Gln Val Phe Asn Thr Val Tyr Asn Ser Asp Asp Asn Val Phe		895
	900	905
Val Gly Ala Pro Thr Gly Ser Gly Lys Thr Ile Cys Ala Glu Phe Ala		910
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Ile Leu Arg Met Leu Leu Gln Ser Ser Glu Gly Arg Cys Val Tyr Ile		925
	930	935
Thr Pro Met Glu Ala Leu Ala Glu Gln Val Tyr Met Asp Trp Tyr Glu		940
945	950	955
Lys Phe Gln Asp Arg Leu Asn Lys Lys Val Val Leu Leu Thr Gly Glu		960
	965	970
Thr Ser Thr Asp Leu Lys Leu Leu Gly Lys Gly Asn Ile Ile Ile Ser		975
	980	985
Thr Pro Glu Lys Trp Asp Ile Leu Ser Arg Arg Trp Lys Gln Arg Lys		990
	995	1000
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Gly Gly Glu Asn Gly Pro Val Leu Glu Val Ile Cys Ser Arg Met Arg		1020
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Tyr Ile Ser Ser Gln Ile Glu Arg Pro Ile Arg Ile Val Ala Leu Ser		1040
	1045	1050
Ser Ser Leu Ser Asn Ala Lys Asp Val Ala His Trp Leu Gly Cys Ser		1055
	1060	1065
Ala Thr Ser Thr Phe Asn Phe His Pro Asn Val Arg Pro Val Pro Leu		1070
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Glu Leu His Ile Gln Gly Phe Asn Ile Ser His Thr Gln Thr Arg Leu		1085
	1090	1095
Leu Ser Met Ala Lys Pro Val Tyr His Ala Ile Thr Lys His Ser Pro		1100
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Lys Lys Pro Val Ile Val Phe Val Pro Ser Arg Lys Gln Thr Arg Leu		1120
	1125	1130
Thr Ala Ile Asp Ile Leu Thr Thr Cys Ala Ala Asp Ile Gln Arg Gln		1135
	1140	1145
Arg Phe Leu His Cys Thr Glu Lys Asp Leu Ile Pro Tyr Leu Glu Lys		1150
	1155	1160
Leu Ser Asp Ser Thr Leu Lys Glu Thr Leu Leu Asn Gly Val Gly Tyr		1165
	1170	1175
Leu His Glu Gly Leu Ser Pro Met Glu Arg Arg Leu Val Glu Gln Leu		1180
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Phe Ser Ser Gly Ala Ile Gln Val Val Val Ala Ser Arg Ser Leu Cys		1200

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 Tyr Tyr Asn Gly Lys Ile His Ala Tyr Val Asp Tyr Pro Ile Tyr Asp  
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 Val Leu Gln Met Val Gly His Ala Asn Arg Pro Leu Gln Asp Asp Glu  
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 Gly Arg Cys Val Ile Met Cys Gln Gly Ser Lys Lys Asp Phe Phe Lys  
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 Lys Phe Leu Tyr Glu Pro Leu Pro Val Glu Ser His Leu Asp His Cys  
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 Lys Gln Asp Ala Val Asp Tyr Leu Thr Trp Thr Phe Leu Tyr Arg Arg  
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 Pro Leu Asn Leu Gly Met Ile Ala Ala Tyr Tyr Tyr Ile Asn Tyr Thr  
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 Thr Ile Glu Leu Phe Ser Met Ser Leu Asn Ala Lys Thr Lys Val Arg  
 1395 1400 1405  
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 Ile Arg His His Glu Asp Asn Leu Leu Arg Gln Leu Ala Gln Lys Val  
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 Pro His Lys Leu Asn Asn Pro Lys Phe Asn Asp Pro His Val Lys Thr  
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 Asn Leu Leu Leu Gln Ala His Leu Ser Arg Met Gln Leu Ser Ala Glu  
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 Lys Asp Ser Tyr Leu Lys Gln Leu Pro His Phe Thr Ser Glu His Ile  
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 Lys Arg Cys Thr Asp Lys Gly Val Glu Ser Val Phe Asp Ile Met Glu  
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 Ile Gly Asp Ala Lys Ser Asn Ser Leu Ile Ser Ile Lys Arg Leu Thr

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 Leu Gln Gln Lys Ala Lys Val Lys Leu Asp Phe Val Ala Pro Ala Thr  
 1650                      1655                      1660  
 Gly Ala His Asn Tyr Thr Leu Tyr Phe Met Ser Asp Ala Tyr Met Gly  
 1665                      1670                      1675                      1680  
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 <211> 586  
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 <211> 123  
 <212> PRT  
 <213> Homo sapiens

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 Glu Val Phe Arg Asp Leu Leu Phe Leu Pro His Ile Ile Gln Ser Gln  
 20                      25                      30  
 Asp Pro Lys Asp Gly Leu Asn Phe Asn Leu Glu Leu Glu Arg Gln Thr  
 35                      40                      45  
 Leu Asp Gln Asp Pro Leu Ser Lys Val Leu Ala Gly Val Ala Leu Gly  
 50                      55                      60  
 Gly Tyr Ser Val Pro Arg Leu His Pro Arg Gln Val Pro Gly Arg Gly  
 65                      70                      75                      80  
 Glu Ala Gly Pro Gly Ala Gly Ala Ala Val Glu Gly Leu His Cys Ala

85 90 95  
 Gly Pro His Leu Leu Gly Pro Pro Ala Leu Ala Glu Arg Ala Thr Met  
 100 105 110  
 Ser Gln Leu Pro Gly Ser Ser Gly Arg Arg Cys  
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 <213> Homo sapiens

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 Phe Pro Thr Leu Leu Pro Thr Arg Leu Leu Thr Gly Gly Leu Ala  
 35 40 45  
 Gln Leu Glu Pro Ile Val Gln Gln Val Leu Ala Glu Glu Pro Leu Ala  
 50 55 60  
 Pro His Cys Pro Thr Pro Asp Gln Gly Asp Ala Leu Glu Glu Gly Leu  
 65 70 75 80  
 Asp Leu Ser Ser Ser Leu Ser Ala Pro Asp His Phe Gln Gly Leu Ser  
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 Pro Ser Trp Pro Ala Leu Leu Arg Pro Lys Arg Ser Val Trp Gly Ala  
 100 105 110  
 Ser Ser Trp Leu Gln Trp Asp Thr Gly Val Pro Ser  
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<210> 2239  
 <211> 623

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2239

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 360  
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 480  
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&lt;210&gt; 2240

&lt;211&gt; 207

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2240

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 Asn Lys Ala Lys Ser Pro Gly Val Arg Gln Pro Gly Ser Ser Ser Ser  
 35 40 45  
 Ser Ala Pro Gly Gln Pro Ser Thr Gly Val Ala Arg Pro Thr Val Ser  
 50 55 60  
 Ser Gly Pro Val Pro Arg Arg Gln Asn Gly Ser Ser Ser Ser Gly Pro  
 65 70 75 80  
 Glu Arg Ser Ile Ser Gly Ser Lys Lys Pro Thr Asn Asp Ser Asn Pro  
 85 90 95  
 Ser Arg Arg Thr Val Ser Gly Thr Cys Gly Pro Gly Gln Pro Ala Ser  
 100 105 110  
 Ser Ser Gly Gly Pro Gly Arg Pro Ile Ser Gly Ser Val Ser Ser Ala  
 115 120 125  
 Arg Pro Leu Gly Ser Ser Arg Gly Pro Gly Arg Pro Val Ser Ser Pro  
 130 135 140  
 His Glu Leu Arg Arg Pro Val Ser Gly Leu Gly Pro Pro Gly Arg Ser  
 145 150 155 160  
 Val Ser Gly Pro Gly Arg Ser Ile Ser Gly Pro Ile Pro Ala Gly Arg



165 170 175  
 Thr Val Ser Asn Ser Val Pro Gly Arg Pro Val Ser Ser Leu Gly Pro  
 180 185 190  
 Gly Gln Thr Val Ser Ser Ser Gly Pro Thr Ile Lys Pro Lys Cys  
 195 200 205  
  
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 <212> DNA  
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 <400> 2241  
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 240  
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 300  
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 420  
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 656

<210> 2242  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

<400> 2242  
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 Lys Ala Leu Arg Ala Lys Thr Asn Thr Tyr Ile Arg Thr Pro Gly Arg  
 35 40 45  
 Gly Glu Glu Pro Val Phe Met Val Thr Gly Arg Arg Glu Asp Val Ala  
 50 55 60  
 Thr Ala Arg Arg Glu Ile Ile Ser Ala Ala Glu His Phe Ser Met Ile  
 65 70 75 80  
 Arg Ala Ser Arg Asn Lys Ser Gly Ala Ala Phe Gly Val Ala Pro Ala  
 85 90 95  
 Leu Pro Gly Gln Val Thr Ile Arg Val Arg Val Pro Tyr Arg Val Val

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      100      105      110
Gly Leu Val Val Gly Pro Lys Gly Ala Thr Ile Lys Arg Ile Gln Gln
      115      120      125
Gln Thr Asn Thr Tyr Ile Ile Thr Pro Ser Arg Asp Arg Asp Pro Val
      130      135      140
Phe Glu Ile Thr Gly Ala Pro Gly Asn Val Glu Arg Ala Arg Glu Glu
      145      150      155      160
Ile Glu Thr His Ile Ala Val Arg Thr Gly Lys Ile Leu Glu Tyr Asn
      165      170      175
Asn Glu Asn Asp Phe Leu Ala Gly Ser Pro Asp Ala Ala Ile Asp Ser
      180      185      190
Arg Tyr Ser Asp Ala Trp Arg Val His Gln Pro Gly Cys Lys Pro Leu
      195      200      205
Ser Thr Phe Arg Gln Asn Ser Leu Gly Cys
      210      215

```

&lt;210&gt; 2243

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2243

```

gaattcagca tttaaagtgc actcgttggc atgcaatttg ctgtcatgaa aacgactgtg
60
gattcatttc ctggtaagaa tcttctgact tattgagctg catgtcagaa gcaaaaagca
120
aaaaaaccaa atatgtacat aaaacagtgt tatcattcct taaaagagaa ggaaaaataaa
180
tccttaaata atgtggactg gaacacagaa atccaaggct ggccgcacgg gtccctggctg
240
ggatggcatc cggggagctg ctgctgggga cgtgcttgcc ggcacaggtc agggggagccg
300
ggttctgcct cctccttgcc cactctcttt gcgccctccc tgtgctcgcc tgtcttggtt
360
tacctcccat cctgggccct tgga
384

```

&lt;210&gt; 2244

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2244

```

Met Gly Gly Lys Thr Arg Gln Ala Ser Thr Gly Arg Ala Gln Arg Glu
  1           5           10           15
Trp Ala Arg Arg Arg Gln Asn Pro Ala Pro Leu Thr Cys Ala Gly Lys
      20      25      30
His Val Pro Ser Ser Ser Pro Asp Ala Ile Pro Ala Arg Thr Arg
      35      40      45
Ala Ala Ser Leu Gly Phe Leu Cys Ser Ser Pro His Tyr Leu Gly Ile
      50      55      60
Tyr Phe Pro Ser Leu Leu Arg Asn Asp Asn Thr Val Leu Cys Thr Tyr
      65      70      75      80
Leu Val Phe Leu Leu Phe Ala Ser Asp Met Gln Leu Asn Lys Ser Glu

```

85 90 95  
 Asp Ser Tyr Gln Glu Met Asn Pro Gln Ser Phe Ser  
 100 105

<210> 2245

<211> 632

<212> DNA

<213> Homo sapiens

<400> 2245

acgcgtgcga ttaccgtcaa ggctgggtgtg gtgagcgctg atctgcacga gcggacgtct  
 60  
 tcgagagaag aggtcggacg cgagaggctc aactatggtc acaccttggc ccacgtatt  
 120  
 gaggcccaca agcatttcac gtggcgctcat ggcgaggctg acgcggtggg catggtgttt  
 180  
 gcggccgaac tgtcgcaccg gtacctggga ctgtccgatg aggtcgttgc gcgcaccgc  
 240  
 actatcctgt ctgagatcgg attgcctgtt acctgtgacg agattaagtg ggcagatctg  
 300  
 cgcaagacga tgaacgtgga caagaaaacc agggtagacc cgcagaccgg gcgtcaagtg  
 360  
 ttgcggtttg tcggtattca caaacccggt caggctcgcca tgatcgtcga ccctgacgag  
 420  
 gccgcttttag ccgagtgcta cgaccggtgt tccgcacggt aaaaacgttc ggaaatgaac  
 480  
 atgtggctgc gggtcagtcg gcattcaggc ctccgtgacg ccgtcgaccc caagtgatgt  
 540  
 gacgattcgg gaaatatctt gttgggcact cttgagcctc gcctgattcc ccataccgga  
 600  
 cttaagttca gtatcgacgg catgaatccg ga  
 632

<210> 2246

<211> 153

<212> PRT

<213> Homo sapiens

<400> 2246

Thr Arg Ala Ile Thr Val Lys Ala Gly Val Val Ser Ala Asp Leu His  
 1 5 10 15  
 Glu Arg Thr Ser Ser Arg Glu Glu Val Gly Arg Glu Arg Leu Asn Tyr  
 20 25 30  
 Gly His Thr Leu Ala His Ala Ile Glu Ala His Lys His Phe Thr Trp  
 35 40 45  
 Arg His Gly Glu Ala Asp Ala Val Gly Met Val Phe Ala Ala Glu Leu  
 50 55 60  
 Ser His Arg Tyr Leu Gly Leu Ser Asp Glu Val Val Ala Arg Thr Arg  
 65 70 75 80  
 Thr Ile Leu Ser Glu Ile Gly Leu Pro Val Thr Cys Asp Glu Ile Lys  
 85 90 95  
 Trp Ala Asp Leu Arg Lys Thr Met Asn Val Asp Lys Lys Thr Arg Val  
 100 105 110  
 Asp Pro Gln Thr Gly Arg Gln Val Leu Arg Phe Val Gly Ile His Lys

115 120 125  
 Pro Gly Gln Val Ala Met Ile Val Asp Pro Asp Glu Ala Ala Leu Ala  
 130 135 140  
 Glu Cys Tyr Asp Arg Cys Ser Ala Arg  
 145 150

<210> 2247

<211> 324

<212> DNA

<213> Homo sapiens

<400> 2247

gggcggttcgc ctccagggtt ctccccgaca ctggatgccca acctgccag gggcagaagg  
 60  
 gaggttgggc gtggggagtg ccgggtacag tcagagttgc caggacagtt tggagcagtg  
 120  
 cctcttaatc ttggccgcac agcacctggg agctttaaat agacccccac gccctgggcg  
 180  
 cccccaccgc tgaccacccc gatctcagct ctgcctttcc cgcctctctg ctgggttgca  
 240  
 taagccagcg attcccaacc ccggctgtac ctggaagcta cccaggagc ttctggagaa  
 300  
 tgtgccgtgt gagccatccc cctg  
 324

<210> 2248

<211> 105

<212> PRT

<213> Homo sapiens

<400> 2248

Met Ala His Thr Ala His Ser Pro Glu Ala Pro Gly Val Ala Ser Arg  
 1 5 10 15  
 Tyr Ser Arg Gly Trp Glu Ser Leu Ala Tyr Ala Thr Gln Gln Arg Gly  
 20 25 30  
 Gly Lys Gly Arg Ala Glu Ile Gly Trp Val Ser Gly Gly Gly Ala Gln  
 35 40 45  
 Gly Val Gly Val Tyr Leu Lys Leu Pro Gly Ala Val Arg Pro Arg Leu  
 50 55 60  
 Arg Gly Thr Ala Pro Asn Cys Pro Gly Asn Ser Asp Cys Thr Arg His  
 65 70 75 80  
 Ser Pro Arg Pro Thr Ser Leu Leu Pro Leu Gly Arg Leu Ala Ser Ser  
 85 90 95  
 Val Gly Glu Asn Pro Gly Gly Glu Arg  
 100 105

<210> 2249

<211> 394

<212> DNA

<213> Homo sapiens

<400> 2249

gaaaaccgga taacagggtg tatacaagcc tctgagttct gggagcaaca accagctcaa  
 60

cccgcaaggg aaagtgagaa agcaattaag ttgggaaccg cgggggttttc ccattccac  
 120  
 ggtggaaacc gcggccagtg aattgaaatc cgcttcctta aggcgaaatg ggcccttaaa  
 180  
 aggcaaggtc aaccgcccgc cagtgtgatg gaatttgcaa gaattcggtt tagcaccctc  
 240  
 ccggcttttc tcccgaccgc gtgcagggtg ggctgcgctg ggctgggag gaactgggag  
 300  
 ctgggggctc atgtcctgta taaaggggct gcaggggagc tgtctcccc cagaagactg  
 360  
 gccacatggg gacaggcctc ctgggggcag atct  
 394

<210> 2250  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 2250  
 Met Ser Pro Gln Leu Pro Val Pro Pro Arg Pro Ser Ala Ala His Pro  
 1 5 10 15  
 Ala Arg Gly Arg Glu Lys Ser Arg Glu Gly Ala Lys Pro Asn Ser Cys  
 20 25 30  
 Lys Phe His His Thr Gly Gly Arg Leu Thr Leu Pro Phe Lys Gly Pro  
 35 40 45  
 Phe Arg Leu Lys Glu Ala Asp Phe Asn Ser Leu Ala Ala Val Ser Thr  
 50 55 60  
 Val Gly Met Gly Lys Pro Arg Gly Ser Gln Leu Asn Cys Phe Leu Thr  
 65 70 75 80  
 Phe Pro Cys Gly Leu Ser Trp Leu Leu Leu Pro Glu Leu Arg Gly Leu  
 85 90 95  
 Tyr Thr Pro Cys Tyr Pro Val Phe  
 100

<210> 2251  
 <211> 654  
 <212> DNA  
 <213> Homo sapiens

<400> 2251  
 acgcgtactt attcgccacc atgattatga ccagtgtttc cagtccgttc agttgttgca  
 60  
 gtggaatagt cagggttaaatt ttaatgtgac cgtttatcgc aatctgccga ccactcgca  
 120  
 ttcaatcatg acttcgtgat aaaagattga gtgtgaggtt ataacgccga agcggtaaaa  
 180  
 attttaattt ttgccgctga ggggttgacc aagcgaagcg cggtaggttt tctgcttagg  
 240  
 agtttaatca tgtttcagac ttttatttct cgccataatt caaacttttt ttctgataag  
 300  
 ctggttctca cttctgttac tccagcttct tcggcacctg ttttacagac acctaaagct  
 360  
 acatcgtaaa cgttatattt tgatagtttg acgggttaatg ctggtaatgg tggttttctt  
 420

cattgcattc agatggatac atctgtcaac gccgctaatac aggttggttc tgttggtgct  
 480  
 gatattgctt ttgatgccga ccctaaattt tttgcctggt tggttcgctt tgagtcttct  
 540  
 tcggttccga ctaccctccc gactgcctat gatgtttatc ctttggatgg tcgccatgat  
 600  
 ggtggttatt ataccgtcaa ggactgtgtg actattgacg tccttcctcg tacg  
 654

<210> 2252

<211> 135

<212> PRT

<213> Homo sapiens

<400> 2252

Met	Phe	Gln	Thr	Phe	Ile	Ser	Arg	His	Asn	Ser	Asn	Phe	Phe	Ser	Asp
1				5					10					15	
Lys	Leu	Val	Leu	Thr	Ser	Val	Thr	Pro	Ala	Ser	Ser	Ala	Pro	Val	Leu
			20					25					30		
Gln	Thr	Pro	Lys	Ala	Thr	Ser	Ser	Thr	Leu	Tyr	Phe	Asp	Ser	Leu	Thr
		35					40					45			
Val	Asn	Ala	Gly	Asn	Gly	Gly	Phe	Leu	His	Cys	Ile	Gln	Met	Asp	Thr
	50					55				60					
Ser	Val	Asn	Ala	Ala	Asn	Gln	Val	Val	Ser	Val	Gly	Ala	Asp	Ile	Ala
65					70					75				80	
Phe	Asp	Ala	Asp	Pro	Lys	Phe	Phe	Ala	Cys	Leu	Val	Arg	Phe	Glu	Ser
			85						90					95	
Ser	Ser	Val	Pro	Thr	Thr	Leu	Pro	Thr	Ala	Tyr	Asp	Val	Tyr	Pro	Leu
			100					105					110		
Asp	Gly	Arg	His	Asp	Gly	Gly	Tyr	Tyr	Thr	Val	Lys	Asp	Cys	Val	Thr
		115					120					125			
Ile	Asp	Val	Leu	Pro	Arg	Thr									
		130				135									

<210> 2253

<211> 327

<212> DNA

<213> Homo sapiens

<400> 2253

ggatcctgct gggcctcttt tacgtgatgt tgacccagcc gctggtgcgc attattcgcg  
 60  
 cactgagcac cagcaagcag gcccgctggt attgcccacc gggtcacgaa aacgatgaaa  
 120  
 tcggcgtatt ggtcaacgtc gcccaaccagc aattcgacaa tatggaaacc gaaatcgagc  
 180  
 agcgccgcca cgccgaggac cgcctcaccg aatacctggg ccaactggaa gatatcgctt  
 240  
 ccgacgcac cctggagctc aaggccagca accaacgctt gagccaatcc aacgatgagc  
 300  
 tggaagcggc aaagttgacc gccttgg  
 327

<210> 2254

<211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 2254  
 Met Leu Thr Gln Pro Leu Val Arg Ile Ile Arg Ala Leu Ser Thr Ser  
 1 5 10 15  
 Lys Gln Ala Arg Leu Asp Cys Pro Pro Gly His Glu Asn Asp Glu Ile  
 20 25 30  
 Gly Val Leu Val Asn Val Ala Asn Gln Gln Phe Asp Asn Met Glu Thr  
 35 40 45  
 Glu Ile Glu Gln Arg Arg His Ala Glu Asp Arg Leu Thr Glu Tyr Leu  
 50 55 60  
 Gly Gln Leu Glu Asp Ile Val Ser Ala Arg Thr Leu Glu Leu Lys Ala  
 65 70 75 80  
 Ser Asn Gln Arg Leu Ser Gln Ser Asn Asp Glu Leu Glu Ala Ala Lys  
 85 90 95  
 Leu Thr Ala Leu  
 100

<210> 2255  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 2255  
 nngctagcac atgagaagtg tgaagtttat actttgcttg ggcgatcacg ccgttttcca  
 60  
 aatatggctc atgcaacttc tggccaaagg ggtcacattg agcgtgctgc tatcaatgct  
 120  
 cctgtacagg gcagtgcagc tgatgttgct atgtgtgcaa tgcttgagat agacaggaat  
 180  
 actcgtctta aggagcttgg ttggacgcta ctcttgacagg tgcattgatga agtgatactg  
 240  
 gaagggcctt cagagtctgc ggagtnggcc aagtccatag ttgttgagtg catgtctaag  
 300  
 cccttctatg gcaccaatat cctgaggggc gaccttgctg ttgatgcaa gtgtgca  
 357

<210> 2256  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 2256  
 Xaa Leu Ala His Glu Lys Cys Glu Val Tyr Thr Leu Leu Gly Arg Ser  
 1 5 10 15  
 Arg Arg Phe Pro Asn Met Ala His Ala Thr Ser Gly Gln Arg Gly His  
 20 25 30  
 Ile Glu Arg Ala Ala Ile Asn Ala Pro Val Gln Gly Ser Ala Ala Asp  
 35 40 45  
 Val Ala Met Cys Ala Met Leu Glu Ile Asp Arg Asn Thr Arg Leu Lys  
 50 55 60  
 Glu Leu Gly Trp Thr Leu Leu Leu Gln Val His Asp Glu Val Ile Leu

```

65          70          75          80
Glu Gly Pro Ser Glu Ser Ala Glu Xaa Ala Lys Ser Ile Val Val Glu
          85          90          95
Cys Met Ser Lys Pro Phe Tyr Gly Thr Asn Ile Leu Arg Val Asp Leu
          100          105          110
Ala Val Asp Ala Lys Cys Ala
          115

```

&lt;210&gt; 2257

&lt;211&gt; 626

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2257

```

nnaatgacaa aaaatatgaa ccaaaatagt gacagtggca gtacaaataa ctataaaagc
60
ctgaaacctta aattagaaaa tctgagttct ttaccaccag attctgacag aacatcagaa
120
gtatatctac atgaagaatt acagcaggac atgcaaaagt ttaagaatga ggtcaacaca
180
ttagaagaag agttcctggc tttgaagaaa gaaaatgttc aacttcataa agagggtgaa
240
gaagaaatgg agaagcacag aagtaatagc acagaattat caggaaccct aactgatggt
300
actactgttg gcaatgatga tgatggacta aatcagcaga ttcctaggaa ggaaaatgaa
360
gagcatgaca ggctgcaga taaaacagct aatgaaaaga acaagggtcaa aaaccaaata
420
tatcctgagg ctgactttgc tgactcaatg gagccatctg aaatagcctc agaggattgt
480
gaattgtctc actctgttta tgagaatttt atgttgctga ttgaacaact tagaatggag
540
tataaaggta ggaccactgc ataaatgcaa ggccttttga tgtatcctgc agtaatgtgt
600
gtatacattg ctgagaactg acgcgt
626

```

&lt;210&gt; 2258

&lt;211&gt; 187

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2258

```

Xaa Met Thr Lys Asn Met Asn Gln Asn Ser Asp Ser Gly Ser Thr Asn
1          5          10          15
Asn Tyr Lys Ser Leu Lys Pro Lys Leu Glu Asn Leu Ser Ser Leu Pro
          20          25          30
Pro Asp Ser Asp Arg Thr Ser Glu Val Tyr Leu His Glu Glu Leu Gln
          35          40          45
Gln Asp Met Gln Lys Phe Lys Asn Glu Val Asn Thr Leu Glu Glu Glu
          50          55          60
Phe Leu Ala Leu Lys Lys Glu Asn Val Gln Leu His Lys Glu Val Glu
65          70          75          80
Glu Glu Met Glu Lys His Arg Ser Asn Ser Thr Glu Leu Ser Gly Thr

```



```

      85              90              95
Leu Thr Asp Gly Thr Thr Val Gly Asn Asp Asp Asp Gly Leu Asn Gln
      100              105              110
Gln Ile Pro Arg Lys Glu Asn Glu Glu His Asp Arg Pro Ala Asp Lys
      115              120              125
Thr Ala Asn Glu Lys Asn Lys Val Lys Asn Gln Ile Tyr Pro Glu Ala
      130              135              140
Asp Phe Ala Asp Ser Met Glu Pro Ser Glu Ile Ala Ser Glu Asp Cys
      145              150              155              160
Glu Leu Ser His Ser Val Tyr Glu Asn Phe Met Leu Leu Ile Glu Gln
      165              170              175
Leu Arg Met Glu Tyr Lys Gly Arg Thr Thr Ala
      180              185

```

<210> 2259  
 <211> 425  
 <212> DNA  
 <213> Homo sapiens

```

<400> 2259
acgcgtcaca atgataaagc cattatatcc atcaagaggt aaatcattct tgaaattttc
60
taaaggtaaa cacttacgtg taacacgttc atcaaagaat tcaggaacca catattctgg
120
acgggtcatct acgactgtaa cagcacagcc aataaacaat agcaaatacag taatagctcg
180
gctaacaatga cctgcaccta atacgagaac tgacggatca ttttctacag gttgtacgaa
240
acactccatt tcgcctacca tgcatagaga attcagcttt gctttatcta cagtaaattc
300
ttcaatagga gttccgtata gaacccttcc atcttcagca taaatagtct tatecccttg
360
acgaggaccg gatagaacgg taaccattac ggtagcttca gtaacctgta gacgattttt
420
catga
425

```

<210> 2260  
 <211> 141  
 <212> PRT  
 <213> Homo sapiens

```

<400> 2260
Met Lys Asn Arg Leu Gln Val Thr Glu Ala Thr Val Met Val Thr Val
1      5      10      15
Leu Ser Gly Pro Arg Gln Gly Asp Lys Thr Ile Tyr Ala Glu Asp Gly
20     25     30
Arg Val Leu Tyr Gly Thr Pro Ile Glu Gly Phe Thr Val Asp Lys Ala
35     40     45
Lys Leu Asn Ser Leu Cys Met Val Gly Glu Met Glu Cys Phe Val Gln
50     55     60
Pro Val Glu Asn Asp Pro Ser Val Leu Val Leu Gly Ala Gly His Val
65     70     75     80
Ser Arg Ala Ile Thr Asp Leu Leu Leu Phe Ile Gly Cys Arg Val Thr

```

				85						90					95				
Val	Val	Asp	Asp	Arg	Pro	Glu	Tyr	Val	Val	Pro	Glu	Phe	Phe	Asp	Glu				
				100						105				110					
Arg	Val	Thr	Arg	Lys	Cys	Leu	Pro	Leu	Glu	Asn	Phe	Lys	Asn	Asp	Leu				
				115				120					125						
Pro	Leu	Asp	Glu	Tyr	Asn	Gly	Phe	Ile	Ile	Val	Thr	Arg							
				130				135					140						

&lt;210&gt; 2261

&lt;211&gt; 660

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2261

```

ngctagctgc tgctcctgag gatcgggcgc agaattattgc tgccgatctg tccgggttgc
60
ttgagcccaa gcgcgaggtc gatgtgtccg gcgaccgcgc gcgttgcggt gggagcatag
120
tgctcgtgca cgctgaccga gaggtccgtg cgagaggtac tcccgatgat atttgcgggc
180
agctcgatgc cgtggccgcc atgatggccc ttgtctatgg gtcgaatgtg actattcccg
240
acgatgccgg gaggtctcttc gacaagcttc actgaacggt gttcaattgg tcccaacggc
300
tgcccatgtg ggcagccgct ctatctcgtc atgggaagga acccgatgtc gtcacgcaat
360
ggtttccagg ccaccgacct ggctcttata gcggtctttg cagccctcat tgctgtgcta
420
gccgtcatcc cgccgatgtt catgggtgggg gcggtccctt ttgcccttca gatgggttgc
480
gtcatgctgg cgccgatggt gctgggaagt atccgtggcg gatgcgcggt aggcttgtat
540
atccttgctg gcgcgctggg gctgcccgtc ttcagcggtg ggtctagcgg gattggcgtc
600
ctgggtgggtc ccaactggtg gtatctatgg ggatggctga tcggcgcttt cgtggcggtt
660

```

&lt;210&gt; 2262

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2262

Met	Pro	Gly	Gly	Ser	Thr	Ser	Phe	Thr	Glu	Arg	Cys	Ser	Ile	Gly					
1				5				10					15						
Pro	Asn	Gly	Cys	Pro	Cys	Gly	Gln	Pro	Leu	Tyr	Leu	Val	Met	Gly	Arg				
				20				25				30							
Asn	Pro	Met	Ser	Ser	Arg	Asn	Gly	Phe	Gln	Ala	Thr	Asp	Leu	Ala	Leu				
				35			40					45							
Ile	Ala	Val	Phe	Ala	Ala	Leu	Ile	Ala	Val	Leu	Ala	Val	Ile	Pro	Pro				
				50			55				60								
Met	Phe	Met	Val	Gly	Ala	Val	Pro	Phe	Ala	Leu	Gln	Met	Val	Ala	Val				
							70				75				80				
Met	Leu	Ala	Pro	Met	Val	Leu	Gly	Ser	Ile	Arg	Gly	Gly	Cys	Ala	Val				

85 90 95  
 Gly Leu Tyr Ile Leu Val Gly Ala Leu Gly Leu Pro Val Phe Ser Gly  
 100 105 110  
 Gly Ser Ser Gly Ile Gly Val Leu Val Gly Pro Thr Gly Gly Tyr Leu  
 115 120 125  
 Trp Gly Trp Leu Ile Gly Ala Phe Val Ala Gly  
 130 135

<210> 2263  
 <211> 491  
 <212> DNA  
 <213> Homo sapiens

<400> 2263  
 naccggttcc cggtcgaccg aggcaaaggc aaaagtaagc aggggtgcccg tagtccccgt  
 60  
 tcccaccgcg gtatggctgg gtcactgctg acagatggcg tccccctgct gatctttccg  
 120  
 gagggcaccc ggtctcgac cggcgcaatg ggcaccttca aacctggggc tgccgcattg  
 180  
 gctatttcac gtgggggttcc gggttatcccg attgcttttag taggagcatg ggcggctatg  
 240  
 ccgtccgagc aagccaggtt accaaaagga cgtccattgg tccacgtggc tattggacac  
 300  
 cctatggacc ctgttcccg cgagatcgcc caccaattct ccgaacggat tcgtcgccag  
 360  
 gtcattgagt tgcacgacca aaccgcccgc gcctacggca tgccaacct tgacgaatac  
 420  
 ggacgccacc gcgcgctaag ccaggcctcc gagagcggcg acaccgcac caccaaccac  
 480  
 tcgacgtgca c  
 491

<210> 2264  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 2264  
 Xaa Ala Phe Pro Val Asp Arg Gly Lys Gly Lys Ser Lys Gln Gly Ala  
 1 5 10 15  
 Arg Ser Pro Arg Ser His Arg Gly Met Ala Gly Ser Leu Leu Thr Asp  
 20 25 30  
 Gly Val Pro Leu Leu Ile Phe Pro Glu Gly Thr Arg Ser Arg Thr Gly  
 35 40 45  
 Ala Met Gly Thr Phe Lys Pro Gly Ala Ala Ala Leu Ala Ile Ser Arg  
 50 55 60  
 Gly Val Pro Val Ile Pro Ile Ala Leu Val Gly Ala Trp Ala Ala Met  
 65 70 75 80  
 Pro Ser Glu Gln Ala Arg Leu Pro Lys Gly Arg Pro Leu Val His Val  
 85 90 95  
 Ala Ile Gly His Pro Met Asp Pro Val Pro Gly Glu Ile Ala His Gln  
 100 105 110  
 Phe Ser Glu Arg Ile Arg Arg Gln Val Ile Glu Leu His Asp Gln Thr

	115		120		125	
Ala	Arg	Ala	Tyr	Gly	Met	Pro
	130		135		140	
Ala	Leu	Ser	Gln	Ala	Ser	Glu
	145		150		155	
Ser	Thr	Cys				

&lt;210&gt; 2265

&lt;211&gt; 328

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2265

```

ccatgggaat aggccaacac ggatggatct actgtataac ttgcctgcca tcaggaaaga
60
gtcaacacgg cagacacatg ctggcagaaa ccctgctgga gttgccctg agcattgatg
120
cataccaccc gagaggagga gaggggtggtg ggagaaatca gatcagagtt caaaatgcac
180
cggaagggtc cgaaatgta agactgcacc ttgcaggaac tgtcaatgcc actaccaata
240
tcactcactt acgtcaagca cttgagagca gctgcgaaca caattctctg actcctaacc
300
tttagcacgt gactgggacc actggaca
328

```

&lt;210&gt; 2266

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2266

Met	Gly	Ile	Gly	Gln	His	Gly	Trp	Ile	Tyr	Cys	Ile	Thr	Cys	Leu	Pro
1				5					10					15	
Ser	Gly	Lys	Ser	Gln	His	Gly	Arg	His	Met	Leu	Ala	Glu	Thr	Leu	Leu
			20				25						30		
Glu	Leu	Pro	Leu	Ser	Ile	Asp	Ala	Tyr	His	Pro	Arg	Gly	Gly	Glu	Gly
		35				40						45			
Gly	Gly	Arg	Asn	Gln	Ile	Arg	Val	Gln	Asn	Ala	Pro	Glu	Gly	Leu	Gly
	50					55				60					
Asn	Val	Arg	Leu	His	Leu	Ala	Gly	Thr	Val	Asn	Ala	Thr	Thr	Asn	Ile
65					70				75					80	
Thr	His	Leu	Arg	Gln	Ala	Leu	Glu	Ser	Ser	Cys	Glu	His	Asn	Ser	Leu
				85				90						95	
Thr	Pro	Asn	Leu												
															100

&lt;210&gt; 2267

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2267

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 240  
 gacagagatg gtgaagcagg catgtcctaa agcctccctt cttaaccctg accttgaagg  
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 370

<210> 2268

<211> 91

<212> PRT

<213> Homo sapiens

<400> 2268

Met	Ala	Asp	His	Gly	Gly	Leu	Met	Gln	Ala	Gly	Lys	Ala	Arg	Gln	Ser
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Ser	Gln	Lys	Gln	Val	Thr	Glu	Gly	Ala	Thr	Thr	Glu	Leu	His	Ser	Arg
			20					25					30		
Trp	Gly	Val	Lys	Pro	Tyr	Pro	Pro	Lys	Thr	Ala	Val	Thr	Gly	Val	Ala
			35					40					45		
Asn	Leu	Tyr	Arg	Asp	Arg	Leu	Lys	Ala	Thr	Ala	Thr	Gln	Gly	Thr	Glu
			50				55				60				
Met	Val	Lys	Gln	Ala	Cys	Pro	Lys	Ala	Ser	Leu	Leu	Asn	Pro	Asp	Leu
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Glu	Gly	Gln	Glu	Thr	Ser	His	Leu	Arg	Met	Leu					
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<210> 2269

<211> 507

<212> DNA

<213> Homo sapiens

<400> 2269

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<210> 2270  
 <211> 169  
 <212> PRT  
 <213> Homo sapiens

<400> 2270  
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 Ile Gly Val Asn Ala Gly Ser Leu Asp Lys Arg Leu Leu Asp Lys Tyr  
 35 40 45  
 Gly Ala Pro Thr Ala Glu Ala Met Val Glu Ser Ala Leu Trp Glu Ala  
 50 55 60  
 Ser Leu Phe Glu Gln Tyr Gly Phe Arg Asp Phe Lys Ile Ser Val Lys  
 65 70 75 80  
 His His Asp Pro Val Val Met Ile Arg Ala Tyr Glu Gln Leu Ala Ala  
 85 90 95  
 Lys Cys Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Ala  
 100 105 110  
 Phe Gln Gly Thr Ile Lys Ser Ala Val Ala Phe Gly His Leu Leu Ala  
 115 120 125  
 Glu Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val  
 130 135 140  
 Glu Glu Val Lys Val Gly Ile Lys Ile Leu Glu Ser Leu Asn Leu Arg  
 145 150 155 160  
 Pro Arg Gly Leu Glu Ile Val Ser Cys  
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<210> 2271  
 <211> 573  
 <212> DNA  
 <213> Homo sapiens

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<210> 2272

<211> 191

<212> PRT

<213> Homo sapiens

<400> 2272

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Asp	Glu	Asp	Ile	Pro	Met	Val	Asp	Glu	Ser	Leu	Glu	Gln	Phe	Ala	Gln
			20					25					30		
Leu	Leu	Lys	Thr	Arg	Thr	Ser	Glu	Glu	Gly	Met	Ala	Pro	Leu	Thr	Ser
		35					40					45			
Asp	Ala	Val	Ala	Arg	Leu	Ala	Thr	Tyr	Ser	Ala	Arg	Leu	Ala	Asp	His
	50					55					60				
Gln	Gly	Arg	Val	Ser	Ala	Arg	Ile	Gly	Asp	Leu	Phe	Gln	Leu	Val	Ser
65				70					75				80		
Glu	Ala	Asp	Phe	Ile	Arg	His	Leu	Ala	Gly	Asp	Glu	Met	Thr	Asp	Ala
			85						90				95		
Gly	His	Ile	Glu	Arg	Ala	Leu	Lys	Ala	Lys	Ala	Thr	Arg	Thr	Gly	Arg
		100					105					110			
Val	Ser	Ala	Arg	Ile	Leu	Asp	Asp	Met	Leu	Ala	Gly	Val	Ile	Leu	Ile
		115				120						125			
Asp	Thr	Ala	Gly	Ala	Ala	Val	Gly	Lys	Cys	Asn	Gly	Leu	Thr	Val	Leu
	130				135						140				
Glu	Val	Gly	Asp	Ser	Ala	Phe	Gly	Val	Pro	Ala	Arg	Ile	Ser	Ala	Thr
145				150					155				160		
Val	Tyr	Pro	Gly	Gly	Ser	Gly	Ile	Val	Asp	Ile	Glu	Arg	Glu	Val	Asn
			165					170					175		
Leu	Gly	Gln	Pro	Ile	His	Ser	Lys	Gly	Val	Met	Ile	Leu	Thr	Gly	
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<210> 2273

<211> 4355

<212> DNA

<213> Homo sapiens

<400> 2273

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 120  
 gagagggagg aggaagtgat cacctgtttt gagagggcct cctggatcgc tcaggtgttc  
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<210> 2274

<211> 158

<212> PRT

<213> Homo sapiens

<400> 2274

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Gln	Arg	Ser	Cys	Arg	Gly	Gly	Leu	Ser	Leu	Glu	Arg	Leu	Pro	Asn	Ser
		20					25						30		
Ile	Ala	Ser	Arg	Phe	Arg	Leu	Thr	Glu	Arg	Glu	Glu	Glu	Val	Ile	Thr
		35				40						45			
Cys	Phe	Glu	Arg	Ala	Ser	Trp	Ile	Ala	Gln	Val	Phe	Leu	Gln	Glu	Leu
		50				55				60					
Glu	Lys	Thr	Thr	Asn	Asn	Ser	Thr	Ser	Arg	His	Leu	Lys	Gly	Cys	His
65				70					75				80		
Pro	Leu	Asp	Tyr	Glu	Leu	Thr	Tyr	Phe	Leu	Glu	Ala	Ala	Leu	Gln	Ser
			85					90					95		
Ala	Tyr	Val	Lys	Asn	Leu	Lys	Lys	Gly	Asn	Ile	Val	Lys	Gly	Met	Arg
		100						105					110		
Glu	Leu	Arg	Glu	Val	Leu	Arg	Thr	Val	Glu	Thr	Lys	Ala	Thr	Gln	Asn
		115				120						125			
Phe	Lys	Val	Met	Ala	Ala	Lys	His	Leu	Ala	Gly	Val	Leu	Leu	His	Ser
		130				135						140			
Leu	Ser	Gly	Val	Leu	Leu	Glu	Pro	Pro	Val	Pro	Pro	Ser	Ala		

145

150

155

&lt;210&gt; 2275

&lt;211&gt; 608

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2275

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120  
aaggagaaca ggagacctca aaaggaagaa ccaggctgtg ccccaacctt ttttccaaac  
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caaagttctg gcttcactac acccactgct atgacacctc ctgttctaac cacagccgaa  
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608

&lt;210&gt; 2276

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2276

Ser	Thr	Asn	Asn	Thr	Lys	Glu	Asn	Arg	Arg	Pro	Gln	Lys	Glu	Glu	Pro
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Gly	Cys	Ala	Pro	Thr	Phe	Phe	Pro	Asn	Gln	Ser	Ser	Gly	Phe	Thr	Thr
			20					25				30			
Pro	Thr	Ala	Met	Thr	Pro	Pro	Val	Leu	Thr	Thr	Ala	Glu	Thr	Ser	Val
		35					40					45			
Lys	Pro	Ser	Val	Ser	Ala	Phe	Thr	His	Ser	Pro	Pro	Glu	Asn	Thr	Thr
		50				55					60				
Gly	Ile	Ser	Ser	Thr	Ile	Ser	Phe	His	Ser	Arg	Thr	Leu	Asn	Leu	Thr
65				70						75				80	
Asp	Val	Ile	Glu	Glu	Leu	Ala	Gln	Ala	Ser	Thr	Gln	Thr	Leu	Lys	Ser
			85					90					95		
Thr	Ile	Ala	Ser	Glu	Thr	Thr	Leu	Ser	Ser	Lys	Ser	His	Gln	Ser	Thr
		100					105					110			
Thr	Thr	Arg	Lys	Ala	Ile	Ile	Arg	His	Ser	Thr	Ile	Pro	Pro	Phe	Leu
		115				120						125			
Ser	Ser	Ser	Ala	Thr	Leu	Ile	Pro	Val	Pro	Ile	Ser	Pro	Pro	Phe	Thr

130 135 140  
 Gln Arg Ala Val Thr Asp Asn Val Ala Thr Pro Ile Ser Gly Leu Met  
 145 150 155 160  
 Thr Asn Thr Val Val Lys Leu  
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<210> 2277

<211> 640

<212> DNA

<213> Homo sapiens

<400> 2277

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 120  
 gacagggaca ctgagggatg aaagccccca cgctctggcc tgccttgctc agtcagggcc  
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<210> 2278

<211> 95

<212> PRT

<213> Homo sapiens

<400> 2278

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 20 25 30  
 Cys Cys Pro Pro Trp Leu Ser Ser Pro Pro Ala Ala Cys Leu Pro Ser  
 35 40 45  
 Ser Leu Leu Ser Pro Tyr Pro Val Leu Pro Ser Pro Ser Cys Lys Val  
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 His Ala Thr Pro Gln Glu Glu Pro Gln Arg Leu Ser Ser Asp Pro Thr  
 65 70 75 80  
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 85 90 95

<210> 2279  
 <211> 331  
 <212> DNA  
 <213> Homo sapiens

<400> 2279  
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 300  
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 331

<210> 2280  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 2280  
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Pro	Glu	Arg	Leu	Ala	Gln	Arg	Gly	Asp	Ser	Ser	Ala	Pro	Ser	Thr	Cys

1677

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 Leu Asn Gly Gly Trp Thr Ile Gln Trp Asn Gly Asp Tyr Gln Val Ala  
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 Gly Thr Thr Phe Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr  
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Ser Thr Pro Ala Trp Asp Ser Pro Ala Asn Ser His Arg Val Pro Glu		
1475	1480	1485
Thr Gln Pro Leu Ala Pro Ser Leu Ala Glu Ala Gly Pro Pro Ala Asp		

1490	1495	1500
Pro Leu Val Val Arg Asn Ala Ser Trp Gln Ala Gly Asn Trp Ser Glu		
1505	1510	1515
Cys Ser Thr Thr Cys Gly Leu Gly Ala Val Trp Arg Pro Val Arg Cys		1520
	1525	1530
Ser Ser Gly Arg Asp Glu Asp Cys Ala Pro Ala Gly Arg Pro Gln Pro		1535
	1540	1545
Ala Arg Arg Cys His Leu Arg Pro Cys Ala Thr Trp His Ser Gly Asn		1550
	1555	1560
Trp Ser Lys Cys Ser Arg Ser Cys Gly Gly Gly Ser Ser Val Arg Asp		1565
	1570	1575
Val Gln Cys Val Asp Thr Arg Asp Leu Arg Pro Leu Arg Pro Phe His		1580
1585	1590	1595
Cys Gln Pro Gly Pro Ala Lys Pro Pro Ala His Arg Pro Cys Gly Ala		1600
	1605	1610
Gln Pro Cys Leu Ser Trp Tyr Thr Ser Ser Trp Arg Glu Cys Ser Glu		1615
	1620	1625
Ala Cys Gly Gly Gly Glu Gln Gln Arg Leu Val Thr Cys Pro Glu Pro		1630
	1635	1640
Gly Leu Cys Glu Glu Ala Leu Arg Pro Asn Thr Thr Arg Pro Cys Asn		1645
	1650	1655
Thr His Pro Cys Thr Gln Trp Val Val Gly Pro Trp Gly Gln Cys Ser		1660
1665	1670	1675
Ala Pro Cys Gly Gly Val Gln Arg Arg Leu Val Lys Cys Val Asn		1680
	1685	1690
Thr Gln Thr Gly Leu Pro Glu Glu Asp Ser Asp Gln Cys Gly His Glu		1695
	1700	1705
Ala Trp Pro Glu Ser Ser Arg Pro Cys Gly Thr Glu Asp Cys Glu Pro		1710
	1715	1720
Val Glu Pro Pro Arg Cys Glu Arg Asp Arg Leu Ser Phe Gly Phe Cys		1725
1730	1735	1740
Glu Thr Leu Arg Leu Leu Gly Arg Cys Gln Leu Pro Thr Ile Arg Thr		1745
	1750	1755
Gln Cys Cys Arg Ser Cys Ser Pro Pro Ser His Gly Ala Pro Ser Arg		1760
	1765	1770
Gly His Gln Arg Val Ala Arg Arg		1775
	1780	

&lt;210&gt; 2287

&lt;211&gt; 750

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2287

tgacacaggt tatttctctt tgggttaaata tcttacaagt cttttttaaa tcttcacttc  
 60  
 tggcctataa aagtatcatc atccccattt tacagaatgg gaaagtaagg cgtggggagg  
 120  
 ttgaggacat ttgtacagag tcaggttaact ggaggaactg gactacaacc ctgctcagt  
 180  
 cagccagtgt gactgagcgc ctctgagag ccaggtggat tctgccctca aggatccatg  
 240  
 ctctgggcaa gaaaccacc catcagcagg tggcttctgc tgagccacaa caggcacaca  
 300

gaggggtcca tgggagccca gaggggagca tctgaccagg ctcaggggaa ggaatgtgtc  
 360  
 cagcagagtc acagaggagc agtatgagtt agccaggtag gggacattcc aggcagggga  
 420  
 gcagcaggac aaaagcatag aggtagcact gccagtgccca agttccaaaa taagaggctg  
 480  
 actgctacag ggtccatata ggaaaataat gggaaataca tttggacagg aggtggggtc  
 540  
 tgtaacaaag gactttaatt ccagggttaag gaatctggat gttaaaacaa cattagctgc  
 600  
 cattttctaca gtgctacttc ccaggctctg tgcctttctg ggagccttga aggtttgtga  
 660  
 gctggaagga gatattagga acaaaacgat gcatgaggat agctcaggta aaggttattg  
 720  
 ataagtaaga atgcctggca ccaaacgcgt  
 750

&lt;210&gt; 2288

&lt;211&gt; 142

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2288

Met	Ala	Ala	Asn	Val	Val	Leu	Thr	Ser	Arg	Phe	Leu	Asn	Leu	Glu	Leu
1			5						10					15	
Lys	Ser	Phe	Val	Thr	Asp	Pro	Thr	Ser	Cys	Pro	Asn	Val	Phe	Pro	Ile
			20					25					30		
Ile	Phe	Leu	Tyr	Gly	Pro	Cys	Ser	Ser	Gln	Pro	Leu	Ile	Leu	Glu	Leu
		35					40					45			
Gly	Thr	Gly	Ser	Ala	Thr	Ser	Met	Leu	Leu	Ser	Cys	Cys	Ser	Pro	Ala
		50				55					60				
Trp	Asn	Val	Pro	Tyr	Leu	Ala	Asn	Ser	Tyr	Cys	Ser	Ser	Val	Thr	Leu
65					70					75				80	
Leu	Asp	Thr	Phe	Leu	Pro	Leu	Ser	Leu	Val	Arg	Cys	Ser	Pro	Leu	Gly
			85						90					95	
Ser	His	Gly	Pro	Leu	Cys	Val	Pro	Val	Val	Ala	Gln	Gln	Lys	Pro	Pro
			100				105						110		
Ala	Asp	Gly	Trp	Val	Ser	Cys	Pro	Glu	His	Gly	Ser	Leu	Arg	Ala	Glu
		115					120					125			
Ser	Thr	Trp	Leu	Ser	Gly	Gly	Ala	Gln	Ser	His	Trp	Leu	His		
		130				135						140			

&lt;210&gt; 2289

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2289

caggacgcgg cctcggcggg gcccgggccg aacggctgcg gacacctggg cgccgaggag  
 60  
 ccgagcgccg ccgcctccgg catggatcat tgcgtgacgg tggagcgcca gctggagaag  
 120  
 gtgctgcaca agttctcggg ctacgggcag ctgtgcgagc gcggcctgga ggagctcatc  
 180



gactacaccg gcggtctcaa gcaccagatc ctgcagagcc acggccaaga tgctgaatta  
 240  
 tcagggacac tttcacttgt tttgacacag ggctgtaaaa gaataanaag gggatactgg  
 300  
 ttcaaaaatt ggcctccgac cacaagaca tccacagcag tgtttctcgg gttggaaaag  
 360  
 ccattgatga ggattcactt t  
 381

<210> 2290

<211> 100

<212> PRT

<213> Homo sapiens

<400> 2290

Met	Asp	His	Cys	Val	Thr	Val	Glu	Arg	Glu	Leu	Glu	Lys	Val	Leu	His
1				5					10					15	
Lys	Phe	Ser	Gly	Tyr	Gly	Gln	Leu	Cys	Glu	Arg	Gly	Leu	Glu	Glu	Leu
			20					25					30		
Ile	Asp	Tyr	Thr	Gly	Gly	Leu	Lys	His	Gln	Ile	Leu	Gln	Ser	His	Gly
		35					40					45			
Gln	Asp	Ala	Glu	Leu	Ser	Gly	Thr	Leu	Ser	Leu	Val	Leu	Thr	Gln	Gly
		50				55					60				
Cys	Lys	Arg	Ile	Xaa	Arg	Gly	Tyr	Trp	Phe	Lys	Asn	Trp	Pro	Pro	Thr
65					70					75				80	
Thr	Lys	Thr	Ser	Thr	Ala	Val	Phe	Leu	Gly	Leu	Glu	Lys	Pro	Leu	Met
			85						90					95	
Arg	Ile	His	Phe												
				100											

<210> 2291

<211> 573

<212> DNA

<213> Homo sapiens

<400> 2291

gcattgctcta ccgcaaagtc gggccccac cgattaataaa tgcccgggtc gaggacagcc  
 60  
 ttcggcagca ccgactcatt atcggcaccg acctagtcaa ttgccaccac ctgcttatgc  
 120  
 aagtggctga tagaagcccc agccggctta agccagttct ggaaaaccac cacatatcgc  
 180  
 acatgttcgt tgtgacgatg cagctgagcc attgaatcga cggtcagcgc catgaacgcc  
 240  
 cgatgctcgt tgacggtaag actcggcgac ccagcaacgt cggcggttgt cgtgccctca  
 300  
 tcggtgtaat ggcgacgagc gacgatgacg tcatgtccgc cggcaaagaa ggctgcggaa  
 360  
 gcctcgcgta attcttgggg accgaggtcc tcggcgcgcc ggtctgaccc caccgccttg  
 420  
 aacttggcgt taaggaccga cctcacgtga gcctcccctg acgggttaga caggtattcc  
 480  
 tctgccagt cccgcgctgc ccgaggcaag ctcatecccc agttgagctg ccaataccgc  
 540

cacgacagga tctcgaaaag attggggacg cgt  
573

<210> 2292

<211> 140

<212> PRT

<213> Homo sapiens

<400> 2292

```
Met Ser Leu Pro Arg Ala Ala Arg Asp Trp Gln Glu Glu Tyr Leu Ser
 1              5              10              15
Asn Pro Ser Gly Glu Ala His Val Arg Ser Val Leu Asn Ala Lys Phe
      20              25              30
Lys Ala Val Gly Ser Asp Arg Arg Ala Glu Asp Leu Gly Pro Gln Glu
      35              40              45
Leu Arg Glu Ala Ser Ala Ala Phe Phe Ala Gly Gly His Asp Val Ile
      50              55              60
Val Ala Arg Arg His Tyr Thr Asp Glu Gly Thr Thr Thr Ala Asp Val
      65              70              75              80
Ala Gly Ser Ala Ser Leu Thr Val Asn Glu His Arg Ala Phe Met Ala
      85              90              95
Leu Thr Val Asp Ser Met Ala Gln Leu His Arg His Asn Glu His Val
      100             105             110
Arg Tyr Val Val Val Phe Gln Asn Trp Leu Lys Pro Ala Gly Ala Ser
      115             120             125
Ile Asp His Leu His Lys Gln Val Val Ala Ile Asp
      130             135             140
```

<210> 2293

<211> 358

<212> DNA

<213> Homo sapiens

<400> 2293

```
acgcgtgaag gaatggaagc tgctctcgtc ggtgcacaca agactggcgg gtgcccattg
60
gtgaacactg tcgctaagaa ctgggtgaac cggctcaaca cgccggatat gaaaccact
120
gaggagatca agcggcagtt ccaaggtctg cattgggttg gacgtaagta tgggctcaac
180
cacggagagt tctatcttga cgacgagcag tgggccacgc tcatggccgg gtcctctttc
240
gaggcgaatc cgcgcatata gagcaacttt gattccgagg gcgctgttgt ggatccggat
300
tccgattcac ttgctggggc tgatcgagat gcccgagggtg cttcggtatgc atgccttc
358
```

<210> 2294

<211> 115

<212> PRT

<213> Homo sapiens

<400> 2294

```
Met Glu Ala Ala Leu Val Gly Ala His Lys Thr Gly Gly Cys Pro Leu
```

```

      1             5             10             15
Val Asn Thr Val Ala Lys Asn Trp Leu Asn Arg Leu Asn Thr Pro Asp
      20             25             30
Met Lys Pro Thr Glu Glu Ile Lys Arg Gln Phe Gln Gly Leu His Trp
      35             40             45
Leu Gly Arg Lys Tyr Gly Leu Asn His Gly Glu Phe Tyr Leu Asp Asp
      50             55             60
Glu Gln Trp Ala Thr Leu Met Ala Gly Ser Ser Phe Glu Ala Asn Pro
      65             70             75             80
Arg Ile Lys Ser Asn Phe Asp Ser Glu Gly Ala Val Val Asp Pro Asp
      85             90             95
Ser Asp Ser Leu Ala Gly Ala Asp Arg Asp Ala Arg Gly Ala Ser Asp
      100             105             110
Ala Cys Leu
      115

```

&lt;210&gt; 2295

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2295

```

ggcaccgatc cgagtgggtg tgccgggatt aggnccgatc tanaaacatt ctccgccctt
60
ggggcgatatg gctgctcgtt cattaccgca ctggtagcgc aaaatacgcg cggcgtgcag
120
tcggtgtatc gtatcgaacc ggattttgtc ggtgcacaac tggactctgt gttcagcgat
180
gtccgcattg attccaccaa aatcggcatg ctggcagagg cggatatcgt ggaagcggtc
240
gcggagcgcc tcaaacatta tcgcgttaaa aacgtggtac ttgatacggg gatgctggcg
300
aaaagtggcg atccgctgct atctcctgct gctgtcgaaa ctctgcgaaa acaccttctg
360
ccacacgtcg cgctgatcac gccaaatttg ccggaggcgg cggcgtgctt ggatgcgcct
420
catgcccgta ccgagcacga gatgaaagag caggggcgcg cacttctggc gcttggctgc
480
gaggcagtgc tgatgaaagg cggccatctt gacgatcctg agagcccgga ctggctcttc
540
acgcgt
546

```

&lt;210&gt; 2296

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2296

```

Gly Thr Asp Pro Ser Gly Gly Ala Gly Ile Arg Xaa Asp Leu Xaa Thr
      1             5             10             15
Phe Ser Ala Leu Gly Ala Tyr Gly Cys Ser Val Ile Thr Ala Leu Val
      20             25             30
Ala Gln Asn Thr Arg Gly Val Gln Ser Val Tyr Arg Ile Glu Pro Asp

```

```

      35          40          45
Phe Val Gly Ala Gln Leu Asp Ser Val Phe Ser Asp Val Arg Ile Asp
      50          55          60
Ser Thr Lys Ile Gly Met Leu Ala Glu Ala Asp Ile Val Glu Ala Val
65          70          75          80
Ala Glu Arg Leu Lys His Tyr Arg Val Lys Asn Val Val Leu Asp Thr
      85          90          95
Val Met Leu Ala Lys Ser Gly Asp Pro Leu Leu Ser Pro Ala Ala Val
      100          105          110
Glu Thr Leu Arg Lys His Leu Leu Pro His Val Ala Leu Ile Thr Pro
      115          120          125
Asn Leu Pro Glu Ala Ala Ala Leu Leu Asp Ala Pro His Ala Arg Thr
      130          135          140
Glu His Glu Met Lys Glu Gln Gly Arg Ala Leu Leu Ala Leu Gly Cys
145          150          155          160
Glu Ala Val Leu Met Lys Gly Gly His Leu Asp Asp Pro Glu Ser Pro
      165          170          175
Asp Trp Leu Phe Thr Arg
      180

```

&lt;210&gt; 2297

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2297

```

gggaattccg ggcccttccc cccaagcccg ggtaattttt tgtattttta aaaaaaagg
60
gaattttccc acgttggggg ggggggggtc ggactttttc ccccaaaaac ccccccccc
120
caccccccca aaggccgaaa agcagggccca aaaccccccg gacccccccc gggggggggca
180
aaaggaaaaa cccctttttt tttttttttt ttttatacac atgagggtct ctggttaata
240
aatgttgaga ttaggggtta ggtgagatta aacagggttct ttttttcatg atttctcgga
300
gtctttatga tgctccacac cagtacttct caaagctgac tgtgtataca aaacactggg
360
gatctgaccc acatgtaaag tctgatttct ttggtctggg gcaggcctga aatn
414

```

&lt;210&gt; 2298

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2298

```

Lys Lys Arg Glu Phe Ser His Val Gly Gly Gly Gly Phe Gly Leu Phe
1          5          10          15
Pro Pro Lys Thr Pro Pro Pro His Pro Pro Lys Gly Arg Lys Ala Gly
20          25          30
Pro Lys Pro Pro Gly Pro Pro Pro Gly Gly Ala Lys Gly Lys Thr Pro
35          40          45
Phe Phe Phe Phe Phe Phe Tyr Thr His Glu Gly Leu Trp Leu Ile Asn

```

50  
Val Glu Met  
65

55

60

<210> 2299  
<211> 987  
<212> DNA  
<213> Homo sapiens

<400> 2299  
ngagatgtct aagttatattt ttttttcccg gaaggcaa at ggctggcgtg gaagcacaac  
60  
ccgctttcac tcttcgaatt tgtgcttagc tcttttcttg taccctgcca ctctgaccca  
120  
acatgctgtg atgtgtgccg agggaggaat tggtcagcta cacaacctgg atcttaccac  
180  
agtttgata tgactgaggc tctccaatgg gccagatata actggcgacg gctgatcaga  
240  
ggtgcaacca gggatgatga ttcagggccca tacaactatt cctcgttgct cgctgtggg  
300  
cgcaagtcct ctccagatccc taaactgtca ggaaggcacc ggattgttgt tccccacatc  
360  
cagcccttca aggatgagta tgagaagttc tccggagcct atgtgaacaa tcgaatacga  
420  
acaacaaagt acacacttct gaattttgtg ccaagaaatt tatttgaaca atttcacaga  
480  
gctgcccaatt tatatttctt gttcctagtt gtcctgaact ggttaccttt ggtagaagcc  
540  
ttccaaaagg aaatcaccat gttgcctctg gtggtgggtcc ttacaattat cgcaattaaa  
600  
gatggcctgg aagattatcg gaaatacaaa attgacaaac agatcaataa ttttaataact  
660  
aaagtttata gtaggaaaga gaaaaaatac attgaccgat gctggaaaga cgttactgtt  
720  
ggggacttta ttgcctctc ctgcaacgag gtcacccctg cagacatggt actactcttt  
780  
tccactgac cagatggaat ctgtcacatt gagacttctg gtcttgatgg agagagcaat  
840  
ttaaacaaga ggcaggtggt tcggggatat gcagaacagg actctgaagt tgatcctgag  
900  
aagttttcca gtaggataga atgtgaaagc ccaacaatg acctcagcag attccgaggc  
960  
ttcctagaac attccaacaa agaacgc  
987

<210> 2300  
<211> 266  
<212> PRT  
<213> Homo sapiens

<400> 2300  
Met Thr Glu Ala Leu Gln Trp Ala Arg Tyr His Trp Arg Arg Leu Ile  
1 5 10 15  
Arg Gly Ala Thr Arg Asp Asp Asp Ser Gly Pro Tyr Asn Tyr Ser Ser

```
<210> 2301
<211> 390
<212> DNA
<213> Homo sapiens
```

<210> 2302

<211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 2302  
 Tyr Pro Lys Arg Phe Lys Phe Asp Ala Asp Glu Phe Tyr Leu Lys Ser  
 1 5 10 15  
 Ser Glu Glu Met Xaa Ala Thr Ser Ser Ala Xaa Phe Pro Glu Ala Cys  
 20 25 30  
 Asp Asn Thr Met Glu Ile Ala Glu Xaa Val Ala Thr Leu Asn Ser Thr  
 35 40 45  
 Gln Thr Gln Xaa Tyr Met Pro Asp Phe Pro Thr Pro Glu Gly Glu Asn  
 50 55 60  
 Glu Glu Ser Trp Phe Val Lys Glu Val Glu Arg Gly Leu His Tyr Arg  
 65 70 75 80  
 Phe Pro Glu Gly Ile Pro Asp Asp Val Arg Lys Gln Ala Asp Tyr Glu  
 85 90 95  
 Val Gly Ile Ile Thr Gln Met Gly Phe Pro Gly Tyr Phe Leu Val Val  
 100 105 110  
 Ala Asp Phe Ile Asn Trp Ala Lys Asn Asn Gly Ile Arg Val Gly Pro  
 115 120 125  
 Gly Arg  
 130

<210> 2303  
 <211> 638  
 <212> DNA  
 <213> Homo sapiens

<400> 2303  
 nnggatccag gctgcccctg tgtgtctcct tcagtcttcg ttagctgcct gctgctgtct  
 60  
 gcacctgtgt ttggctacct gggcgaccga catagccgca aggctaccat gagcttcggt  
 120  
 atcttgctgt ggtcaggagc tggcctctct agctccttca tctccccccg gtattcttgg  
 180  
 ctctttcttc tgtccccggg catcgagggc actggctcgg ccagctactc caccatcgcg  
 240  
 cccaccgtcc tgggcgacct cttcgtgagg gaccagcgca cccgcgtgct ggctgtcttc  
 300  
 tacatcttta tccccgttgg aagtggctct ggctacgtgc tggggtcggc tgtgacgatg  
 360  
 ctgactggga actggcgctg ggcctccga gtcatgccct gcctggaggc cgtggccttg  
 420  
 atcctgctta tctgctggt tccagacca ccccggggag ctgccgagac acagggggag  
 480  
 ggggccgtgg gaggcttcag aagcagctgg tgtgaggacg tcagatacct ggggaaaaac  
 540  
 tggagttttg tgtggctgac cctcggagtg accgccatgg cctttgtgac tggagcctg  
 600  
 gggttctggg cccccaagtt tctgctcgag gcacgcgt  
 638

<210> 2304

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2304

```

Xaa Asp Pro Gly Cys Pro Cys Val Ser Pro Ser Val Phe Val Ser Cys
 1          5          10          15
Leu Leu Leu Ser Ala Pro Val Phe Gly Tyr Leu Gly Asp Arg His Ser
 20          25          30
Arg Lys Ala Thr Met Ser Phe Gly Ile Leu Leu Trp Ser Gly Ala Gly
 35          40          45
Leu Ser Ser Ser Phe Ile Ser Pro Arg Tyr Ser Trp Leu Phe Phe Leu
 50          55          60
Ser Arg Gly Ile Glu Gly Thr Gly Ser Ala Ser Tyr Ser Thr Ile Ala
 65          70          75          80
Pro Thr Val Leu Gly Asp Leu Phe Val Arg Asp Gln Arg Thr Arg Val
 85          90          95
Leu Ala Val Phe Tyr Ile Phe Ile Pro Val Gly Ser Gly Leu Gly Tyr
100          105          110
Val Leu Gly Ser Ala Val Thr Met Leu Thr Gly Asn Trp Arg Trp Ala
115          120          125
Leu Arg Val Met Pro Cys Leu Glu Ala Val Ala Leu Ile Leu Leu Ile
130          135          140
Leu Leu Val Pro Asp Pro Pro Arg Gly Ala Ala Glu Thr Gln Gly Glu
145          150          155          160
Gly Ala Val Gly Gly Phe Arg Ser Ser Trp Cys Glu Asp Val Arg Tyr
165          170          175
Leu Gly Lys Asn Trp Ser Phe Val Trp Ser Thr Leu Gly Val Thr Ala
180          185          190
Met Ala Phe Val Thr Gly Ala Leu Gly Phe Trp Ala Pro Lys Phe Leu
195          200          205
Leu Glu Ala Arg
210

```

&lt;210&gt; 2305

&lt;211&gt; 340

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2305

```

gccccgcct ctatcttccg gcatcgtcac agtcgcatcg tgacggtact ggctggagtc
60
tcggaccagc acactttgac cgtcgtggtc gctcgtgac atggggtaac gcgaacctcg
120
tcgctcctgt tcttgacctc ttccgtgccc ccattgacaa cgatcgggca agttcactgg
180
cccgcaacgc tattggtgac gcagcactcg cagctggtct cgaccgactc gtccacacca
240
cggcgctcggc gcgcgacgag ggcgatgagt tggtcgtcgt tactcgcagc gctgctgccg
300
ccgcacgcaa ttccatgacg acaacgtgga gttggcgcgc
340

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&lt;210&gt; 2306



<211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 2306  
 Met Glu Leu Arg Ala Ala Ala Ala Leu Arg Val Thr Thr Thr Asn  
 1 5 10 15  
 Ser Ser Pro Ser Ser Arg Thr Asp Ala Val Val Trp Thr Ser Arg Ser  
 20 25 30  
 Arg Pro Ala Ala Ser Ala Ala Ser Pro Ile Ala Leu Arg Ala Ser Glu  
 35 40 45  
 Leu Ala Arg Ser Leu Ser Met Gly Ala Arg Lys Arg Ser Arg Thr Gly  
 50 55 60  
 Ala Thr Arg Phe Ala Leu Pro His Val Thr Arg Arg Pro Arg Arg Ser  
 65 70 75 80  
 Lys Cys Ala Gly Pro Arg Leu Gln Pro Val Pro Ser Arg Cys Asp Cys  
 85 90 95  
 Asp Asp Ala Gly Arg  
 100

<210> 2307  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 2307  
 ngcttctcag ctgaaggggg agataaagct ctacataaga tgggtccagg tgggggcaaa  
 60  
 gccaaaggcac tgggtggggc tggcagtggg agcaagggtc cagcaggtgg cggaagcaag  
 120  
 cgacggctga gcagcgaaga cagctccctg gagccagacc tggccgagat gagcctggat  
 180  
 gacagcagcc tggccctggg cgcagaggcc aggaccttcg ggggattccc tgagagccct  
 240  
 ccaccctgtc ctctccacgg tggctcccgga ggcccttcca ctttccttcc tgagccccca  
 300  
 gatacttatg aagaagatgg tgatgagagt ggcaatgggc ttcccaaaac caaagaggca  
 360

<210> 2308  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 2308  
 Xaa Phe Ser Ala Glu Gly Gly Asp Lys Ala Leu His Lys Met Gly Pro  
 1 5 10 15  
 Gly Gly Gly Lys Ala Lys Ala Leu Gly Gly Ala Gly Ser Gly Ser Lys  
 20 25 30  
 Gly Ser Ala Gly Gly Gly Ser Lys Arg Arg Leu Ser Ser Glu Asp Ser  
 35 40 45  
 Ser Leu Glu Pro Asp Leu Ala Glu Met Ser Leu Asp Asp Ser Ser Leu  
 50 55 60  
 Ala Leu Gly Ala Glu Ala Arg Thr Phe Gly Gly Phe Pro Glu Ser Pro

```

65          70          75          80
Pro Pro Cys Pro Leu His Gly Gly Ser Arg Gly Pro Ser Thr Phe Leu
          85          90          95
Pro Glu Pro Pro Asp Thr Tyr Glu Glu Asp Gly Asp Glu Ser Gly Asn
          100          105          110
Gly Leu Pro Lys Thr Lys Glu Ala
          115          120

```

&lt;210&gt; 2309

&lt;211&gt; 395

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2309

```

ggatccctac aaatggggcc ctgctctgag cacattccca tgagggtgc ctgcctgtg
60
cactctctgc cctgggcccgc ggggcctgac tgggttccca cctcctccta cccactgggg
120
tcttttccag caggcacagg gattcctcat gggggaggca gagccaccc gtctgtcctc
180
ggtgacggcc tgagctgtgc acggcctccc ctgcctcctc gttctcaggc ccccagggt
240
ccatccagcc ccagcgtgtg gcgttctggc tcttccctgg agtctcctcc cagaccacgc
300
gactccactc aactgtgcc tagcggactg tgtggttgat gcagccggct cacttgagtg
360
tgttggtgta tgcccacaac aggcttgccg tcacc
395

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&lt;210&gt; 2310

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2310

```

Met Gly Pro Cys Ser Glu His Ile Pro Met Arg Ala Ala Cys Pro Val
 1          5          10          15
His Ser Leu Pro Trp Ala Ala Gly Pro Asp Trp Val Pro Thr Ser Ser
          20          25          30
Tyr Pro Leu Gly Ser Phe Pro Ala Gly Thr Gly Ile Pro His Gly Gly
          35          40          45
Gly Arg Ala His Pro Ser Val Leu Gly Asp Gly Leu Ser Cys Ala Arg
          50          55          60
Pro Pro Leu Pro Ser Cys Ser Gln Ala Pro Gln Gly Pro Ser Ser Pro
65          70          75          80
Ser Val Trp Arg Ser Gly Ser Ser Leu Glu Ser Pro Pro Arg Pro Arg
          85          90          95
Asp Ser Thr His Thr Val Pro Ser Gly Leu Cys Gly
          100          105

```

&lt;210&gt; 2311

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2311

gtgcacgccg agatgctgcc gcaagacaag cagcgtgtcg tcggcgagtt gaagcgccag  
60  
ggcttctcag tgatcaaggt cggcgatggc atcaatgatt gcgacgctct cgccgeggcg  
120  
gatgtcggca gtcccatggg cggcagcgcg gacgtggctc tcgaaacggc cgatgctgcc  
180  
gtccttcacg gacgggtggg ggacgtcttc gcgatgatcg ccctatcgaa gcgaaccatg  
240  
gccaacattc gacagaacat cgcgatcgcg atcgggctaa aggcggtgtt ccttgtaacg  
300  
accgtcgtcg gcatcacggg gctttggcct gcaatcctcg ccgatacggg gaccacggag  
360  
cttgtgacca tgaacgcg  
378

&lt;210&gt; 2312

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2312

Val	His	Ala	Glu	Met	Leu	Pro	Gln	Asp	Lys	Gln	Arg	Val	Val	Gly	Glu
1				5					10					15	
Leu	Lys	Arg	Gln	Gly	Phe	Ser	Val	Ile	Lys	Val	Gly	Asp	Gly	Ile	Asn
			20					25					30		
Asp	Cys	Asp	Ala	Leu	Ala	Ala	Ala	Asp	Val	Gly	Ser	Pro	Met	Gly	Gly
		35					40					45			
Ser	Ala	Asp	Val	Ala	Leu	Glu	Thr	Ala	Asp	Ala	Ala	Val	Leu	His	Gly
	50					55					60				
Arg	Val	Gly	Asp	Val	Phe	Ala	Met	Ile	Ala	Leu	Ser	Lys	Arg	Thr	Met
65					70					75				80	
Ala	Asn	Ile	Arg	Gln	Asn	Ile	Ala	Ile	Ala	Ile	Gly	Leu	Lys	Ala	Val
				85				90					95		
Phe	Leu	Val	Thr	Thr	Val	Val	Gly	Ile	Thr	Gly	Leu	Trp	Pro	Ala	Ile
			100					105					110		
Leu	Ala	Asp	Thr	Gly	Thr	Thr	Glu	Leu	Val	Thr	Met	Asn	Ala		
			115					120					125		

&lt;210&gt; 2313

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2313

ctagtggcat ggtctcgtcg gtctttagtg gagcataccg acacatcggt gactcaaacg  
60  
atccgaatca tggctcgtcc tggttggcct ggaaccatta acgtacgcct caccatcg  
120  
ttaagcgacg ccggtctagc tgtcgaagtc accgcgcgca atgtcggtag gacagcgggg  
180  
ccgcttgat acgcagcaca ccctatctc tgtctgggtg gcaccatcga cgactggaca  
240

gtcgacgccc cgtttacctc gtggttacag gtcgatgac ggctgctacc aatgcagatg  
 300  
 cgcgagatgg acagcatcca cgcgctgaac ggtctcacgg gcggacagcg caccttcgat  
 360  
 accgcttaca ccgtgaaagg aggcaggaac cgtcggatcg cccgcatggc gtatccgggt  
 420  
 ctcaacggtg aaacgagcca cgaattgtgg ggcgacgccg cgatgagctg ggtgcaagtc  
 480  
 tacactccag acgaccgcca cagtctggcc atcgagccaa tgacctgcgg ccagatgca  
 540  
 tttaatgagg gcccagacca cgggtgacgtc attcgactgg agcccggtaa tgacgtcaca  
 600  
 ctgcactggg gcatcgcta acccgcgga gctcgaaagg acaaggacgg gaaggcagga  
 660  
 ttcacgcgt  
 669

&lt;210&gt; 2314

&lt;211&gt; 206

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2314

Leu	Val	Ala	Trp	Ser	Arg	Trp	Ser	Leu	Val	Glu	His	Thr	Asp	Thr	Ser
1				5					10					15	
Val	Thr	Gln	Thr	Ile	Arg	Ile	Met	Ala	Arg	Pro	Gly	Trp	Pro	Gly	Thr
		20					25						30		
Ile	Asn	Val	Arg	Leu	Thr	His	Arg	Leu	Ser	Asp	Ala	Gly	Leu	Ala	Val
	35					40						45			
Glu	Val	Thr	Ala	Arg	Asn	Val	Gly	Thr	Thr	Ala	Gly	Pro	Leu	Gly	Tyr
	50				55						60				
Ala	Ala	His	Pro	Tyr	Leu	Cys	Leu	Gly	Gly	Thr	Ile	Asp	Asp	Trp	Thr
65				70					75					80	
Val	Asp	Ala	Pro	Phe	Thr	Ser	Trp	Leu	Gln	Val	Asp	Asp	Arg	Leu	Leu
			85					90					95		
Pro	Met	Gln	Met	Arg	Glu	Met	Asp	Ser	Ile	His	Ala	Leu	Asn	Gly	Leu
		100					105						110		
Thr	Gly	Gly	Gln	Arg	Thr	Phe	Asp	Thr	Ala	Tyr	Thr	Val	Lys	Gly	Gly
	115					120						125			
Arg	Asn	Arg	Arg	Ile	Ala	Arg	Met	Ala	Tyr	Pro	Gly	Leu	Asn	Gly	Glu
	130					135					140				
Thr	Ser	His	Glu	Leu	Trp	Gly	Asp	Ala	Ala	Met	Ser	Trp	Val	Gln	Val
145				150					155					160	
Tyr	Thr	Pro	Asp	Asp	Arg	His	Ser	Leu	Ala	Ile	Glu	Pro	Met	Thr	Cys
			165					170					175		
Gly	Pro	Asp	Ala	Phe	Asn	Glu	Gly	Pro	Thr	His	Gly	Asp	Val	Ile	Arg
		180					185					190			
Leu	Glu	Pro	Gly	Asn	Asp	Val	Thr	Leu	His	Trp	Gly	Ile	Ala		
	195					200						205			

&lt;210&gt; 2315

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2315

nacgcgtccc tcacgatac cgagcccgga atgggaaaac ggggtgatcg cgttgaggcc  
 60  
 acccaaggcc gaccaattcg catcgataag gcggtcgctt atcacacttc tcgcggcgctg  
 120  
 ccggtacatg aactgtttga ccgagtgcgc cgcagcttag accgagtgcg tgaacagggg  
 180  
 cacaacgtct actacgacga acagcgtgca tggcttgacg attactgggc aacggctgat  
 240  
 gttgaggtcg agggtgcccc gaccgggtatt cagcaggctg tcaggtggaa cttttccag  
 300  
 attgctcagg catcagcccg tgcagatcaa cttggcattc cggcaaaggg tgtaaccggg  
 360  
 tcaggctatg aaggccacta cttttgggac actgaggttt atgtcatccc gatgttgacc  
 420  
 tacactcatc caagaatcgc tgagaatgcg ctgagattcc ggggtgaatac ctttccgcaa  
 480  
 gctcgacgcc gggctaagga attgtctgaa cgaggcgccc ttttcccgctg gcgaacaatc  
 540  
 accggt  
 546

&lt;210&gt; 2316

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2316

Xaa Ala Ser Leu Ile Asp Thr Glu Pro Gly Met Gly Lys Arg Val Tyr  
 1 5 10 15  
 Arg Val Glu Ala Thr Gln Gly Arg Pro Ile Arg Ile Asp Lys Ala Val  
 20 25 30  
 Ala Tyr His Thr Ser Arg Gly Val Pro Val His Glu Leu Phe Asp Arg  
 35 40 45  
 Val Arg Arg Ser Leu Asp Arg Val Arg Glu Gln Gly His Asn Val Tyr  
 50 55 60  
 Tyr Asp Glu Gln Arg Ala Trp Leu Asp Asp Tyr Trp Ala Thr Ala Asp  
 65 70 75 80  
 Val Glu Val Glu Gly Ala Pro Thr Gly Ile Gln Gln Ala Val Arg Trp  
 85 90 95  
 Asn Leu Phe Gln Ile Ala Gln Ala Ser Ala Arg Ala Asp Gln Leu Gly  
 100 105 110  
 Ile Pro Ala Lys Gly Val Thr Gly Ser Gly Tyr Glu Gly His Tyr Phe  
 115 120 125  
 Trp Asp Thr Glu Val Tyr Val Ile Pro Met Leu Thr Tyr Thr His Pro  
 130 135 140  
 Arg Ile Ala Glu Asn Ala Leu Arg Phe Arg Val Asn Thr Leu Pro Gln  
 145 150 155 160  
 Ala Arg Arg Arg Ala Lys Glu Leu Ser Glu Arg Gly Ala Leu Phe Pro  
 165 170 175  
 Trp Arg Thr Ile Thr Gly  
 180

<210> 2317  
 <211> 496  
 <212> DNA  
 <213> Homo sapiens

<400> 2317  
 gccggcgggc tcgggaacgg tcaactgacct gcagcaggca atggcggtcg cggtttaatc  
 60  
 agggttctgc acggagtttt ggatagtcgg tccagtcgcc actggcaagg cgcgaccagg  
 120  
 cagctgctga cgctgctgtg atgccgagga gatcggagac gattcgtggg tgcattctgcc  
 180  
 gggtcagttc gatcagcgcg gtcgttcgag cgcttcctga acgcagcccc tgctggcgca  
 240  
 gacgtcggct gagtgggcct ggtgtgagat gcaaccccg attcctgcc ggaaagagcc  
 300  
 atccctcggg tcggtgtctc gatgtgtcag cgagctcggc gatcgcatc ccgaggacct  
 360  
 cgggcagttc gattggctcg gtcctgatgg tgagcttccc cggctcgtgat gtcacgtcga  
 420  
 cctgctcacg ggtgagcgcg acgatgcgag tgaggtggag gccgtagagg agcacgagca  
 480  
 acccagcggc acgcgt  
 496

<210> 2318  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 2318  
 Met Pro Arg Arg Ser Glu Thr Ile Arg Gly Cys Ile Cys Arg Val Ser  
 1 5 10 15  
 Ser Ile Ser Ala Val Val Arg Ala Leu Pro Glu Arg Ser Pro Cys Trp  
 20 25 30  
 Arg Arg Arg Arg Leu Ser Gly Pro Gly Val Arg Cys Asn Pro Gly Phe  
 35 40 45  
 Leu Pro Gly Lys Ser His Pro Ser Gly Arg Cys Leu Asp Val Ser Ala  
 50 55 60  
 Ser Ser Ala Ile Ala Phe Pro Arg Thr Ser Gly Ser Ser Ile Gly Ser  
 65 70 75 80  
 Ala Pro Met Val Ser Phe Pro Gly Arg Asp Val Thr Ser Thr Cys Ser  
 85 90 95  
 Arg Val Ser Ala Thr Met Arg Val Arg Trp Arg Pro  
 100 105

<210> 2319  
 <211> 1748  
 <212> DNA  
 <213> Homo sapiens

<400> 2319  
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 60

gaatatactc aattccaaaa ttatgtgaaa gaattgaaga aaaaacggaa gcagaaaact  
120  
ttttagtgga aaccagctaa tgggtgcaatg ggtcatggga tttctttgat aagaaatggt  
180  
gacaaacttc catctcagga tcatttgatt gttcaagaat acattgaaaa gcctttccta  
240  
atggaagggtt acaagtttga cttacgaatt tatattctgg ttacatcgtg tgatccacta  
300  
aaaatatttc tctaccatga tgggcttggt cgaatgggta cagagaagta cattccacct  
360  
aatgagtcca atttgaccca gttatacatg catctgacaa actactccgt gaacaagcat  
420  
aatgagcatt ttgaacggga tgaaactgag aacaaaggca gcaaactgtc catcaaattg  
480  
tttacagaat tccttcaagc aaatcaacat gatgttgcta agttttggag tgatatttca  
540  
gaattggtgg taaagaccct gattgtagca gaacctcatg tcctgcatgc ctatcgaatg  
600  
tgtagacctg gtcaacctcc aggaagcgaa agtgtctgct ttgaagtcct gggatttgat  
660  
attttggtgg atagaaaact aaagccatgg cttctggaga ttaaccgagc cccaagcttt  
720  
ggaactgac agaaaataga ctatgatgta aaaaggggag tgctgctaaa tgcgttgaag  
780  
ctactaaaca taaggaccag tgacaaaaga agaaacttgg ccaaacaaaa agctgaggct  
840  
caaaggaggc tctatggtca aaattcaatt aaaaggctct taccaggctc ctcagactgg  
900  
gaacagcaga gacaccagtt ggagaggcgg aaagaagagt tgaaagagag actcgctcaa  
960  
gtacgaaagc agatctcacg agaagaacat gaaaatcgac atatggggaa ttatagacga  
1020  
atttatcctc ctgaagataa agcattactt gaaaagtatg aaaatttggt agctgttgcc  
1080  
tttcagacct tcctttcagg aagagcagct tcattccagc gagagttgaa taatcctttg  
1140  
aaaaggatga aggaagaaga tattttggat cttctggagc aatgtgaaat tgatgatgaa  
1200  
aagttgatgg gaaaaactac caagactcga ggaccaaagc ctctgtgttc tatgcctgag  
1260  
agtactgaga taatgaaaag accaaagtac tgcagcagtg acagcagtta tgatagtagc  
1320  
agcagctctt cagaatctga cgaaaatgaa aaagaagagt accaaaataa gaaaagagaa  
1380  
aagcaagtta catataatct taaacctcc aaccactaca aattaattca acaaccagc  
1440  
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1500  
gacaccgccc cattttctgc tcaacaaatg atatctgtgt cacggccaac ttctgcatct  
1560  
cggtcacatt ccttaaaccg gggccttccct cctacatgag gcactctgct cacagtaatg  
1620  
atgcctgtc taccaactct caagtgagt agtctttgcg gcaactgaaa acaaaagaac  
1680

aagaagatga tctaacaagt cagaccttat ttgttctcaa agacatgaag atccggtttc  
 1740  
 caggaaag  
 1748

<210> 2320

<211> 532

<212> PRT

<213> Homo sapiens

<400> 2320

Xaa	Ile	Lys	Ser	Arg	Ser	Leu	Asp	Tyr	Thr	Phe	Val	Pro	Arg	Thr	Trp
1				5					10					15	
Ile	Phe	Pro	Ala	Glu	Tyr	Thr	Gln	Phe	Gln	Asn	Tyr	Val	Lys	Glu	Leu
			20					25					30		
Lys	Lys	Lys	Arg	Lys	Gln	Lys	Thr	Phe	Ile	Val	Lys	Pro	Ala	Asn	Gly
		35					40					45			
Ala	Met	Gly	His	Gly	Ile	Ser	Leu	Ile	Arg	Asn	Gly	Asp	Lys	Leu	Pro
	50					55					60				
Ser	Gln	Asp	His	Leu	Ile	Val	Gln	Glu	Tyr	Ile	Glu	Lys	Pro	Phe	Leu
65				70					75					80	
Met	Glu	Gly	Tyr	Lys	Phe	Asp	Leu	Arg	Ile	Tyr	Ile	Leu	Val	Thr	Ser
			85					90						95	
Cys	Asp	Pro	Leu	Lys	Ile	Phe	Leu	Tyr	His	Asp	Gly	Leu	Val	Arg	Met
		100						105					110		
Gly	Thr	Glu	Lys	Tyr	Ile	Pro	Pro	Asn	Glu	Ser	Asn	Leu	Thr	Gln	Leu
	115						120					125			
Tyr	Met	His	Leu	Thr	Asn	Tyr	Ser	Val	Asn	Lys	His	Asn	Glu	His	Phe
	130				135						140				
Glu	Arg	Asp	Glu	Thr	Glu	Asn	Lys	Gly	Ser	Lys	Arg	Ser	Ile	Lys	Trp
145				150					155					160	
Phe	Thr	Glu	Phe	Leu	Gln	Ala	Asn	Gln	His	Asp	Val	Ala	Lys	Phe	Trp
			165					170						175	
Ser	Asp	Ile	Ser	Glu	Leu	Val	Val	Lys	Thr	Leu	Ile	Val	Ala	Glu	Pro
		180						185					190		
His	Val	Leu	His	Ala	Tyr	Arg	Met	Cys	Arg	Pro	Gly	Gln	Pro	Pro	Gly
	195					200					205				
Ser	Glu	Ser	Val	Cys	Phe	Glu	Val	Leu	Gly	Phe	Asp	Ile	Leu	Leu	Asp
	210					215					220				
Arg	Lys	Leu	Lys	Pro	Trp	Leu	Leu	Glu	Ile	Asn	Arg	Ala	Pro	Ser	Phe
225				230					235					240	
Gly	Thr	Asp	Gln	Lys	Ile	Asp	Tyr	Asp	Val	Lys	Arg	Gly	Val	Leu	Leu
			245					250						255	
Asn	Ala	Leu	Lys	Leu	Leu	Asn	Ile	Arg	Thr	Ser	Asp	Lys	Arg	Arg	Asn
		260					265						270		
Leu	Ala	Lys	Gln	Lys	Ala	Glu	Ala	Gln	Arg	Arg	Leu	Tyr	Gly	Gln	Asn
	275					280						285			
Ser	Ile	Lys	Arg	Leu	Leu	Pro	Gly	Ser	Ser	Asp	Trp	Glu	Gln	Gln	Arg
	290					295					300				
His	Gln	Leu	Glu	Arg	Arg	Lys	Glu	Glu	Leu	Lys	Glu	Arg	Leu	Ala	Gln
305				310					315					320	
Val	Arg	Lys	Gln	Ile	Ser	Arg	Glu	Glu	His	Glu	Asn	Arg	His	Met	Gly
			325					330						335	
Asn	Tyr	Arg	Arg	Ile	Tyr	Pro	Pro	Glu	Asp	Lys	Ala	Leu	Leu	Glu	Lys



340 345 350  
 Tyr Glu Asn Leu Leu Ala Val Ala Phe Gln Thr Phe Leu Ser Gly Arg  
 355 360 365  
 Ala Ala Ser Phe Gln Arg Glu Leu Asn Asn Pro Leu Lys Arg Met Lys  
 370 375 380  
 Glu Glu Asp Ile Leu Asp Leu Leu Glu Gln Cys Glu Ile Asp Asp Glu  
 385 390 395 400  
 Lys Leu Met Gly Lys Thr Thr Lys Thr Arg Gly Pro Lys Pro Leu Cys  
 405 410 415  
 Ser Met Pro Glu Ser Thr Glu Ile Met Lys Arg Pro Lys Tyr Cys Ser  
 420 425 430  
 Ser Asp Ser Ser Tyr Asp Ser Ser Ser Ser Ser Glu Ser Asp Glu  
 435 440 445  
 Asn Glu Lys Glu Glu Tyr Gln Asn Lys Lys Arg Glu Lys Gln Val Thr  
 450 455 460  
 Tyr Asn Leu Lys Pro Ser Asn His Tyr Lys Leu Ile Gln Gln Pro Ser  
 465 470 475 480  
 Ser Ile Arg Arg Ser Val Ser Cys Pro Arg Ser Ile Ser Ala Gln Ser  
 485 490 495  
 Pro Ser Ser Gly Asp Thr Arg Pro Phe Ser Ala Gln Gln Met Ile Ser  
 500 505 510  
 Val Ser Arg Pro Thr Ser Ala Ser Arg Ser His Ser Leu Asn Pro Gly  
 515 520 525  
 Leu Pro Pro Thr  
 530

<210> 2321  
 <211> 433  
 <212> DNA  
 <213> Homo sapiens

<400> 2321  
 caattgtgtg gacgtgtcta tgttgttttc taattctata ctatcttgaa aatgggttcag  
 60  
 cgttctagaa atacagccac ataatttttt ttgttttgaa aaactgctca gcaaatgcat  
 120  
 acaggtcata atggcaggta acagaccatt tattgaagtg ctgaaacaaa tagaaaacaa  
 180  
 agtccaggac accatcacag agcagtactt cccttgtag atactctcag ctaagtaaga  
 240  
 attgagtgag acaacaataa aacaaatacc cataggcttt tcaaacagta acaaccgct  
 300  
 caggggttagc agcatttcta gaccttgatg gtaaaatgat gttctcaacc tttgctttca  
 360  
 gacactggat cactgcttaa gtagccttta tcttttcccc ctaatttttg ttgaagatgc  
 420  
 cagaggtgga gtg  
 433

<210> 2322  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 2322

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Met Leu Leu Thr Leu Ser Gly Leu Leu Leu Phe Glu Lys Pro Met Gly
 1             5             10             15
Ile Cys Phe Ile Val Val Ser Leu Asn Ser Tyr Leu Ala Glu Ser Ile
             20             25             30
Ser Gln Gly Lys Tyr Cys Ser Val Met Val Ser Trp Thr Leu Phe Ser
             35             40             45
Ile Cys Phe Ser Thr Ser Ile Asn Gly Leu Leu Pro Ala Ile Met Thr
             50             55             60
Cys Met His Leu Leu Ser Ser Phe Ser Lys Gln Lys Lys Leu Cys Gly
65             70             75             80
Cys Ile Ser Arg Thr Leu Asn His Phe Gln Asp Ser Ile Glu Leu Glu
             85             90             95
Thr His Ile Asp Thr Ser Thr Gln Leu
             100             105

```

&lt;210&gt; 2323

&lt;211&gt; 532

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2323

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acgcgtcaaa actggcaaaag ctggcggtt agggggaggg gcaagtggac ttggaggccc
60
tcctccactg tgcacccctt tggaaaaaaa gcggaggggg catcaagtaa aagtttcttg
120
ccaggcagag ccagctcggc ggccccccgc acatagctgg ggtagcagg ggttgettct
180
ctgccgggca cagcgtcttc caggagccag ccggggagag ctgagccaag gccgaaggag
240
ccgcctgcgg gcttagccgc cccctccgc ccgttgcccc cagagcggac gctgggacgc
300
ccggggtctg gcagctctgc gcccggttag gagcggggcg gcgagcatta gcctgcgtcc
360
tggaagaagg gcgcagcgcc gcagttgagg ccgaagcagc ccctcgcggg ctaggatac
420
ctgtcagtga gcgcccggat tgcacggccc ccgggtagt cctgccggcg aggggcggga
480
gctcgggtga cttggccatc cccatccccg gcccgggccc ggaggcgggc cg
532

```

&lt;210&gt; 2324

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2324

```

Thr Arg Gln Asn Trp Gln Ser Trp Arg Leu Arg Gly Arg Gly Lys Trp
 1             5             10             15
Thr Trp Arg Pro Ser Ser Thr Val His Pro Leu Gly Lys Lys Ala Glu
             20             25             30
Gly Ala Ser Ser Lys Ser Phe Leu Pro Gly Arg Ala Ser Ser Ala Ala
             35             40             45
Pro Arg Thr

```

50

&lt;210&gt; 2325

&lt;211&gt; 459

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2325

nnacgcgtgc aggaccgcat gagcgccatc tgggagagag gagtgggttg aggaaagatg  
 60  
 gatgagaacc gttttgtggc cgttaccagt tccaacgcag ctaagcttct gaacctgtat  
 120  
 ccccgcaagg gccgcattat tcccggagcc gatgctgatg tgggtggtgtg ggaccagaa  
 180  
 gccacaaaga ccatctcagc cagcacgcag gtccagggag gagacttcaa cctgtatgag  
 240  
 aacatgcgt gccacggcgt gccactggc accatcagcc gggggcgcgt cgtgtatgag  
 300  
 aacggcgtct tcatgtgcgc cgagggcacc ggcaagttct gtccctgag gtccttccca  
 360  
 gacactgtct acaagaagct ggtccagaga gagaagactt taaaggtag aggagtggcc  
 420  
 cgcactccct acctggggga tgctgctgtt gtcgtgcac  
 459

&lt;210&gt; 2326

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2326

Xaa Arg Val Gln Asp Arg Met Ser Ala Ile Trp Glu Arg Gly Val Val  
 1 5 10 15  
 Gly Gly Lys Met Asp Glu Asn Arg Phe Val Ala Val Thr Ser Ser Asn  
 20 25 30  
 Ala Ala Lys Leu Leu Asn Leu Tyr Pro Arg Lys Gly Arg Ile Ile Pro  
 35 40 45  
 Gly Ala Asp Ala Asp Val Val Val Trp Asp Pro Glu Ala Thr Lys Thr  
 50 55 60  
 Ile Ser Ala Ser Thr Gln Val Gln Gly Gly Asp Phe Asn Leu Tyr Glu  
 65 70 75 80  
 Asn Met Arg Cys His Gly Val Pro Leu Val Thr Ile Ser Arg Gly Arg  
 85 90 95  
 Val Val Tyr Glu Asn Gly Val Phe Met Cys Ala Glu Gly Thr Gly Lys  
 100 105 110  
 Phe Cys Pro Leu Arg Ser Phe Pro Asp Thr Val Tyr Lys Lys Leu Val  
 115 120 125  
 Gln Arg Glu Lys Thr Leu Lys Val Arg Gly Val Ala Arg Thr Pro Tyr  
 130 135 140  
 Leu Gly Asp Val Ala Val Val Val His  
 145 150

&lt;210&gt; 2327

&lt;211&gt; 599

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2327

gaattccaga agatcaagta ttctacgat gccctggaga agaagcagtt tctccccgtg  
 60  
 gcctttctctg tgggaaacgc cttctcatac tatcagagca acagaggctt ccaggaagac  
 120  
 tcagagatcc gagcagctga gaagaaattt gggagcaaca aggccgagat ggtggtgcct  
 180  
 gactttctcgg agctttttcaa ggagagagcc acagccccct tctttgtatt tcaggtgttc  
 240  
 tgtgtggggc tctggtgcct ggatgagtac tgggtactaca gcgtctttac gctatccatg  
 300  
 ctggtggcgt tcgaggcctc gctggtgcag cagcagatgc ggaacatgtc ggagatccgg  
 360  
 aagatgggca acaagcccca catgatccag gtctaccgaa gccgcaagtg gaggccatt  
 420  
 gccagtgatg agatcgtacc aggggacatc gtctccatcg gtgaggccgg gttccgctca  
 480  
 gtcccagtgg gagccccagc ctcagggcct ctggccaacc ctctgcctc tgccctgcag  
 540  
 gccgctcccc acaggagaac ctggtgccat gtgacgtgct tctgctgcga ggccgctgc  
 599

&lt;210&gt; 2328

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2328

Glu Phe Gln Lys Ile Lys Tyr Ser Tyr Asp Ala Leu Glu Lys Lys Gln  
 1 5 10 15  
 Phe Leu Pro Val Ala Phe Pro Val Gly Asn Ala Phe Ser Tyr Tyr Gln  
 20 25 30  
 Ser Asn Arg Gly Phe Gln Glu Asp Ser Glu Ile Arg Ala Ala Glu Lys  
 35 40 45  
 Lys Phe Gly Ser Asn Lys Ala Glu Met Val Val Pro Asp Phe Ser Glu  
 50 55 60  
 Leu Phe Lys Glu Arg Ala Thr Ala Pro Phe Phe Val Phe Gln Val Phe  
 65 70 75 80  
 Cys Val Gly Leu Trp Cys Leu Asp Glu Tyr Trp Tyr Tyr Ser Val Phe  
 85 90 95  
 Thr Leu Ser Met Leu Val Ala Phe Glu Ala Ser Leu Val Gln Gln Gln  
 100 105 110  
 Met Arg Asn Met Ser Glu Ile Arg Lys Met Gly Asn Lys Pro His Met  
 115 120 125  
 Ile Gln Val Tyr Arg Ser Arg Lys Trp Arg Pro Ile Ala Ser Asp Glu  
 130 135 140  
 Ile Val Pro Gly Asp Ile Val Ser Ile Gly Glu Ala Gly Phe Arg Ser  
 145 150 155 160  
 Val Pro Val Gly Ala Pro Ala Ser Gly Pro Leu Ala Asn Pro Pro Ala  
 165 170 175  
 Ser Ala Leu Gln Ala Ala Pro His Arg Arg Thr Trp Cys His Val Thr

180  
Cys Phe Cys Cys Glu Ala Ala  
195

185

190

<210> 2329  
<211> 392  
<212> DNA  
<213> Homo sapiens

<400> 2329  
acgcgttcca tgaatgctgg tgcggctgcc gcgattgcta tgtacgcctg gacgacgcag  
60  
tggtgtccaa agccacgcac tagctgatcg gggagaaccg tcacctcta ggctcgtgtc  
120  
atgagcacgc aaccactga ggaaccactc cgactagttg tggcattcaa tccagtgcct  
180  
agtgcctccc gggttgctca tcatcatgcg acgagatttc gcctggcggt gcaggccttc  
240  
attgtcgtcg tcattggtgg tttgttgctg gcgttgacgg ccgacgcctt ccagttatcg  
300  
acggtgatgt ggatgctcgg ggcattgggtg gtgctattcc tcgtgctttt cgtcatccag  
360  
aatctgcggc tgcacgccgc tcgcaaggat cc  
392

<210> 2330  
<211> 90  
<212> PRT  
<213> Homo sapiens

<400> 2330  
Met Ser Thr Gln Pro Thr Glu Glu Pro Leu Arg Leu Val Val Ala Phe  
1 5 10 15  
Asn Pro Val Pro Ser Ala Ser Arg Val Ala His His His Ala Thr Arg  
20 25 30  
Phe Arg Leu Ala Val Gln Ala Phe Ile Val Val Val Ile Gly Gly Leu  
35 40 45  
Leu Trp Ala Leu Thr Ala Asp Ala Phe Gln Leu Ser Thr Val Met Trp  
50 55 60  
Met Leu Gly Ala Trp Val Val Leu Phe Leu Val Leu Phe Val Ile Gln  
65 70 75 80  
Asn Leu Arg Leu His Ala Ala Arg Lys Asp  
85 90

<210> 2331  
<211> 2813  
<212> DNA  
<213> Homo sapiens

<400> 2331  
nnggagcaag agagttatta aaagtgggtg gaagacttcc tgggtgcagga ggctcactcc  
60  
gatttaaggt gcccgagtcc acgctgatgg actgccgtag acaactgaaa gacagtaagc  
120

aaattttatc tattacaaag aacttttaaag ttgagaatat tggacctctt cctataactg  
180  
tttctgtctc gaaaattaat ggggtataact gccaaaggta tggattcgag gtgctggatt  
240  
gggattcagt ttcccttga cccaaacaca tcccgcgata tcagcattgt gttcactcca  
300  
gactttacct cctcctgggt aattcgggac ctaagtcttg taaccgcagc ggacctagaa  
360  
tttctgttca ctctcaatgt gactctccct catcacctgt tgccttcttg tgcagacgtg  
420  
gttccaggac ccagctggga ggagtcattt tggaggctca cggctcttct tgtcagtttg  
480  
tccctgttgg gtgtgatttt aatagccttc caacaagcac agtacattct catggaattc  
540  
atgaaaacaa gacagaggca aaatgctagc tctcttcac agcaaaacaa tggctctatg  
600  
gatgtaatca gccccattc ttacaaaagc aattgcaaga actttctcga tacatatggc  
660  
ccctctgata aaggcagggg gaagaactgc cttccagtga acactcccca aagcaggatc  
720  
cagaatgctg caaagaggag ccagccacc tatggtcatt ctcagaagaa gcacaaatgc  
780  
tcagtgtatt acagtaaaca caaaaccagc acagctgcgg ccagcagcac cagcagcact  
840  
actgaggaaa aacagacttc acccctgggc agctcactgc ctgctgctaa agaggacatt  
900  
tgcactgatg ccatgcgtga gaactggatc agcctcagat atgcaagtgg cataaatgtc  
960  
aacctgcaga agaatttaac ccttcccaa aacttactga ataaagaaga aaacacactg  
1020  
aaaaacacaa ttgttttcag taatccttct tcagaatgta gtatgaagga gggaatacag  
1080  
acatgtatgt ttcctaagga aactgacatt aaaacttcag agaacacagc tgagtccaag  
1140  
gaacgggagc tctgtccact gaagacctcc aagaaactac ctgaaaacca tttaccaaga  
1200  
aactcacctc agtaccacca gccagacttg ccagaaattt ccaggaaaaa taatgggaat  
1260  
aaccagcaag tacctgtcaa gaatgaagta gatcattgtg aaaatttgaa gaagggtggc  
1320  
acaaagcctt cttcagaaaa gaagattcac aaaacatcta gagaagacat gttttctgag  
1380  
aaacaggaca tacctttcgt agagcaagaa gatccttata ggaagaaaaa gcttcaggag  
1440  
aaaagagaag gaaatttaca aaatttaaag tggagtaaaa gtcgaacatg tagaaagaac  
1500  
aagaaaaggg gtgttgctcc agtctcaagg cctcctgaac agagtgatct aaagcttgtg  
1560  
tgcagtgact ttgagaggtc tgagctgagc agtgacatca atgtaagaag ctggtgtata  
1620  
caggaaagca ctagggaggt ttgtaaagca gatgccgaaa ttgcaagcag tttacctgct  
1680  
gcccagagag aggcagggtta ctaccagaag cctgagaaga aatgtgtgga caagttctgc  
1740

tccgattcca gctctgactg tgggagctcc tctggcagcg tgcgtgccag ccggggcagc  
 1800  
 tgggggagct ggagcagcac cagcagctcc gacggggata agaagcccat ggtggagccc  
 1860  
 cagcacttcc tgccggccgg agacagtgtt tcacaaaatg attttccttc tgaagctccc  
 1920  
 atctccttga atctttctca taacatctgc aatcccatga ccgtgaatag tctcccacaa  
 1980  
 tacgcagagc cttcctgtcc cagccttcct gccgggccc caggtgttga agaagataaa  
 2040  
 ggtctttact cacctggaga cctgtggccc actccgccag tgtgtgtgac aagcagctta  
 2100  
 aactgcaccc tggagaacgg cgtgccttgt gtgattcagg agtcggcccc gggttcataat  
 2160  
 agtttcattg attggagtgc aacatgcgaa ggccagtttt ccagcgcata ctgtccattg  
 2220  
 gaattgaacg attacaatgc ctttcagaa gaaaacatga actatgcaa tggcttcccc  
 2280  
 tgtcctgcag atgttcagac agactttatt gatcacaact ctcagtctac ctggaaçacc  
 2340  
 ccaccaaca tgctgtgtgc ctggggacat gccagtttca tcagctctcc gccctacctc  
 2400  
 acaagcacc gaagcttgtc tccaatgtct ggactttttg gttccatctg ggccccgcaa  
 2460  
 agcgatgtgt atgaaaattg ctgccccatc aacccaccca cggaacattc gaccacatg  
 2520  
 gaaaaccaag cggtcgtgtg caaggaatac taccgggggt tcaaccggtt tcgcgcctat  
 2580  
 atgaacctgg acatatggac taccacagcg aataggaatg caaatttccc actgtctaga  
 2640  
 gactcgagtt actgtgggaa tgtgtgaaaa taattggatt tttaaacaat gtgaataaag  
 2700  
 aggcttgtgt tttgattact agtgtaaact ggttattgag atagattatg acattggtgg  
 2760  
 atattttggc actttttatat gaaaataaat tttttaatga aaaaaaaaaa aaa  
 2813

&lt;210&gt; 2332

&lt;211&gt; 789

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2332

Pro	Asp	Phe	Thr	Ser	Ser	Trp	Val	Ile	Arg	Asp	Leu	Ser	Leu	Val	Thr
1				5					10					15	
Ala	Ala	Asp	Leu	Glu	Phe	Arg	Phe	Thr	Leu	Asn	Val	Thr	Leu	Pro	His
			20					25					30		
His	Leu	Leu	Pro	Leu	Cys	Ala	Asp	Val	Val	Pro	Gly	Pro	Ser	Trp	Glu
		35					40					45			
Glu	Ser	Phe	Trp	Arg	Leu	Thr	Val	Phe	Phe	Val	Ser	Leu	Ser	Leu	Leu
	50					55				60					
Gly	Val	Ile	Leu	Ile	Ala	Phe	Gln	Gln	Ala	Gln	Tyr	Ile	Leu	Met	Glu
65					70					75				80	
Phe	Met	Lys	Thr	Arg	Gln	Arg	Gln	Asn	Ala	Ser	Ser	Ser	Ser	Gln	Gln

1705



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      515      520      525
Asp Ser Val Ser Gln Asn Asp Phe Pro Ser Glu Ala Pro Ile Ser Leu
 530      535      540
Asn Leu Ser His Asn Ile Cys Asn Pro Met Thr Val Asn Ser Leu Pro
 545      550      555      560
Gln Tyr Ala Glu Pro Ser Cys Pro Ser Leu Pro Ala Gly Pro Thr Gly
      565      570      575
Val Glu Glu Asp Lys Gly Leu Tyr Ser Pro Gly Asp Leu Trp Pro Thr
      580      585      590
Pro Pro Val Cys Val Thr Ser Ser Leu Asn Cys Thr Leu Glu Asn Gly
      595      600      605
Val Pro Cys Val Ile Gln Glu Ser Ala Pro Val His Asn Ser Phe Ile
 610      615      620
Asp Trp Ser Ala Thr Cys Glu Gly Gln Phe Ser Ser Ala Tyr Cys Pro
 625      630      635      640
Leu Glu Leu Asn Asp Tyr Asn Ala Phe Pro Glu Glu Asn Met Asn Tyr
      645      650      655
Ala Asn Gly Phe Pro Cys Pro Ala Asp Val Gln Thr Asp Phe Ile Asp
      660      665      670
His Asn Ser Gln Ser Thr Trp Asn Thr Pro Pro Asn Met Pro Ala Ala
      675      680      685
Trp Gly His Ala Ser Phe Ile Ser Ser Pro Pro Tyr Leu Thr Ser Thr
 690      695      700
Arg Ser Leu Ser Pro Met Ser Gly Leu Phe Gly Ser Ile Trp Ala Pro
 705      710      715      720
Gln Ser Asp Val Tyr Glu Asn Cys Cys Pro Ile Asn Pro Thr Thr Glu
      725      730      735
His Ser Thr His Met Glu Asn Gln Ala Val Val Cys Lys Glu Tyr Tyr
      740      745      750
Pro Gly Phe Asn Pro Phe Arg Ala Tyr Met Asn Leu Asp Ile Trp Thr
      755      760      765
Thr Thr Ala Asn Arg Asn Ala Asn Phe Pro Leu Ser Arg Asp Ser Ser
 770      775      780
Tyr Cys Gly Asn Val
 785

```

&lt;210&gt; 2333

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2333

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cgtatgattg gtgtgggaca aatactattc aacaagagta cctaaatcat tgtttaaggc
60
gaagtaataa atatgaatgg ggtgtatcat ataatgaaca acgaatatcc atatagtga
120
gacgaagttc ttcacaaagc aaaatcatat ttgtcagcag atgaatatga gtatgtttta
180
aaaagctatc atattgctta tgaagcacat aaaggctcagt tccgaaaaaa cggattacca
240
tacattatgc atcctataca agttgcaggt attttaacag aaatgcgatt agacggaccg
300
acgattgtcg caggtttttt gcatgatgta attgaagata caccgtatac atttgaagat
360

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gtaaaagaaa tgttcaatga agaagttgct cgaattgttg atgggtgtgac gaagcttaaa  
 420  
 aaaataaaaat accgctcaaa agaagaacaa caagctgaaa atcatcgcaa gttatttatt  
 480  
 gcgattgccca aagatgtacg c  
 501

<210> 2334  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 2334  
 Met Asn Gly Val Tyr His Ile Met Asn Asn Glu Tyr Pro Tyr Ser Ala  
 1 5 10 15  
 Asp Glu Val Leu His Lys Ala Lys Ser Tyr Leu Ser Ala Asp Glu Tyr  
 20 25 30  
 Glu Tyr Val Leu Lys Ser Tyr His Ile Ala Tyr Glu Ala His Lys Gly  
 35 40 45  
 Gln Phe Arg Lys Asn Gly Leu Pro Tyr Ile Met His Pro Ile Gln Val  
 50 55 60  
 Ala Gly Ile Leu Thr Glu Met Arg Leu Asp Gly Pro Thr Ile Val Ala  
 65 70 75 80  
 Gly Phe Leu His Asp Val Ile Glu Asp Thr Pro Tyr Thr Phe Glu Asp  
 85 90 95  
 Val Lys Glu Met Phe Asn Glu Glu Val Ala Arg Ile Val Asp Gly Val  
 100 105 110  
 Thr Lys Leu Lys Lys Ile Lys Tyr Arg Ser Lys Glu Glu Gln Gln Ala  
 115 120 125  
 Glu Asn His Arg Lys Leu Phe Ile Ala Ile Ala Lys Asp Val Arg  
 130 135 140

<210> 2335  
 <211> 387  
 <212> DNA  
 <213> Homo sapiens

<400> 2335  
 ggatcctgag cgtgggggact tctttgcact ccacagaacc ctcaattgta cctctacttt  
 60  
 tctctgcaga tggaccacac agcattcccc tgtggctgct gcagggaggg ctgtgagaac  
 120  
 cccatggggcc gtgtggaatt taatcaggca agagtccaga cccatttcat ccacacactc  
 180  
 acccgctgac agttggaaca ggaggctgag agcttttaggg agctggaggg ccctgcccag  
 240  
 ggcagcccac ccagccctgg tgaggaggcc ctggtcccta ctttcccact ggccaagccc  
 300  
 cccatgaaca atgagctggg agacaacagc tgcagcagcg acatgactga ttcttccaca  
 360  
 gcatttcat cagcatcggg cactagt  
 387

<210> 2336

<211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 2336  
 Met Asp His Thr Ala Phe Pro Cys Gly Cys Cys Arg Glu Gly Cys Glu  
 1 5 10 15  
 Asn Pro Met Gly Arg Val Glu Phe Asn Gln Ala Arg Val Gln Thr His  
 20 25 30  
 Phe Ile His Thr Leu Thr Arg Leu Gln Leu Glu Gln Glu Ala Glu Ser  
 35 40 45  
 Phe Arg Glu Leu Glu Ala Pro Ala Gln Gly Ser Pro Pro Ser Pro Gly  
 50 55 60  
 Glu Glu Ala Leu Val Pro Thr Phe Pro Leu Ala Lys Pro Pro Met Asn  
 65 70 75 80  
 Asn Glu Leu Gly Asp Asn Ser Cys Ser Ser Asp Met Thr Asp Ser Ser  
 85 90 95  
 Thr Ala Ser Ser Ser Ala Ser Gly Thr Ser  
 100 105

<210> 2337  
 <211> 359  
 <212> DNA  
 <213> Homo sapiens

<400> 2337  
 ngagaagagg aggagtcac gccaggggcc gccatctcca gccctcgcca agccgctggg  
 60  
 accatgtgca gctcaagaat gccctccggc ccatcggcct cggggcaggg gaagggcagc  
 120  
 ttctctgcac cagcttcctt gctgggctcc agggcccaca ggctgaggcc gggggcccag  
 180  
 gggccaatgc caggcaccct gctattgagg aacctatcca ggaggaagga ctcgggcaga  
 240  
 cctgcgggat cctcgtcttc ccacgggtcc tcatggcaga agcagaagga gctggagtcg  
 300  
 ctgaggtccg tgggcaggcg ggctggggcc aacgtggggt caccgacctc ctcaaagct  
 359

<210> 2338  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 2338  
 Met Cys Ser Ser Arg Met Ala Ser Gly Pro Ser Ala Ser Gly Gln Gly  
 1 5 10 15  
 Lys Gly Ser Phe Ser Ala Pro Ala Ser Leu Leu Gly Ser Arg Ala His  
 20 25 30  
 Arg Leu Arg Pro Gly Ala Gln Gly Ser Met Pro Gly Thr Leu Leu Leu  
 35 40 45  
 Arg Asn Leu Ser Arg Arg Lys Asp Ser Gly Arg Pro Ala Gly Ser Ser  
 50 55 60  
 Ser Ser His Gly Ser Ser Trp Gln Lys Gln Lys Glu Leu Glu Ser Leu

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<210> 2339
<211> 439
<212> DNA
<213> Homo sapiens
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<210> 2340
<211> 92
<212> PRT
<213> Homo sapiens
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<210> 2341
<211> 411
<212> DNA
<213> Homo sapiens
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1709

gccaaacctc ccctccatcc tgcccaagat ggatcttgct gaggctccct ggcatatgcc  
 60  
 tctgcaggag gagccagagg aggtcacgga ggaggaggag gaaagggag aagaggagag  
 120  
 ggagaaggaa gcagaggagg aggaggaaga ggaagagctg ctctgtgag cgggtcccca  
 180  
 ggagccaccg cacaggccca tgccccttca cctagcacca gcagcagcac cagcagccag  
 240  
 agtcctgggg ccacccggca caggcaggag gattctggag accaggccac atcaggcnat  
 300  
 ggaagtggag agcagtgtga aaccacacct gtcagtgtcc tcagtcaccc caagtacagt  
 360  
 ggccccgggg gttcagaact atagccagga gtctgggggc actgagtggc n  
 411

&lt;210&gt; 2342

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2342

Ala Ser Leu Ala Tyr Ala Ser Ala Gly Gly Ala Arg Gly Gly His Gly  
 1 5 10 15  
 Gly Gly Gly Gly Lys Gly Arg Arg Gly Glu Gly Glu Gly Ser Arg Gly  
 20 25 30  
 Gly Gly Gly Arg Gly Arg Ala Ala Pro Val Ser Gly Ser Pro Gly Ala  
 35 40 45  
 Thr Ala Gln Ala His Ala Pro Ser Pro Ser Thr Ser Ser Thr Ser  
 50 55 60  
 Ser Gln Ser Pro Gly Ala Thr Arg His Arg Gln Glu Asp Ser Gly Asp  
 65 70 75 80  
 Gln Ala Thr Ser Gly Xaa Gly Ser Gly Glu Gln Cys Glu Thr His Leu  
 85 90 95  
 Val Ser Ala Leu Ser His Pro Lys Tyr Ser Gly Pro Gly Gly Ser Glu  
 100 105 110  
 Leu

&lt;210&gt; 2343

&lt;211&gt; 522

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2343

ggcccgagc agatgctgat gccttcacag tttcccaacc agggccagca gggattctct  
 60  
 ggaggccagg gaccctacca agccatgtcc caggacatgg gcaataccca agacatgttc  
 120  
 agccctgatc agagctcaat gcccatgagc aacgtgggca ccacccggct cagccacatg  
 180  
 cctctgcccc ctgcgtccaa tcctcctggg accgtgcatt cagccccaaa ccgggggcta  
 240  
 ggcaggcggc cttcggacct caccatcagt attaatacaga tggggtcacc gggcatgggg  
 300

cacttgaagt cgcccaccct tagccagggtg cactcaccctc tggtcacctc gccctctgcc  
 360  
 aacctcaagt caccacagac tcctcacag atggtgcctt tgccttctgc caaccgcga  
 420  
 ggacctctca agtcgccccca ggtcctcggc tctccctca gtgtccgttc accactggc  
 480  
 tcgcccagca ggctcaagtc tccttccatg gcggtgcctt ct  
 522

<210> 2344

<211> 174

<212> PRT

<213> Homo sapiens

<400> 2344

Gly	Pro	Gln	Lys	Met	Leu	Met	Pro	Ser	Gln	Phe	Pro	Asn	Gln	Gly	Gln
1				5					10					15	
Gln	Gly	Phe	Ser	Gly	Gly	Gln	Gly	Pro	Tyr	Gln	Ala	Met	Ser	Gln	Asp
			20					25					30		
Met	Gly	Asn	Thr	Gln	Asp	Met	Phe	Ser	Pro	Asp	Gln	Ser	Ser	Met	Pro
		35					40					45			
Met	Ser	Asn	Val	Gly	Thr	Thr	Arg	Leu	Ser	His	Met	Pro	Leu	Pro	Pro
		50				55					60				
Ala	Ser	Asn	Pro	Pro	Gly	Thr	Val	His	Ser	Ala	Pro	Asn	Arg	Gly	Leu
65					70					75				80	
Gly	Arg	Arg	Pro	Ser	Asp	Leu	Thr	Ile	Ser	Ile	Asn	Gln	Met	Gly	Ser
				85					90				95		
Pro	Gly	Met	Gly	His	Leu	Lys	Ser	Pro	Thr	Leu	Ser	Gln	Val	His	Ser
			100					105					110		
Pro	Leu	Val	Thr	Ser	Pro	Ser	Ala	Asn	Leu	Lys	Ser	Pro	Gln	Thr	Pro
		115						120				125			
Ser	Gln	Met	Val	Pro	Leu	Pro	Ser	Ala	Asn	Pro	Pro	Gly	Pro	Leu	Lys
		130				135					140				
Ser	Pro	Gln	Val	Leu	Gly	Ser	Ser	Leu	Ser	Val	Arg	Ser	Pro	Thr	Gly
145				150						155				160	
Ser	Pro	Ser	Arg	Leu	Lys	Ser	Pro	Ser	Met	Ala	Val	Pro	Ser		
				165					170						

<210> 2345

<211> 561

<212> DNA

<213> Homo sapiens

<400> 2345

nagatctccg tcttgatctt gagcaccgag gcactggggg gggaggacag cagccgcggg  
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 ggctccacc agcccgcgtc caggccgcct gggctcgacg cgctggacag gcgcccggcg  
 120  
 ctggcgctgc cgcccttttg ccgtttccgc cttttcttgc gcttctggtg cttgctggag  
 180  
 gctgcgcgc ccgcctcgcc tgcgctgtcc gagtccttgg cgctgtcgga cgtgagtgc  
 240  
 tcgcagttct gcagccgcag gtccgactcg ctctccacca tagctattaa tgccaagaat  
 300

gcaaatgaaa agaatatcat ctgggtgaat taccttctta gcaatcctga gtacaaggac  
 360  
 acaccatgg acatcgacaca gctcccccat ctgccggaga aaacttccga atcctcggag  
 420  
 acatccgact ctgagtcaga ctctaaagac acctcaggta ttacagagga caacgagaac  
 480  
 tccaagnntc cgacgagaag gggaaccagt ccgagaacag cgaagacccg gagcccgacc  
 540  
 ggaagaagtc gggcaacgcg t  
 561

<210> 2346

<211> 187

<212> PRT

<213> Homo sapiens

<400> 2346

Xaa Ile Ser Val Leu Ile Leu Ser Thr Glu Ala Leu Gly Gly Glu Asp  
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 Asp Ala Leu Asp Arg Arg Arg Arg Leu Ala Leu Pro Pro Phe Cys Arg  
 35 40 45  
 Phe Arg Leu Phe Leu Arg Phe Trp Cys Leu Leu Glu Ala Cys Ala Pro  
 50 55 60  
 Ala Ser Pro Ala Leu Ser Glu Ser Leu Ala Leu Ser Asp Val Ser Asp  
 65 70 75 80  
 Ser Gln Phe Cys Ser Arg Arg Ser Asp Ser Leu Ser Thr Ile Ala Ile  
 85 90 95  
 Asn Ala Lys Asn Ala Asn Glu Lys Asn Ile Ile Trp Val Asn Tyr Leu  
 100 105 110  
 Leu Ser Asn Pro Glu Tyr Lys Asp Thr Pro Met Asp Ile Ala Gln Leu  
 115 120 125  
 Pro His Leu Pro Glu Lys Thr Ser Glu Ser Ser Glu Thr Ser Asp Ser  
 130 135 140  
 Glu Ser Asp Ser Lys Asp Thr Ser Gly Ile Thr Glu Asp Asn Glu Asn  
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<210> 2347

<211> 375

<212> DNA

<213> Homo sapiens

<400> 2347

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 gtcgggtccga acatcgacgc ctggtccgat ttccagccgc tgggcgtggt ggcggggatc  
 180

acgccattca acttcccggc gatggtgccc ctgtggatgt atccggtggc gatcgtttgc  
 240  
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<210> 2348

<211> 125

<212> PRT

<213> Homo sapiens

<400> 2348

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Lys	Arg	Gly	Ile	Glu	Asn	Val	Glu	Tyr	Ala	Cys	Ala	Ala	Pro	Glu	Val
		20					25						30		
Leu	Lys	Gly	Glu	Tyr	Ser	Arg	Asn	Val	Gly	Pro	Asn	Ile	Asp	Ala	Trp
	35					40					45				
Ser	Asp	Phe	Gln	Pro	Leu	Gly	Val	Val	Ala	Gly	Ile	Thr	Pro	Phe	Asn
	50				55				60						
Phe	Pro	Ala	Met	Val	Pro	Leu	Trp	Met	Tyr	Pro	Leu	Ala	Ile	Val	Cys
65				70					75					80	
Gly	Asn	Cys	Phe	Ile	Leu	Lys	Pro	Ser	Glu	Arg	Asp	Pro	Ser	Ser	Thr
		85					90						95		
Leu	Leu	Ile	Ala	Gln	Leu	Leu	Gln	Glu	Ala	Gly	Leu	Pro	Lys	Gly	Val
		100					105					110			
Leu	Asn	Val	Val	His	Gly	Asp	Lys	Thr	Ala	Val	Asp	Ala			
	115					120					125				

<210> 2349

<211> 417

<212> DNA

<213> Homo sapiens

<400> 2349

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 300  
 actggggcac ctactcgagc tgtagaacia gaaggcaaac acgttcacca ttcccttggc  
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<210> 2350



<211> 139  
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 Tyr Ser Ala Gly Ala Asp Lys Val Phe Gly Val Pro Gly Asp Phe Asn  
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 Leu Ala Phe Leu Asp Asp Ile Ile Ala His Asn His Ile Lys Trp Ile  
 35 40 45  
 Gly Asn Thr Asn Glu Leu Asn Ala Ser Tyr Ala Ala Asp Gly Tyr Ala  
 50 55 60  
 Arg Ile Asn Gly Ile Gly Ala Met Val Thr Thr Phe Gly Val Gly Glu  
 65 70 75 80  
 Leu Ser Ala Val Asn Gly Ile Ala Gly Ser Tyr Ala Glu Arg Val Pro  
 85 90 95  
 Val Ile Ala Ile Thr Gly Ala Pro Thr Arg Ala Val Glu Gln Glu Gly  
 100 105 110  
 Lys Tyr Val His His Ser Leu Gly Glu Gly Thr Phe Asp Asp Tyr Arg  
 115 120 125  
 Lys Met Phe Glu Pro Ile Thr Thr Ala Gln Ala  
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<210> 2351  
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 <212> DNA  
 <213> Homo sapiens

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 360  
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 480  
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 540  
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 600  
 gacgtcatcc acgctggcca cctaggcggg atgccccga tgcccgacct gaatgccgag  
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<210> 2352  
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 <213> Homo sapiens

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 Asp Gln Tyr Asp Arg Phe Val Arg Gly Asn Thr Val Leu Ala Gln Pro  
 35 40 45  
 Asn Asp Ala Gly Met Ile Arg Ile Asp Asp Asn Leu Gly Ile Ala Leu  
 50 55 60  
 Ser Leu Asp Ala Asn Gly Arg Gln Thr Thr Leu Asn Pro Tyr Leu Gly  
 65 70 75 80  
 Ala Gln Leu Ala Leu Cys Glu Ala Tyr Arg Asn Val Ala Val Ser Gly  
 85 90 95  
 Ala Thr Pro Val Ala Val Thr Asp Cys Leu Asn Tyr Gly Ser Pro Tyr  
 100 105 110  
 Asp Pro Asp Val Met Trp Gln Phe Asp Glu Thr Ile Leu Gly Leu Val  
 115 120 125  
 Asp Gly Cys Arg Glu Leu Gly Val Pro Val Thr Gly Gly Asn Val Ser  
 130 135 140  
 Leu His Asn Arg Thr Gly Asp Glu Ser Ile Arg Pro Thr Pro Leu Val  
 145 150 155 160  
 Gly Val Leu Gly Val Ile Asp Asp Val His Arg Arg Ile Pro Ser Ala  
 165 170 175  
 Phe Ala His Asp Gly Asp Ala Val Leu Leu Leu Gly Thr Thr Lys Cys  
 180 185 190  
 Glu Phe Gly Gly Ser Val Tyr Glu Asp Val Ile His Ala Gly His Leu  
 195 200 205  
 Gly Gly Met Pro Pro Met Pro Asp Leu Asn Ala Glu Lys Ala Leu Ala  
 210 215 220  
 Ala Val Met Val Glu Ala Ser Lys  
 225 230

<210> 2353  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

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 120  
 gaactcgggtt ctgttgatgt cttgggtcaac aatgctggga tcaactcaaga tacgcttatg  
 180  
 ctcaagatga ccgaagaaga ctttgaaaaa gtgattaaga tcaacttgac aggtgccttc  
 240  
 aacatgacgc aagcagtctt gaaacagatg atcaaggcac gtgaagggtgc gattatcaac  
 300

atgtctagtg tggtcggttt gatgggaaat atcggacaag ccaactatgc agcttctaaa  
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 422

<210> 2354

<211> 140

<212> PRT

<213> Homo sapiens

<400> 2354

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Lys	Val	Val	Pro	Ile	Ser	Gly	Asp	Val	Ser	Asp	Phe	Ala	Asp	Ala	Lys
			20				25					30			
Arg	Met	Val	Asp	Gln	Ala	Ile	Thr	Glu	Leu	Gly	Ser	Val	Asp	Val	Leu
		35				40					45				
Val	Asn	Asn	Ala	Gly	Ile	Thr	Gln	Asp	Thr	Leu	Met	Leu	Lys	Met	Thr
	50				55				60						
Glu	Glu	Asp	Phe	Glu	Lys	Val	Ile	Lys	Ile	Asn	Leu	Thr	Gly	Ala	Phe
65				70				75					80		
Asn	Met	Thr	Gln	Ala	Val	Leu	Lys	Gln	Met	Ile	Lys	Ala	Arg	Glu	Gly
			85					90					95		
Ala	Ile	Ile	Asn	Met	Ser	Ser	Val	Val	Gly	Leu	Met	Gly	Asn	Ile	Gly
			100				105						110		
Gln	Ala	Asn	Tyr	Ala	Ala	Ser	Lys	Ala	Gly	Leu	Ile	Gly	Phe	Thr	Lys
		115				120						125			
Ser	Val	Ala	Arg	Glu	Val	Ala	Asn	Arg	Asn	Val	Arg				
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<210> 2355

<211> 5191

<212> DNA

<213> Homo sapiens

<400> 2355

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 420  
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 480

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&lt;210&gt; 2356

&lt;211&gt; 1000

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<400> 2356  
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 Leu Asp Lys Phe Ser Gly Thr Leu Tyr Trp Lys Glu Asn Lys Phe Pro  
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 Leu Ser Asn Gln Asn Met Leu Leu Arg Gly Cys Val Leu Arg Asn Thr  
 35 40 45  
 Glu Trp Cys Phe Gly Leu Val Ile Phe Ala Gly Pro Asp Thr Lys Leu  
 50 55 60  
 Met Gln Asn Ser Gly Arg Thr Lys Phe Lys Arg Thr Ser Ile Asp Arg  
 65 70 75 80  
 Leu Met Asn Thr Leu Val Leu Trp Ile Phe Gly Phe Leu Val Cys Met  
 85 90 95  
 Gly Val Ile Leu Ala Ile Gly Asn Ala Ile Trp Glu His Glu Val Gly  
 100 105 110  
 Met Arg Phe Gln Val Tyr Leu Pro Trp Asp Glu Ala Val Asp Ser Ala  
 115 120 125  
 Phe Phe Ser Gly Phe Leu Ser Phe Trp Ser Tyr Ile Ile Ile Leu Asn  
 130 135 140  
 Thr Val Val Pro Ile Ser Leu Tyr Val Ser Val Glu Val Ile Arg Leu  
 145 150 155 160  
 Gly His Ser Tyr Phe Ile Asn Trp Asp Lys Lys Met Phe Cys Met Lys  
 165 170 175  
 Lys Arg Thr Pro Ala Glu Ala Arg Thr Thr Thr Leu Asn Glu Glu Leu  
 180 185 190  
 Gly Gln Val Glu Tyr Ile Phe Ser Asp Lys Thr Gly Thr Leu Thr Gln  
 195 200 205  
 Asn Ile Met Val Phe Asn Lys Cys Ser Ile Asn Gly His Ser Tyr Gly  
 210 215 220  
 Asp Val Phe Asp Val Leu Gly His Lys Ala Glu Leu Gly Glu Arg Pro  
 225 230 235 240  
 Glu Pro Val Asp Phe Ser Phe Asn Pro Leu Ala Asp Lys Lys Phe Leu  
 245 250 255  
 Phe Trp Asp Pro Ser Leu Leu Glu Ala Val Lys Ile Gly Asp Pro His  
 260 265 270  
 Thr His Glu Phe Phe Arg Leu Leu Ser Leu Cys His Thr Val Met Ser  
 275 280 285  
 Glu Glu Lys Asn Glu Gly Glu Leu Tyr Tyr Lys Ala Gln Ser Pro Asp  
 290 295 300  
 Glu Gly Ala Leu Val Thr Ala Ala Arg Asn Phe Gly Phe Val Phe Arg  
 305 310 315 320  
 Ser Arg Thr Pro Lys Thr Ile Thr Val His Glu Met Gly Thr Ala Ile  
 325 330 335  
 Thr Tyr Gln Leu Leu Ala Ile Leu Asp Phe Asn Asn Ile Arg Lys Arg  
 340 345 350  
 Met Ser Val Ile Val Arg Asn Pro Glu Gly Lys Ile Arg Leu Tyr Cys  
 355 360 365  
 Lys Gly Ala Asp Thr Ile Leu Leu Asp Arg Leu His His Ser Thr Gln  
 370 375 380  
 Glu Leu Leu Asn Thr Thr Met Asp His Leu Asn Glu Tyr Ala Gly Glu  
 385 390 395 400  
 Gly Leu Arg Thr Leu Val Leu Ala Tyr Lys Asp Leu Asp Glu Glu Tyr  
 405 410 415  
 Tyr Glu Glu Trp Ala Glu Arg Arg Leu Gln Ala Ser Leu Ala Gln Asp

420 425 430  
 Ser Arg Glu Asp Arg Leu Ala Ser Ile Tyr Glu Glu Val Glu Asn Asn  
 435 440 445  
 Met Met Leu Leu Gly Ala Thr Ala Ile Glu Asp Lys Leu Gln Gln Gly  
 450 455 460  
 Val Pro Glu Thr Ile Ala Leu Leu Thr Leu Ala Asn Ile Lys Ile Trp  
 465 470 475 480  
 Val Leu Thr Gly Asp Lys Gln Glu Thr Ala Val Asn Ile Gly Tyr Ser  
 485 490 495  
 Cys Lys Met Leu Thr Asp Asp Met Thr Glu Val Phe Ile Val Thr Gly  
 500 505 510  
 His Thr Val Leu Glu Val Arg Glu Glu Xaa Gln Glu Ser Pro Gly Glu  
 515 520 525  
 Asp Asp Gly Leu Ile Xaa Arg Ser Val Gly Asn Gly Phe Thr Tyr Gln  
 530 535 540  
 Asp Lys Leu Ser Ser Ser Lys Leu Thr Ser Val Leu Glu Ala Val Ala  
 545 550 555 560  
 Gly Glu Tyr Ala Leu Val Ile Asn Gly His Ser Leu Ala His Ala Leu  
 565 570 575  
 Glu Ala Asp Met Glu Leu Glu Phe Leu Glu Thr Ala Cys Ala Cys Lys  
 580 585 590  
 Ala Val Ile Cys Cys Arg Val Thr Pro Leu Gln Lys Ala Gln Val Val  
 595 600 605  
 Glu Leu Val Lys Lys Tyr Lys Lys Ala Val Thr Leu Ala Ile Gly Asp  
 610 615 620  
 Gly Ala Asn Asp Val Ser Met Ile Lys Thr Ala His Ile Gly Val Gly  
 625 630 635 640  
 Ile Ser Gly Gln Glu Gly Ile Gln Ala Val Leu Ala Ser Asp Tyr Ser  
 645 650 655  
 Phe Ser Gln Phe Lys Phe Leu Gln Arg Leu Leu Leu Val His Gly Arg  
 660 665 670  
 Trp Ser Tyr Leu Arg Met Cys Lys Phe Leu Cys Tyr Phe Phe Tyr Lys  
 675 680 685  
 Asn Phe Ala Phe Thr Met Val His Phe Trp Phe Gly Phe Phe Cys Gly  
 690 695 700  
 Phe Ser Ala Gln Thr Val Tyr Asp Gln Tyr Phe Ile Thr Leu Tyr Asn  
 705 710 715 720  
 Ile Val Tyr Thr Ser Leu Pro Val Leu Ala Met Gly Val Phe Asp Gln  
 725 730 735  
 Asp Val Pro Glu Gln Arg Ser Met Glu Tyr Pro Lys Leu Tyr Glu Pro  
 740 745 750  
 Gly Gln Leu Asn Leu Leu Phe Asn Lys Arg Glu Phe Phe Ile Cys Ile  
 755 760 765  
 Ala Gln Gly Ile Tyr Thr Ser Val Leu Met Phe Phe Ile Pro Tyr Gly  
 770 775 780  
 Val Phe Ala Asp Ala Thr Arg Asp Asp Gly Thr Gln Leu Ala Asp Tyr  
 785 790 795 800  
 Gln Ser Phe Ala Val Thr Val Ala Thr Ser Leu Val Ile Val Val Ser  
 805 810 815  
 Val Gln Ile Gly Leu Asp Thr Gly Tyr Trp Thr Ala Ile Asn His Phe  
 820 825 830  
 Phe Ile Trp Gly Ser Leu Ala Val Tyr Phe Ala Ile Leu Phe Ala Met  
 835 840 845  
 His Ser Asn Gly Leu Phe Asp Met Phe Pro Asn Gln Phe Arg Phe Val



```

      850              855              860
Gly Asn Ala Gln Asn Thr Leu Ala Gln Pro Thr Val Trp Leu Thr Ile
865              870              875              880
Val Leu Thr Thr Val Val Cys Ile Met Pro Val Val Ala Phe Arg Phe
      885              890              895
Leu Arg Leu Asn Leu Lys Pro Asp Leu Ser Asp Thr Val Arg Tyr Thr
      900              905              910
Gln Leu Val Arg Lys Lys Gln Lys Ala Gln His Arg Cys Met Arg Arg
      915              920              925
Val Gly Arg Thr Gly Ser Arg Arg Ser Gly Tyr Ala Phe Ser His Gln
      930              935              940
Glu Gly Phe Gly Glu Leu Ile Met Ser Gly Lys Asn Met Arg Leu Ser
945              950              955              960
Ser Leu Ala Leu Ser Ser Phe Thr Thr Arg Ser Ser Ser Ser Trp Ile
      965              970              975
Glu Ser Leu Arg Arg Lys Lys Ser Asp Ser Ala Ser Ser Pro Ser Gly
      980              985              990
Gly Ala Asp Lys Pro Leu Lys Gly
      995              1000

```

<210> 2357  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

```

<400> 2357
naccggttac gttgctggag gtcaatgcgt catgccgata catcatcaga tccgcactgt
60
ggcgaccatc cttgccacca ttaccattgc cgccctagtg ctcacgggct gtaatacggc
120
ggtgcgccaa acggtgaaga cgaggtttcc cgcaagctca tcaccgtgtg ggggtgctgag
180
ccacaaaacc cactcctgcc agccgacacc aatgaaaccg gcggcacgaa agtcatcacc
240
gccttggttcg ccggcctggg gtattacgac gccgacggca aaaccataa tgatgtggcc
300
aaatccattg acttcgatgg cgaccgcacc tacacggtga cgctgcggaa aaccagattc
360
gccgacggta ctgaggtgaa ggcccataat tttgtgaaag ctgccgca
408

```

<210> 2358  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

```

<400> 2358
Tyr Gly Gly Ala Pro Asn Gly Glu Asp Glu Val Ser Arg Lys Leu Ile
1      5      10      15
Thr Val Trp Gly Ala Glu Pro Gln Asn Pro Leu Leu Pro Ala Asp Thr
20      25      30
Asn Glu Thr Gly Gly Thr Lys Val Ile Thr Ala Leu Phe Ala Gly Leu
35      40      45
Val Tyr Tyr Asp Ala Asp Gly Lys Thr His Asn Asp Val Ala Lys Ser

```

```

      50              55              60
Ile Asp Phe Asp Gly Asp Arg Thr Tyr Thr Val Thr Leu Arg Lys Thr
65              70              75              80
Arg Phe Ala Asp Gly Thr Glu Val Lys Ala His Asn Phe Val Lys Ala
      85              90              95
Ala Ala

```

<210> 2359  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

```

<400> 2359
aacetgaaca tgttgggatt gagagagccc gaggtgtatg ggtcggaaac attggccgac
60
gttgagcaga cgtgtcgtga gtacggcgaa gaacttgggc ttgtaattga gtttcagcaa
120
accaatcacg aagggcaaat gattgaatgg attcaccacg cccgtagaag gattgcgggg
180
attgtgatca atccaggagc atggacccat acatcggcag ccatccacga tgcgttgatt
240
gcagccgagg taccggtgat tgaggttcac atctcaaag tccacaggcg tgaagatttc
300
aggcattttt cctacgtgtc acgc
324

```

<210> 2360  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

```

<400> 2360
Asn Leu Asn Met Leu Gly Leu Arg Glu Pro Glu Val Tyr Gly Ser Glu
1              5              10              15
Thr Leu Ala Asp Val Glu Gln Thr Cys Arg Glu Tyr Gly Glu Glu Leu
      20              25              30
Gly Leu Val Ile Glu Phe Gln Gln Thr Asn His Glu Gly Gln Met Ile
      35              40              45
Glu Trp Ile His His Ala Arg Arg Arg Ile Ala Gly Ile Val Ile Asn
      50              55              60
Pro Gly Ala Trp Thr His Thr Ser Ala Ala Ile His Asp Ala Leu Ile
65              70              75              80
Ala Ala Glu Val Pro Val Ile Glu Val His Ile Ser Asn Val His Arg
      85              90              95
Arg Glu Asp Phe Arg His Phe Ser Tyr Val Ser Arg
      100              105

```

<210> 2361  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens

<400> 2361

tccggatggg actccaacct acttgggggt actgggggtg cagaaagaac gcggccctgt  
 60  
 gtcagggacc ggtatggaag cctcagtagg gctggagccc catcatgccc cttccgagca  
 120  
 gatcaacaca gaccagctgg tcaaggggga cctccatccc tgcctgtcc tcaaggagct  
 180  
 gtagggagag tcccaaaggc aggtgggtgg gctggggcct ccaacagctg ggtcctctca  
 240  
 tatcacttaa ggcccaacag cacacagtct cccaagtgtg ccaggtgcca caacacggcc  
 300  
 atcccgtctt cacagctcca ccccgctgc ctgcctgcca ccatctccac aaacatatgc  
 360  
 tgcagctcca caccgggaa acaccacatg ctgcgttt  
 398

<210> 2362

<211> 98

<212> PRT

<213> Homo sapiens

<400> 2362

Met	Pro	Leu	Pro	Ser	Arg	Ser	Thr	Gln	Thr	Ser	Trp	Ser	Arg	Gly	Thr
1			5				10				15				
Ser	Ile	Pro	Ala	Leu	Ser	Ser	Arg	Ser	Cys	Arg	Glu	Ser	Pro	Lys	Gly
		20					25				30				
Arg	Trp	Trp	Gly	Trp	Gly	Leu	Gln	Gln	Leu	Gly	Pro	Leu	Ile	Ser	Leu
		35				40					45				
Lys	Ala	Gln	Gln	His	Thr	Val	Ser	Gln	Val	Cys	Gln	Val	Pro	Gln	His
	50					55				60					
Gly	His	Pro	Ala	Leu	Thr	Ala	Pro	Pro	Arg	Leu	Pro	Ala	Cys	His	His
65				70					75					80	
Leu	His	Lys	His	Met	Leu	Gln	Leu	His	Thr	Arg	Glu	Thr	Pro	His	Ala
			85					90					95		

Arg Phe

<210> 2363

<211> 833

<212> DNA

<213> Homo sapiens

<400> 2363

nngactcctc tagctcccaa cgcaaaagcg tttaaagatg cagctcagaa gcataccag  
 60  
 cagcacaagg ggaggtccca agaaccagaa cttacatcac tgcctccgag ttcagaggtt  
 120  
 tcctttccca ccttctcaga actttctgtt tccatggcct cctctgccac ctctgccacc  
 180  
 tcccctgatg tgctggcctc cgtttccatc gcttctcat ggcgttcttc cgcccgtgt  
 240  
 tccaagccca ctgcangtcg aagcaaacgt gattgcgta ccaactcagaa ggtggcacag  
 300  
 ggactggcag cggtgccatc tgggagtctg tgtgctcagc ctccgagtgc aggcttcccc  
 360

ggcccctgct gtggtgctag gtccccagat gagagatcac ggcatgaag atcagcccc  
 420  
 aaggcagccc cttccnttcc agcctgggct ctggcgtgtt ctaggtgctc acttccatgg  
 480  
 ctggcctgct cacagagccc tacctcagcc tgtggtgaagc gcacctgctc ggccctgggtg  
 540  
 ctctatgatg agccaccagt cagttctgca gatgtgtccc cgagctcctg ccgagggacg  
 600  
 aaacacggtg gccctgctcc tagtgctgtg gcacgccacg ctccacacct gccatctgcc  
 660  
 cttccaccac ctgctcccc aggggctccg cctcgtgact cacgctcagg caagtctccg  
 720  
 ggcgcaaca gctggctgat ggtgacatgc tgcagcctgg tcacatcaga aacctgagg  
 780  
 gtggatctcc ggaggtcatc gatgtggaca gactgccaca gcccttcacg cgt  
 833

&lt;210&gt; 2364

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2364

Xaa	Thr	Pro	Leu	Ala	Pro	Asn	Ala	Lys	Ala	Phe	Lys	Asp	Ala	Ala	Gln
1				5					10					15	
Lys	His	His	Gln	Gln	His	Lys	Gly	Arg	Ser	Gln	Glu	Pro	Glu	Leu	Thr
			20					25					30		
Ser	Leu	Pro	Pro	Ser	Ser	Glu	Val	Ser	Phe	Pro	Thr	Phe	Ser	Glu	Leu
		35					40					45			
Ser	Val	Ser	Met	Ala	Ser	Ser	Ala	Thr	Ser	Ala	Thr	Ser	Pro	Asp	Val
		50				55					60				
Leu	Ala	Ser	Val	Ser	Ile	Ala	Ser	Ser	Trp	Arg	Ser	Ser	Ala	Arg	Cys
65					70					75				80	
Ser	Lys	Pro	Thr	Ala	Xaa	Arg	Ser	Lys	Arg	Asp	Cys	Val	Thr	Thr	Gln
				85					90					95	
Lys	Val	Ala	Gln	Gly	Leu	Ala	Ala	Val	Pro	Ser	Gly	Ser	Leu	Cys	Ala
			100					105					110		
Gln	Pro	Pro	Ser	Ala	Gly	Phe	Pro	Gly	Pro	Cys	Cys	Gly	Ala	Arg	Ser
		115					120						125		
Pro	Asp	Glu	Arg	Ser	Arg	Ser									
		130				135									

&lt;210&gt; 2365

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2365

accggtgccc agctcccacg gctcgtccag acctacgttg agaaacttcg acgagacagt  
 60  
 ctccgtcagt tcgcccaca acctctgaac gaagtcaaga ttctccggca ctggagccaa  
 120  
 ggtgcttgcc ctggcatgaa cgccccaggg gaggtcgacg ccgtcgggat tctcacaccg  
 180

atggtgatgg gactcggttt ccaaccacgg ttccatgtga cccagacagt tctggttggc  
 240  
 cccgagctcg atgcctcgtc cgcgacacag accatcgagc cacctcatgt cctccgccgt  
 300  
 cacggggctg cggtcggccc acacctctc ctcaccgagg taggcaaata ccgcttcacc  
 360  
 atagagctca aggtgattga gaccacaccg cgccatgacg cgcgtcagga aatcaagagt  
 420  
 ggaacgcgt  
 429

<210> 2366

<211> 132

<212> PRT

<213> Homo sapiens

<400> 2366

Met Ala Arg Cys Gly Leu Asn His Leu Glu Leu Tyr Gly Glu Ala Gly  
 1 5 10 15  
 Phe Ala Tyr Arg Gly Glu Glu Glu Val Trp Ala Asp Arg Ser Pro Val  
 20 25 30  
 Thr Ala Glu Asp Met Arg Trp Leu Asp Gly Leu Cys Arg Gly Arg Gly  
 35 40 45  
 Ile Glu Leu Gly Ala Asn Gln Asn Cys Leu Gly His Met Glu Pro Trp  
 50 55 60  
 Leu Glu Thr Glu Ser His His His Arg Cys Glu Asn Pro Asp Gly Val  
 65 70 75 80  
 Asp Leu Pro Trp Gly Val His Ala Arg Ala Ser Thr Leu Ala Pro Val  
 85 90 95  
 Pro Glu Asn Leu Asp Phe Val Gln Arg Leu Leu Gly Glu Leu Thr Glu  
 100 105 110  
 Thr Val Ser Ser Lys Phe Leu Asn Val Gly Leu Asp Glu Pro Trp Glu  
 115 120 125  
 Leu Gly Thr Gly  
 130

<210> 2367

<211> 474

<212> DNA

<213> Homo sapiens

<400> 2367

ngtgacaggg agaagacgtg cgcgcagttc ggcggaacct atccgggttc ggccggcagt  
 60  
 gggggtcacg agctcaccga cgcgcgcgcg ttcgcctcgt ggggcgtcga tttcgtcaaa  
 120  
 tacgatcggg gctccggtga ctccgcgcac gacgaccagg tcgcctcgtt caccgcgatg  
 180  
 cgtgacgcaa tccgatccac cggacgcccc atggtgtaca gcatcaaccc caacagcgaa  
 240  
 tcgccggatc ggtccggagc ccaattcgat tggggcgggtg tggcaaccat gacacgtacc  
 300  
 accaacgaca tctcgcgggt gtggaccact cggccggcgg gtgccgatgc gacaccggca  
 360

tcgggggtatc aggggatccg cgacatcatc gacgccgtgg ccccgatcgg cgcacggggt  
 420  
 gcgacggcag cttcgtcgac atggacatgc tcgtcgtcgg tgcgggaac gcgt  
 474

<210> 2368  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<400> 2368  
 Xaa Ala Arg Glu Lys Thr Cys Ala Gln Phe Gly Gly Thr Tyr Pro Gly  
 1 5 10 15  
 Ser Ala Gly Ser Gly Gly His Glu Leu Thr Asp Ala Arg Ala Phe Ala  
 20 25 30  
 Ser Trp Gly Val Asp Phe Val Lys Tyr Asp Arg Cys Ser Gly Asp Ser  
 35 40 45  
 Ala His Asp Asp Gln Val Ala Ser Phe Thr Ala Met Arg Asp Ala Ile  
 50 55 60  
 Arg Ser Thr Gly Arg Pro Met Val Tyr Ser Ile Asn Pro Asn Ser Glu  
 65 70 75 80  
 Ser Pro Asp Arg Ser Gly Ala Gln Phe Asp Trp Gly Gly Val Ala Thr  
 85 90 95  
 Met Thr Arg Thr Thr Asn Asp Ile Ser Pro Val Trp Thr Thr Arg Pro  
 100 105 110  
 Ala Gly Ala Asp Ala Thr Pro Ala Ser Gly Tyr Gln Gly Ile Arg Asp  
 115 120 125  
 Ile Ile Asp Ala Val Ala Pro Ile Gly Ala Arg Val Ala Thr Ala Ala  
 130 135 140  
 Ser Ser Thr Trp Thr Cys Ser Ser Ser Val Ser Ala Thr Arg  
 145 150 155

<210> 2369  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

<400> 2369  
 ctgaatggca ggcaggcaga ggccaccaga gccagcccc cgagaagccc tgctgagcca  
 60  
 aaggggagcg ccctgggacc taaccagag ccccatctca cttcccccg ttctttcaaa  
 120  
 gtgcctcccc caaccccagt caggacttcg tccatcccag ttcaggaagc acaagagggt  
 180  
 cccgaaagga agagggggcc accaagaagg ctcccagccg actcccactg cctcccagct  
 240  
 tccacatccg ccccgctcc caggtctacc cagacagggc ccccgagcnc agactgcct  
 300  
 ggggagctca aggccacagc accagccagc ccaaggcttg gccagtccca gtcccaagca  
 360  
 gatgaacgag ctgggactcc gctccagcc cctcccctgc ccctcct  
 408

<210> 2370

<211> 136  
 <212> PRT  
 <213> Homo sapiens

<400> 2370  
 Leu Asn Gly Arg Gln Ala Glu Ala Thr Arg Ala Ser Pro Pro Arg Ser  
 1 5 10 15  
 Pro Ala Glu Pro Lys Gly Ser Ala Leu Gly Pro Asn Pro Glu Pro His  
 20 25 30  
 Leu Thr Phe Pro Arg Ser Phe Lys Val Pro Pro Pro Thr Pro Val Arg  
 35 40 45  
 Thr Ser Ser Ile Pro Val Gln Glu Ala Gln Glu Ala Pro Glu Arg Lys  
 50 55 60  
 Arg Gly Pro Pro Arg Arg Leu Pro Ala Asp Ser His Cys Leu Pro Ala  
 65 70 75 80  
 Ser Thr Ser Ala Pro Pro Pro Arg Ser Thr Gln Thr Gly Pro Pro Ser  
 85 90 95  
 Xaa Asp Cys Pro Gly Glu Leu Lys Ala Thr Ala Pro Ala Ser Pro Arg  
 100 105 110  
 Leu Gly Gln Ser Gln Ser Gln Ala Asp Glu Arg Ala Gly Thr Pro Pro  
 115 120 125  
 Pro Ala Pro Pro Leu Pro Pro Pro  
 130 135

<210> 2371  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

<400> 2371  
 gaattcggtg tgcgatgcga gctgcagcc tgggagcaga gacaaggagc aaaggcggtg  
 60  
 agagggttgc cagggcaccc agttacagct ggagctgcag gggacccatc cctcgagaga  
 120  
 ggcaggcact agtcatgagg caagagatgc ctcaagaagag gatgctggcc gcagggcaca  
 180  
 gcagagaggg agatagcccg gggcactcct caggaccggg cctcagggga cagcaaacia  
 240  
 gattcctgat agacgcgccc aggtcatgcc ttttcagtgg tgtgagccag gttctggcgt  
 300  
 caggcgggcc aagggttttca tgcagcn  
 327

<210> 2372  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 2372  
 Met Arg Ala Cys Ser Leu Gly Ala Glu Thr Arg Ser Lys Gly Gly Glu  
 1 5 10 15  
 Arg Val Ala Arg Ala Pro Ser Tyr Ser Trp Ser Cys Arg Gly Pro Ile  
 20 25 30  
 Pro Arg Glu Arg Gln Ala Leu Val Met Arg Gln Glu Met Pro Gln Lys

```

      35              40              45
Arg Met Leu Ala Ala Gly His Ser Arg Glu Gly Asp Ser Pro Gly His
      50              55              60
Ser Ser Gly Pro Gly Leu Arg Gly Gln Gln Thr Arg Phe Leu Ile Asp
65              70              75              80
Ala Pro Arg Ser Cys Leu Phe Ser Gly Val Ser Gln Val Leu Ala Ser
      85              90              95
Gly Gly Pro Arg Phe Ser Cys Ser
      100

```

&lt;210&gt; 2373

&lt;211&gt; 591

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2373

```

gaattctgac attcaggaag tcaattgcag aaggtttaac caagttgatt ctgttttacc
60
aaatcctgtc tattctgaaa agcggccaat gccagactca tctcatgatg tgaaagttct
120
cacttcaaag acatcagctg ttgagatgac ccaggcagta ttgaatactc agcttttcac
180
agaaaatggt accaaagtgt agcaaaatcc accagcagtt tgtgaaacaa tttctgttcc
240
caagtccatg tccactgagg aatataaatc aaaaattcaa aatgaaaata tgctacttct
300
cgcttttgctt tcacaggcac gtaagactca gaagacagta ttaaaagatg ctaatcaaac
360
tattcaggat tctaaaccag acagttgtga aatgaatcca aatacccaaa tgactggtaa
420
ccaactgaat ttgaagaaca tggaaactcc aagtacttct aatgtaagtg gcagggtttt
480
ggacaactcc ttttgcagtg gacaagaatc ctcaacaaaa ggaatgcctg ctaaaagtga
540
cagtagctgt tccatggaag tgctagcaac ctgtctttcc ctgtggaaaa a
591

```

&lt;210&gt; 2374

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2374

```

Met Pro Asp Ser Ser His Asp Val Lys Val Leu Thr Ser Lys Thr Ser
1              5              10              15
Ala Val Glu Met Thr Gln Ala Val Leu Asn Thr Gln Leu Ser Ser Glu
      20              25              30
Asn Val Thr Lys Val Glu Gln Asn Ser Pro Ala Val Cys Glu Thr Ile
      35              40              45
Ser Val Pro Lys Ser Met Ser Thr Glu Glu Tyr Lys Ser Lys Ile Gln
      50              55              60
Asn Glu Asn Met Leu Leu Leu Ala Leu Leu Ser Gln Ala Arg Lys Thr
65              70              75              80
Gln Lys Thr Val Leu Lys Asp Ala Asn Gln Thr Ile Gln Asp Ser Lys

```



```

      85              90              95
Pro Asp Ser Cys Glu Met Asn Pro Asn Thr Gln Met Thr Gly Asn Gln
      100              105              110
Leu Asn Leu Lys Asn Met Glu Thr Pro Ser Thr Ser Asn Val Ser Gly
      115              120              125
Arg Val Leu Asp Asn Ser Phe Cys Ser Gly Gln Glu Ser Ser Thr Lys
      130              135              140
Gly Met Pro Ala Lys Ser Asp Ser Ser Cys Ser Met Glu Val Leu Ala
      145              150              155              160
Thr Cys Leu Ser Leu Trp Lys
      165

```

&lt;210&gt; 2375

&lt;211&gt; 535

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2375

```

ntggccatgt cggtgctcag cagcggcacc ctggacagtt accttgagcg tcacaaacaa
60
ctggacgcga tgcgcatgct gcacttcttc gccctcgacg aagaaaaccc cgccagcatc
120
tataactgcc tgcgcgccgc gcggggcaat gccacgcggg tacgcggggc gatcaccgcc
180
gacatgtggg aaaacctcaa cgccacctgg ctggaaatgc gcagcatcgc cgccgggggc
240
ctggccccgc atggcatcag ccacttctgt gactgggtca agcagcggtc gcacctgttc
300
cgccggggcaa cctcgggcac catcatgcgc aacgacgctt accggtttat tcgcctgggc
360
acgtttgtcg agcgcgcgga caacacctg cgctgctgg atgcgcgcta cgaaatgttt
420
ggtagaggag cggaagaggt cagcgacctg tcggcacgcg ggtattacca gtggagcgcc
480
ctgctgcggg ccttgctcgc attcgaggcg tataccgaac tgtaccccaa cgcg
535

```

&lt;210&gt; 2376

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2376

```

Xaa Ala Met Ser Leu Leu Ser Ser Gly Thr Leu Asp Ser Tyr Leu Glu
  1              5              10              15
Arg His Lys Gln Leu Asp Ala Met Arg Met Leu His Phe Phe Ala Leu
      20              25              30
Asp Glu Glu Asn Pro Ala Ser Ile Tyr Asn Cys Leu Arg Ala Ala Arg
      35              40              45
Gly Asn Ala His Ala Val Arg Gly Arg Ile Thr Ala Asp Met Trp Glu
      50              55              60
Asn Leu Asn Ala Thr Trp Leu Glu Met Arg Ser Ile Ala Ala Gly Gly
      65              70              75              80
Leu Ala Arg His Gly Ile Ser His Phe Cys Asp Trp Val Lys Gln Arg

```

<400> 2378  
Met Ser Phe Ile Met Pro Leu Lys Ser Phe Arg Ala Lys Asn Ile Ile  
1 5 10 15  
Phe Thr Phe Gln Phe Tyr Val Cys Gln Ser Ile Leu Phe Tyr Ala Phe  
20 25 30  
Ser Cys Ile His Ile Phe Lys Asn Ile Ser Pro Asn Arg Lys Ile Pro

```

      35              40              45
Thr Ser Ile Cys Trp Phe His Phe Ile Arg Arg Val Lys Tyr Phe Phe
      50              55              60
Met Ser His His His Arg Ser Phe Pro Phe Val Cys Gln Gly Leu Ile
65              70              75              80
Ser Leu Val Gln Asp His Pro Gly Leu Val Pro Phe Ile Ser Trp Val
      85              90              95
Leu Pro Gln Lys Gly Ala Ser Val Leu Pro Tyr His Phe
      100              105

```

&lt;210&gt; 2379

&lt;211&gt; 342

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2379

```

tcatgacctg gagacttcgg aaactcaaca agactgcagg gcacccaggg gcaccagccc
60
cggtcaccgc agaggatcag tgcactttgc catctggcag atcaactcat ggcacaactg
120
ggaaacataa cattcacgct tgtgaaccga gacgccatac cccagcgggtg ccgagagcaa
180
cagtgcctgtg caggtctggg cagatgaggg cctccaggac acgaggactc actcgtcac
240
cctgccact gggcagctgc tcgccactcc cctcctggag ggcaggacgg acaccacaca
300
cacacacaag caggaagct gtgcagcagt ggggagaaaag ca
342

```

&lt;210&gt; 2380

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2380

```

Met Thr Trp Arg Leu Arg Lys Leu Asn Lys Thr Ala Gly His Pro Gly
  1              5              10              15
Ala Pro Ala Pro Val Thr Ala Glu Asp Gln Cys Thr Leu Pro Ser Gly
      20              25              30
Arg Ser Thr His Gly Thr Thr Gly Lys His Asn Ile His Ala Cys Glu
      35              40              45
Pro Arg Arg His Thr Pro Ala Val Pro Arg Ala Thr Val Leu Cys Arg
      50              55              60
Ser Gly Gln Met Arg Ala Ser Arg Thr Arg Gly Leu Thr Arg Ser Pro
65              70              75              80
Cys Pro Leu Gly Ser Cys Ser Pro Leu Pro Ser Trp Arg Ala Gly Arg
      85              90              95
Thr Pro His Thr His Thr Ser Arg Glu Ala Val Gln Gln Trp Gly Glu
      100              105              110
Ser

```

&lt;210&gt; 2381

&lt;211&gt; 434

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2381

gtgcaccctg gccatatgga cgccagcgac gtcggcgtct tgcgtgacgt ggaaccgatc  
 60  
 ggcccaagta gagagatgga ttttgaatgg tgacgatgta cccgccgcag caagtggatg  
 120  
 ccgtcctctt tgacatggac ggaaccctgc tcaacaccct gccggcctgg tgcgtggcat  
 180  
 ctgagcatct gtggggcact tctctggctg acgtgacag cgccaagggt gacgggggca  
 240  
 ccgtcgacga cgtcgttgag ctgtatctgc gagaccacc tcaggcagat cccagggcca  
 300  
 ccacgagcgt tttcatggac atccttgacg ccaacctggc tggccacacc gagccgatgc  
 360  
 ccggagctga ccgcctcgtg aagaggctgt caggatcatgt acccatcgct gtggtgtcga  
 420  
 attccccgac gcgt  
 434

&lt;210&gt; 2382

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2382

Met	Val	Thr	Met	Tyr	Pro	Pro	Gln	Gln	Val	Asp	Ala	Val	Leu	Phe	Asp
1				5					10					15	
Met	Asp	Gly	Thr	Leu	Leu	Asn	Thr	Leu	Pro	Ala	Trp	Cys	Val	Ala	Ser
			20					25					30		
Glu	His	Leu	Trp	Gly	Thr	Ser	Leu	Ala	Asp	Ala	Asp	Ser	Ala	Lys	Val
		35					40					45			
Asp	Gly	Gly	Thr	Val	Asp	Asp	Val	Val	Glu	Leu	Tyr	Leu	Arg	Asp	His
	50					55					60				
Pro	Gln	Ala	Asp	Pro	Gln	Ala	Thr	Ile	Glu	Arg	Phe	Met	Asp	Ile	Leu
65					70					75				80	
Asp	Ala	Asn	Leu	Ala	Gly	His	Thr	Glu	Pro	Met	Pro	Gly	Ala	Asp	Arg
			85						90				95		
Leu	Val	Lys	Arg	Leu	Ser	Gly	His	Val	Pro	Ile	Ala	Val	Val	Ser	Asn
		100						105					110		
Ser	Pro	Thr	Arg												
			115												

&lt;210&gt; 2383

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2383

acgcgtgcgt tcagatgagc gccggacgaa actcctcggc cgcttcggca ggcattggatt  
 60  
 catgtcggca cgggcctttg aacaggatcg ccgtcgcgtg gctatccgcc gcgggtgggg  
 120

cagaaaacgc ccactctccc ttccccaggc gccggccgtc gagtcgtcta cgcaacgcac  
 180  
 gtctacatag gtgacttttt cataccccca ctttcgtact cggatgggct cggcgtgctc  
 240  
 gatgtcggca cgaaaaatta aatgcactga atgcgggttg tcgcacagga tgcattctgt  
 300  
 ctttcttgat gccacccacc ttgttacata ttctgccatg caaaacacct tgtgattttt  
 360  
 ggccggagtgc aacatgggtat gtgtatgccca ctg  
 393

<210> 2384

<211> 125

<212> PRT

<213> Homo sapiens

<400> 2384

Met	Leu	His	Ser	Ala	Lys	Asn	His	Lys	Val	Phe	Cys	Met	Ala	Glu	Tyr
1				5					10					15	
Val	Thr	Arg	Trp	Val	Ala	Ser	Arg	Lys	Thr	Arg	Cys	Ile	Leu	Cys	Asp
			20					25					30		
Asn	Pro	His	Ser	Val	His	Leu	Ile	Phe	Arg	Ala	Asp	Ile	Glu	His	Ala
		35					40				45				
Glu	Pro	Ile	Arg	Val	Arg	Lys	Trp	Gly	Tyr	Glu	Lys	Val	Thr	Tyr	Val
	50					55					60				
Asp	Val	Arg	Cys	Val	Asp	Asp	Ser	Thr	Ala	Gly	Ala	Trp	Gly	Arg	Glu
65				70					75					80	
Ser	Gly	Arg	Phe	Leu	Pro	His	Pro	Arg	Arg	Ile	Ala	Thr	Arg	Arg	Arg
			85					90					95		
Ser	Cys	Ser	Lys	Ala	Arg	Ala	Asp	Met	Asn	Pro	Cys	Leu	Pro	Lys	Arg
			100					105				110			
Pro	Arg	Ser	Phe	Val	Arg	Arg	Ser	Ser	Glu	Arg	Thr	Arg			
			115				120					125			

<210> 2385

<211> 347

<212> DNA

<213> Homo sapiens

<400> 2385

acgcgttccc aaagtaggat ggctgggata gagggaaagg acatctttca ggcttggttat  
 60  
 gcaactgtgct gtggactctt gtgtgtgggt cctaggtctg cccagcattt tggggttcac  
 120  
 cccgtgaccc tctacgggtt tccatgcccc cagcaccacg tccatcatca tttctggggg  
 180  
 cccctcacct cagagagcct gcttcctatg actgcgtggg ccagctggag aaggacgacc  
 240  
 caagacccct caagtttctg tgtcctgacc ccaagcatag gcctgagtgc tcttggggcc  
 300  
 caagggcctt tacgcactac tctctggggc ccaactgtctg cactctt  
 347

<210> 2386

<211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 2386  
 Met Ala Gly Ile Glu Gly Lys Asp Ile Phe Gln Ala Cys Tyr Ala Leu  
 1 5 10 15  
 Cys Cys Gly Leu Leu Trp Gly Pro Arg Ser Ala Gln His Phe Gly  
 20 25 30  
 Val His Pro Val Thr Leu Tyr Gly Phe Pro Cys Pro Gln His His Val  
 35 40 45  
 His His His Phe Trp Gly Pro Leu Thr Ser Glu Ser Leu Leu Pro Met  
 50 55 60  
 Thr Ala Trp Ala Ser Trp Arg Arg Thr Thr Gln Asp Pro Ser Ser Phe  
 65 70 75 80  
 Cys Val Leu Thr Pro Ser Ile Gly Leu Ser Ala Pro Gly Ala Gln Gly  
 85 90 95  
 Pro Leu Arg Thr Thr Leu Trp Gly Pro Leu Ser Ala Leu  
 100 105

<210> 2387  
 <211> 715  
 <212> DNA  
 <213> Homo sapiens

<400> 2387  
 ncggccgcac ttcaccttac ggaggggaga taatgagatc aattagaggc gccgtcaccg  
 60  
 cgccggagac agctgccgcc gcatagtaat caccgcggg ctgggtgcgc gggggctccc  
 120  
 cgctacctgc gcgcctgctg ctcccaccac gcggcaccga cccgggcgcg ccccgggccc  
 180  
 ctgtccgcag cccacagcca caccgcgcac cctacaccct ccttgccgct ctgctgggga  
 240  
 getcaccccc tccactcgca cagtgcgctg cgccccgggg tgtgggaggt cccgggactt  
 300  
 ggggtgtgag tgccgtgtgtg ggggtagggg caggtgtccg cttgtgcgca tatgggcatg  
 360  
 agttacatg gcgtgtgcct ggagatgggc gagtgcaggc tggaatgtgc cggcgtggca  
 420  
 cgtgtgtggg cccaaataga tgcgtgtgtg atcacatgtt gtgttcgtgt ttgcacctcg  
 480  
 tgtgcctgtg tgtccgtatt tgagtgttta caggaatgtg ggtgggtgagt acccgatatg  
 540  
 ggggtgcatc gcacttgtgc gtgtgtgtgt gtaggcgcgt gtgtgtgcgt gtgtgtgtta  
 600  
 ngggatacgt gtagatgtgc attagtgtga ctgtgtgtgc tcatgtgcct gtgcacgtgt  
 660  
 gtttgaggtt tgtgtgcatg ggtagcgtct gtgagagcca tgtgtatatc tgcag  
 715

<210> 2388  
 <211> 58  
 <212> PRT

<213> Homo sapiens

<400> 2388

```

Met Gly Met Ser Val His Gly Val Cys Leu Glu Met Gly Glu Cys Arg
 1           5           10           15
Leu Glu Cys Ala Gly Val Ala Arg Val Trp Ala Gln Ile Asp Ala Cys
      20           25           30
Val Ile Thr Cys Cys Val Arg Val Cys Thr Ser Cys Ala Cys Val Ser
      35           40           45
Val Phe Glu Cys Leu Gln Glu Cys Gly Trp
      50           55

```

<210> 2389

<211> 336

<212> DNA

<213> Homo sapiens

<400> 2389

```

ntcaccctgc cgccggaagg ttgctcgtac cgcattggcca tcgtcaccat gaagaagtcg
60
tatccggggcc acgccaagcg cgtcatgttg ggtgtctggt cgtttttgcg acagttcatg
120
tataccaagt tcgttatcgt caccgacgac gatatacaacg cccgcgactg gaacgacgtg
180
atctggggcca tcaccacgcg catggacccc aagcgcgaca cggtgatgat cgataacacg
240
ccgatcgact acctcgactt cgccctcgccg gtgtccggcc tgggttcgaa gatggggctc
300
gatccacgac acaaattggcc cggccacacc acccgn
336

```

<210> 2390

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2390

```

Xaa Thr Leu Pro Pro Glu Gly Cys Ser Tyr Arg Met Ala Ile Val Thr
 1           5           10           15
Met Lys Lys Ser Tyr Pro Gly His Ala Lys Arg Val Met Leu Gly Val
      20           25           30
Trp Ser Phe Leu Arg Gln Phe Met Tyr Thr Lys Phe Val Ile Val Thr
      35           40           45
Asp Asp Asp Ile Asn Ala Arg Asp Trp Asn Asp Val Ile Trp Ala Ile
      50           55           60
Thr Thr Arg Met Asp Pro Lys Arg Asp Thr Val Met Ile Asp Asn Thr
      65           70           75           80
Pro Ile Asp Tyr Leu Asp Phe Ala Ser Pro Val Ser Gly Leu Gly Ser
      85           90           95
Lys Met Gly Leu Asp Pro Thr His Lys Trp Pro Gly His Thr Thr Arg
      100          105          110

```

<210> 2391

<211> 388

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2391

gtcgactaac ctgcgtacag ccgccaccct acgttttagtc gcgaagcgtg tcggctccat  
60  
gttcattccg gagctacacc atgaataaag tactacctga tccacccatc gatccccgaa  
120  
aagaccgctg cgctttcaac cgcgccatcg accattacct gcctaccag ggcttcact  
180  
gcgtcaacga agacctgagt ttcgaagacg ccctgctcta caccgccagc ctgctcgaca  
240  
gtgcctctgc cacggcgctg gattgcggtg agctgctgca aagccctgaa cgggcgaaga  
300  
tcctggccgt gtggcatttg ctggaaattg caaaaaccac cgtagatcgc ttccccatcg  
360  
agtgcctgac cgcaccaaag ccctgcct  
388

&lt;210&gt; 2392

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2392

Met Asn Lys Val Leu Pro Asp Pro Pro Ile Asp Pro Ala Lys Asp Arg  
1 5 10 15  
Val Ala Phe Asn Arg Ala Ile Asp His Tyr Leu Pro Thr Gln Gly Phe  
20 25 30  
His Cys Val Asn Glu Asp Leu Ser Phe Glu Asp Ala Leu Leu Tyr Thr  
35 40 45  
Ala Ser Leu Leu Asp Ser Ala Ser Ala Thr Ala Leu Asp Cys Gly Glu  
50 55 60  
Leu Leu Gln Ser Pro Glu Arg Ala Lys Ile Leu Ala Val Trp His Leu  
65 70 75 80  
Leu Glu Ile Ala Lys Thr Thr Val Asp Arg Phe Pro Ile Glu Cys Leu  
85 90 95  
Thr Ala Pro Lys Pro Cys  
100

&lt;210&gt; 2393

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2393

aacctgtcta ccgaggacca ggccgagcag gtagagattg tgaagcgtc tgagtccggc  
60  
atgggtcaccg accccatcac tgcgcgcccg gatatgacca tcggggaagt agacgcgctg  
120  
tgcgccgct tccgcctctc cggcctgccg gtggtagacg aggacggcac cctgatgggc  
180  
atttgacca cccgcgatat gcgcttcgag cctgactttg accgcaaggt cagcgaggtc  
240



atgacggcta tgccgcttgt tgttgcgcgc gaggggtgtat ctaagaagga agccctcgaa  
 300  
 ctgctctcgg ccaataaggt ggaaaagctg cccatcgtcg atgcggataa taagctcacc  
 360  
 ggccctgatta ccgtcaagga ctttgtcaag accgagcagt accccaacgc g  
 411

<210> 2394

<211> 137

<212> PRT

<213> Homo sapiens

<400> 2394

Asn	Leu	Ser	Thr	Glu	Asp	Gln	Ala	Glu	Gln	Val	Glu	Ile	Val	Lys	Arg
1				5				10					15		
Ser	Glu	Ser	Gly	Met	Val	Thr	Asp	Pro	Ile	Thr	Ala	Arg	Pro	Asp	Met
			20					25					30		
Thr	Ile	Gly	Glu	Val	Asp	Ala	Leu	Cys	Ala	Arg	Phe	Arg	Ile	Ser	Gly
			35				40					45			
Leu	Pro	Val	Val	Asp	Glu	Asp	Gly	Thr	Leu	Met	Gly	Ile	Cys	Thr	Thr
	50					55					60				
Arg	Asp	Met	Arg	Phe	Glu	Pro	Asp	Phe	Asp	Arg	Lys	Val	Ser	Glu	Val
65					70					75				80	
Met	Thr	Ala	Met	Pro	Leu	Val	Val	Ala	Arg	Glu	Gly	Val	Ser	Lys	Lys
			85					90						95	
Glu	Ala	Leu	Glu	Leu	Leu	Ser	Ala	Asn	Lys	Val	Glu	Lys	Leu	Pro	Ile
			100					105					110		
Val	Asp	Ala	Asp	Asn	Lys	Leu	Thr	Gly	Leu	Ile	Thr	Val	Lys	Asp	Phe
			115				120					125			
Val	Lys	Thr	Glu	Gln	Tyr	Pro	Asn	Ala							
			130				135								

<210> 2395

<211> 362

<212> DNA

<213> Homo sapiens

<400> 2395

aagctttcag aggagtttgc taaagtgtta aggatttgca tattttcaac tttagtcata  
 60  
 tctaagtgcc ccaataaaac agcgcggcgc attgggggct ggctttcatc aacaactaac  
 120  
 ttagcaatat taatctgacc ttttcctggt gattgggcat ttagtaataa tgcggggcca  
 180  
 atatcatcat actttccaaa tttttttgat tttttagaca tcaactgaag ttgtgaccat  
 240  
 ttactgtctt tgtcttgatg gcaatctaaa caaacatctc ttgtattaag ttgttcactt  
 300  
 acccaaggat taggcactct aaaggcatga tcgcgtcgat catcgactcc catgtaacgc  
 360  
 gt  
 362

<210> 2396

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2396

```

Met Gly Val Asp Asp Arg Arg Asp His Ala Phe Arg Val Pro Asn Pro
 1           5           10           15
Trp Val Ser Glu Gln Leu Asn Thr Arg Asp Val Cys Leu Asp Cys His
          20           25           30
Gln Asp Lys Asp Ser Lys Trp Ser Gln Leu Gln Leu Met Ser Lys Lys
          35           40           45
Ser Lys Ile Phe Gly Lys Tyr Asp Asp Ile Gly Pro Ala Leu Leu Leu
          50           55           60
Asn Ala Gln Ser Pro Gly Lys Gly Gln Ile Asn Ile Ala Lys Leu Val
65           70           75           80
Val Asp Glu Ser Gln Pro Pro Met Arg Arg Ala Val Leu Leu Gly His
          85           90           95
Leu Asp Met Thr Lys Val Glu Asn Met Gln Ile Leu Asn Thr Leu Ala
          100          105          110
Asn Ser Ser Glu Ser
          115

```

&lt;210&gt; 2397

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2397

```

nacagcacac tccgcctcct ccgacgatca tagctttcac gtcggacatg atcccccgcc
60
tagtgtacta ctggtccttc tccgtccctc cctacgggga ccacacttcc tacaccatgg
120
aagggtacat caacaacact ctctccatct tcaaagtcgc agacttcaaa aacaaaagca
180
agggaaaccc gtactctgac ctgggtaacc ataccacatg caggtatcgt gatttccgat
240
acccacctgg acacccccag gagtataaac acaacatcta ctattggcat gtgattgcag
300
ccaagctggc ttttatcatt gtcatggagc acgtcatcta ctctgtgaaa tttttcattt
360
catatgcaat tcccgatgta tcaaagcgca caaagagcaa gatccagaga gaaaaatacc
420
taacccaaaa gcttcttcat gagaatcac
449

```

&lt;210&gt; 2398

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2398

```

Cys Thr Thr Gly Pro Ser Pro Ser Leu Pro Thr Gly Thr Thr Leu Pro
 1           5           10           15
Thr Pro Trp Lys Gly Thr Ser Thr Thr Leu Ser Pro Ser Ser Lys Ser

```

```

      20      25      30
Gln Thr Ser Lys Thr Lys Ala Arg Glu Thr Arg Thr Leu Thr Trp Val
      35      40      45
Thr Ile Pro His Ala Gly Ile Val Ile Ser Asp Thr His Leu Asp Thr
      50      55      60
Pro Arg Ser Ile Asn Thr Thr Ser Thr Ile Gly Met
      65      70      75

```

&lt;210&gt; 2399

&lt;211&gt; 344

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2399

```

acgcgtcatg cttcacgaaa cgggtcacgc gcttcattac caagcagctg gcaaacacaa
60
cttgatatttc gagcgggttg cgccagtcga gatcatggag ttcgtggcct actgcttgca
120
gtttctgacg atcgagcgcc tggccatgtc aggggaactt tcgggtaaag aacaggaact
180
agtcaaaccc tttgctggtc cggccaggct tggaggggtt cgaaaaccta caacgccaca
240
aaacgggttc agcactgggt ttataaacag cctaaaatcc cgacaagtaa agaactcgat
300
accgtatggc ttgagatgcg acacacgctc ggggtggatt gggtc
344

```

&lt;210&gt; 2400

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2400

```

Met Leu His Glu Thr Gly His Ala Leu His Tyr Gln Ala Ala Gly Lys
 1      5      10      15
His Asn Leu Tyr Phe Glu Arg Val Ala Pro Val Glu Ile Met Glu Phe
      20      25      30
Val Ala Tyr Cys Leu Gln Phe Leu Thr Ile Glu Arg Leu Ala Met Ser
      35      40      45
Gly Glu Leu Ser Gly Lys Glu Gln Leu Val Lys Pro Phe Ala Gly
      50      55      60
Pro Ala Arg Leu Gly Gly Val Arg Lys Pro Thr Thr Pro Gln Asn Gly
      65      70      75      80
Ser Ser Thr Gly Phe Ile Asn Ser Leu Lys Ser Arg Gln Val Lys Asn
      85      90      95
Ser Ile Pro Tyr Gly Leu Arg Cys Asp Thr Arg Ser Gly Trp Ile Gly
      100      105      110

```

&lt;210&gt; 2401

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2401

nntaccgagg taaaactcga tagcctcggt gtcaccgacc agatgcgctc tgggcgctgc  
 60  
 tggatgtttg ccgcgctcaa cgtattccgc caccgcgcgg ccaaggagct caacatcgat  
 120  
 gactttgagt ttctctttac ctacctgcag tacttcgaca aactagagcg cgccaacttc  
 180  
 gcgctcaacc aactgctgga tctcaccgaa gacggcaccg actgggatga ccgcgacgtg  
 240  
 gctacttccc tcgagctcac aggcgacgac ggcggtggt ggtcattttt caccaacctc  
 300  
 gtggacaagt acggcgagcgt cccggccgag gtcatgcctg aggtgcactc gtccggccac  
 360  
 accgaccaga tgaatcgca tatcgccacc atcatccgcc gcgccgcgca ccgtgcggtg  
 420  
 gaaggcgagg gggatcgcg gggcatcgtc aagcaagccc gccccgatat ccaacgcgt  
 479

<210> 2402

<211> 159

<212> PRT

<213> Homo sapiens

<400> 2402

Xaa	Thr	Glu	Val	Lys	Leu	Asp	Ser	Leu	Gly	Val	Thr	Asp	Gln	Met	Arg
1				5					10					15	
Ser	Gly	Arg	Cys	Trp	Met	Phe	Ala	Ala	Leu	Asn	Val	Phe	Arg	His	Arg
			20					25					30		
Ala	Ala	Lys	Glu	Leu	Asn	Ile	Asp	Asp	Phe	Glu	Phe	Ser	Phe	Thr	Tyr
		35				40						45			
Leu	Gln	Tyr	Phe	Asp	Lys	Leu	Glu	Arg	Ala	Asn	Phe	Ala	Leu	Asn	Gln
	50					55					60				
Leu	Leu	Asp	Leu	Thr	Glu	Asp	Gly	Thr	Asp	Trp	Asp	Asp	Arg	Asp	Val
65					70					75				80	
Ala	Thr	Ser	Leu	Glu	Leu	Thr	Gly	Asp	Asp	Gly	Gly	Trp	Trp	Ser	Phe
			85					90						95	
Phe	Thr	Asn	Leu	Val	Asp	Lys	Tyr	Gly	Ala	Val	Pro	Ala	Glu	Val	Met
			100					105					110		
Pro	Glu	Val	His	Ser	Ser	Gly	His	Thr	Asp	Gln	Met	Asn	Arg	Asp	Ile
		115					120						125		
Ala	Thr	Ile	Ile	Arg	Arg	Ala	Ala	His	Arg	Ala	Val	Glu	Gly	Glu	Gly
	130					135					140				
Asp	Arg	Gly	Gly	Ile	Val	Lys	Gln	Ala	Arg	Pro	Asp	Ile	Gln	Arg	
145					150					155					

<210> 2403

<211> 387

<212> DNA

<213> Homo sapiens

<400> 2403

ntcataaacg gcgataaccc gctggactcg tctgcggttc acccggaagc ctacccgctg  
 60  
 gtgcagcgta ttgccgccga gaccggccgt gatatccgtt cgctgatcgg tgacgcccg  
 120

ttcctcaagc gcctggaccc gaagaagtac accgacgaaa ccttcgggtgt gccgaccatc  
 180  
 accgacatcc tgcaagagct ggaaaaacct ggccgcgacc cgcgtcccga gttcaagacc  
 240  
 gccgagttcc aggacggtgt tgaagacctc aaggacctgc agccgggcat gatcctcgaa  
 300  
 ggcggtgtca ccaacgtgac caactttggc gcctttgtgg atatcggcgt gcacaggac  
 360  
 ggtttggtgc acatctctgc actttcg  
 387

<210> 2404

<211> 129

<212> PRT

<213> Homo sapiens

<400> 2404

Xaa	Met	Asn	Gly	Asp	Asn	Pro	Leu	Asp	Ser	Ser	Ala	Val	His	Pro	Glu
1				5					10					15	
Ala	Tyr	Pro	Leu	Val	Gln	Arg	Ile	Ala	Ala	Glu	Thr	Gly	Arg	Asp	Ile
			20					25					30		
Arg	Ser	Leu	Ile	Gly	Asp	Ala	Ala	Phe	Leu	Lys	Arg	Leu	Asp	Pro	Lys
		35				40						45			
Lys	Tyr	Thr	Asp	Glu	Thr	Phe	Gly	Val	Pro	Thr	Ile	Thr	Asp	Ile	Leu
	50					55					60				
Gln	Glu	Leu	Glu	Lys	Pro	Gly	Arg	Asp	Pro	Arg	Pro	Glu	Phe	Lys	Thr
65				70					75					80	
Ala	Glu	Phe	Gln	Asp	Gly	Val	Glu	Asp	Leu	Lys	Asp	Leu	Gln	Pro	Gly
			85					90					95		
Met	Ile	Leu	Glu	Gly	Val	Val	Thr	Asn	Val	Thr	Asn	Phe	Gly	Ala	Phe
		100					105					110			
Val	Asp	Ile	Gly	Val	His	Gln	Asp	Gly	Leu	Val	His	Ile	Ser	Ala	Leu
		115				120					125				

Ser

<210> 2405

<211> 859

<212> DNA

<213> Homo sapiens

<400> 2405

ttgcaagtaa catcaaaagt catctacaga agcaaaagac aaaaaggccc ctccacctgc  
 60  
 aaattaaatg gaataatttg ctttatgaga agctcaccat tggggtcatt cttatttttt  
 120  
 ctactccac atttactac aaaccaagga aagctccctc atggaccgac atctggtgag  
 180  
 ccttcacttc tccctggca atgcctggcc acctgacacc tggcctccct cctctttcca  
 240  
 gcaatcctgg taccaacgaa tggctcacca ccaccaccc caatgcccag accgcagacc  
 300  
 tgcatcctc ccatctcaca gcccctaatc caaacgtta ttcattctac ctccatcct  
 360

actcctcacg aattttcttcc accgtagact ctggttaatt ggactgactg aagcccaggg  
 420  
 gtcagtttct gtcctaagag cgctccaggt ggctgcaccc tgtgcccaga gccaggcccc  
 480  
 ctgctatagg ctgctgcac tccccctgca ggtgctgggg acaccgcaac cctcctcctg  
 540  
 gggacaccta cttgcctttg caggccctcg ggggtcactt ctcccaggaa gccgcctctg  
 600  
 ggtgaggtaa tatccctcta tcacagcatt ggccacacca cattgcaaac gctgctgggg  
 660  
 tccactgtct tcaccaatta caccatgagc tccacagact ccaggaccat ggcttctacc  
 720  
 tctcagttcc cagtgttagc tatggggccc agcacacagg gaacagcagt tcaattaccc  
 780  
 agttcactga agggcagacc tgggatcata caggagagcaa ggaagcttga gccccctcag  
 840  
 gagaagggga agaacgcgt  
 859

<210> 2406

<211> 149

<212> PRT

<213> Homo sapiens

<400> 2406

Met	Asp	Arg	His	Leu	Val	Ser	Leu	His	Leu	Ser	Pro	Gly	Asn	Ala	Trp
1				5					10					15	
Pro	Pro	Asp	Thr	Trp	Pro	Pro	Ser	Ser	Phe	Gln	Gln	Ser	Trp	Tyr	Gln
			20					25					30		
Arg	Met	Ala	His	His	His	Pro	Pro	Gln	Cys	Pro	Asp	Arg	Arg	Pro	Ala
		35					40				45				
Phe	Leu	Pro	Ser	His	Ser	Pro	Lys	Ser	Lys	Pro	Leu	Phe	Ile	Leu	Pro
	50					55				60					
Pro	Ile	Leu	Leu	Leu	Thr	Asn	Phe	Phe	His	Arg	Arg	Leu	Trp	Leu	Ile
65					70				75					80	
Gly	Leu	Thr	Glu	Ala	Gln	Gly	Ser	Val	Ser	Val	Leu	Arg	Ala	Leu	Gln
			85					90					95		
Val	Ala	Ala	Pro	Cys	Ala	Gln	Ser	Gln	Ala	Pro	Cys	Tyr	Arg	Leu	Ala
		100						105					110		
Ala	Leu	Pro	Leu	Gln	Val	Leu	Gly	Thr	Pro	Gln	Pro	Ser	Ser	Trp	Gly
		115					120					125			
His	Leu	Leu	Ala	Phe	Ala	Gly	Pro	Arg	Gly	Ser	Leu	Leu	Pro	Gly	Ser
	130					135					140				
Arg	Leu	Trp	Val	Arg											
145															

<210> 2407

<211> 303

<212> DNA

<213> Homo sapiens

<400> 2407

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gtattcatcg agcaaggcca gcgacgtatc ccggtgcagt acgccaagcg gatggtgggg  
 120  
 cgccgaatgt ttggtggctc gacgacgtac attccgctca aggtaaacca atctggcggt  
 180  
 atccccgtca tctttgcctc gtcgatcctg taccttcggg tgctctacgc aactttccgg  
 240  
 ccgcagacgt ccgcggcaaa gtggatcggg cactacttca cgcgcggtga ccatccgggtg  
 300  
 tac  
 303

<210> 2408

<211> 101

<212> PRT

<213> Homo sapiens

<400> 2408

Xaa	Ala	Trp	Phe	Ile	Phe	Ser	Met	Val	Ile	Ala	Ile	Gly	Leu	Ala	Val
1			5					10					15		
Met	Ala	Ala	Val	Val	Phe	Ile	Glu	Gln	Gly	Gln	Arg	Arg	Ile	Pro	Val
		20					25					30			
Gln	Tyr	Ala	Lys	Arg	Met	Val	Gly	Arg	Arg	Met	Phe	Gly	Gly	Ser	Thr
	35					40					45				
Thr	Tyr	Ile	Pro	Leu	Lys	Val	Asn	Gln	Ser	Gly	Val	Ile	Pro	Val	Ile
	50				55					60					
Phe	Ala	Ser	Ser	Ile	Leu	Tyr	Leu	Pro	Val	Leu	Tyr	Ala	Thr	Phe	Arg
65				70				75					80		
Pro	Gln	Thr	Ser	Ala	Ala	Lys	Trp	Ile	Gly	His	Tyr	Phe	Thr	Arg	Gly
			85					90					95		
Asp	His	Pro	Val	Tyr											
			100												

<210> 2409

<211> 322

<212> DNA

<213> Homo sapiens

<400> 2409

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 120  
 cttccggcca aatgaccctc cctaggctac caagaccctg gcctaagggg agccgaggtc  
 180  
 tcggcccgac tgcagacgcc cgcaccctga ctccagatgc ctccgaggca tccaggtggg  
 240  
 ccctgagggg cctgctgtgg ctttgttctt gttggctggg ctgggggtct gacctgtga  
 300  
 gggacatgag tgtcagtgtg gg  
 322

<210> 2410

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2410

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Met Val Ser Ser Pro His Cys Val Ser Pro Glu Ser Asn Trp Arg Pro
 1           5           10           15
Ser Asp Thr Thr Ser Arg Pro Asn Arg Arg Gly Ser Arg Asn Ser Asp
           20           25           30
Cys Gly Asn Cys Leu Gln Phe Ser Ser Gly Gln Met Thr Leu Pro Arg
           35           40           45
Leu Pro Arg Pro Trp Pro Lys Gly Ser Arg Gly Leu Gly Pro Thr Ala
           50           55           60
Asp Ala Arg Thr Leu Thr Pro Asp Ala Ser Glu Ala Ser Arg Trp Ala
65           70           75           80
Leu Arg Gly Leu Leu Trp Leu Cys Ser Cys Trp Leu Gly Trp Gly Ser
           85           90           95
Asp Leu Val Arg Asp Met Ser Val Ser Val
           100           105

```

<210> 2411

<211> 371

<212> DNA

<213> Homo sapiens

<400> 2411

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gggtctgcgg cagacagggg gacagagggg gctgtgagag ccctgaggct gagtggcttt
120
ctggggaagc accatcccta gggacctccg cgttcgggtca gtggccgctg ctgtcgggtg
180
gcagagcaga ggctggggcg agagtgggtc gcaggcctgc tgggtggcagc ttgtgcagga
240
agggaggatg gaggttggct tgtggctggc aagaggggtg catgcacgtc gctgaaaggg
300
aggcctgggc ccgaggcctg ggtgtgggga cgctgagga gactgtacag tgtggagtcg
360
ggggggctgc g
371

```

<210> 2412

<211> 123

<212> PRT

<213> Homo sapiens

<400> 2412

```

Met Gly Trp Val Leu Glu Thr Arg Asp Gln Ala Gly Pro Ala Pro Gly
 1           5           10           15
Ala His Ser Arg Val Cys Gly Arg Gln Gly Asp Arg Gly Ser Cys Glu
           20           25           30
Ser Pro Glu Ala Glu Trp Leu Ser Gly Glu Ala Pro Ser Leu Gly Thr
           35           40           45
Ser Ala Phe Gly Gln Trp Pro Leu Leu Ser Val Cys Arg Ala Glu Ala
           50           55           60
Gly Ala Arg Val Val Ser Arg Pro Ala Gly Gly Ser Leu Cys Arg Lys

```



65                      70                      75                      80  
 Gly Gly Trp Arg Leu Ala Cys Gly Trp Gln Glu Gly Gly Met His Val  
                                  85                      90                      95  
 Ala Glu Arg Gln Ala Trp Ala Arg Gly Leu Gly Val Gly Thr Pro Glu  
                                  100                      105                      110  
 Glu Thr Val Gln Cys Gly Val Gly Gly Ala Ala  
                                  115                      120

<210> 2413  
 <211> 784  
 <212> DNA  
 <213> Homo sapiens

<400> 2413  
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 gtggctggat ttaggggtgca tataaaggca gtgaggctgg agaagtattc taggtctgct  
 120  
 taggctcact gaggaattgg gggttcttcc gaagagcatg gagcccttgg aggacctcca  
 180  
 cagcaggcag agagacggca gcctcctggg atctgattgc ccagccccac ttacacaggc  
 240  
 ggctgagggtg agctcttccc atggagtgc tcttctctga tcagcctgag gagagcaggg  
 300  
 ccccaccatc ctgcacctgg tgcagaaaaa ccctgtgaag ctgcactaca gaaagacacc  
 360  
 accaggtggc aggcttggag attgcatgga ggccccgcc cccccaacca attctttgat  
 420  
 aatagcacag tgttgaagag agggggccat aaaagactga atccctgttc atgccaggct  
 480  
 ggctctgccc aacatatatg agactgcaag ttctgccact gtgggctgtg taccacaag  
 540  
 ccacaggtcc ctctgaacct gtgaatcagg tcttggggagc tattcgagca ggctggattt  
 600  
 tctctctgac ctggggggac ctgagagtaa gttacagact tcatgaccct tcaccccaaa  
 660  
 acatttgagt atgtatcacc taagaacaag ggcattctcc tgtagaacca caatgcaatt  
 720  
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 780  
 gcgt  
 784

<210> 2414  
 <211> 137  
 <212> PRT  
 <213> Homo sapiens

<400> 2414  
 Met Lys Ser Val Thr Tyr Ser Gln Val Pro Arg Gly Arg Gly Glu Asn  
 1                      5                      10                      15  
 Pro Ala Cys Ser Asn Ser Ser Gln Asp Leu Ile His Arg Phe Arg Gly  
                                  20                      25                      30  
 Thr Cys Gly Leu Trp Val His Ser Pro Gln Trp Gln Asn Leu Gln Ser

```

      35              40              45
His Ile Cys Trp Ala Glu Pro Ala Trp His Glu Gln Gly Phe Ser Leu
      50              55              60
Leu Trp Pro Pro Leu Phe Asn Thr Val Leu Leu Ser Lys Asn Trp Leu
65              70              75              80
Gly Gly Ala Gly Pro Pro Cys Asn Leu Gln Ala Cys His Leu Val Val
      85              90              95
Ser Phe Cys Ser Ala Ala Ser Gln Gly Phe Ser Ala Pro Gly Ala Gly
      100              105              110
Trp Trp Gly Pro Ala Leu Leu Arg Leu Ile Arg Lys Asp Ala Leu His
      115              120              125
Gly Lys Ser Ser Pro Gln Pro Pro Val
      130              135

```

&lt;210&gt; 2415

&lt;211&gt; 2164

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2415

```

ctcgtgccag cgtcctcgcg ggtctgaatg gaagggtcga ggtcgtcgtc ggcgggcgagc
60
agatcctgaa gccagaactc caccccggcg ccgcgcgccat gcggcgggag aggtgcgggcg
120
ccccccaccc gcgtcgccgc catggagggtg ctgcggcgct ctteggtctt cgctgcgggag
180
atcatggagc cctttgatcg ctggcccaca gacaaggagc tgggtggcca ggctaaagca
240
ctaggccggg agtacgtgca cgcgcggctt ttgcgcgcgc gcctctcttg gagcgctcca
300
gagcgtgcct cgctgcccc tggaggagcg ctggctgagg tgtgcgcggg gctgctgcgc
360
ctgggcatg agctggagat gatccggccc agcgtctacc gcaacgtggc gcgtcagctg
420
cacatctccc tgcagtctga gcctgtggtg accgatgcgt tcttggcgtt ggctggccac
480
atcttctctg caggcatcac gtggggcaag gtggtgtccc tgtatgcggg ggccgcgggg
540
ctggccgtgg actgtgtgag gcaggcccag cctgccatgg tccacgcctt cgtggactgc
600
ctgggggagt tcgtgcgcaa gacctggca acctggctgc ggagacgcgg cggtaggact
660
gatgtcctca agtgtgtggt cagcacagac cctggcctcc gctcccactg gctggtggct
720
gcactctgca gcttcggccg ctctctgaag getgccttct tcgtgctgct gccagagaga
780
tgagctgccc acctggcagt ggccgcagcc tggccctctg ggcccaacgc aggaggccct
840
cagcaccgga acacatcttc ctctcccca cccgagcctg gagcactcta acctcgga
900
ccccctaagc cccgttcttc cgcagacca ggccctccgg aagggtgagt ggggaggggc
960
tttctgagc ctggagctgg gctttggggc agcctgcgac cctcccgcgt tgtgtccctt
1020

```

ctctgtgat ctctgtgttt tcccttttct ttctggggcc aggaagtcag ggtcaactcc  
 1080  
 caggcctcag gtgaaggggc ccagaacacc tgctctcacc tgagccccag gtgaaggggc  
 1140  
 ccgggaacac ctgctctcac ctgagcccca ggtgaagggg cccgggaaca cctgctctca  
 1200  
 cctgagcccc tggatgaagg gcccgggaaca cctgctctca cctgagcccc aggtgaaggg  
 1260  
 gcccgggaaca cctgctctca cctgagcccc aggtgaaggg gcccgggaaca cttgctctca  
 1320  
 cctgagcccc aggtgaaggg gcccgggaac acctctcacc tgaacccggg ggtcccatcc  
 1380  
 caggaagaag ggccatctca ggacatgagt cctcaggggc cctgcacatt caatctgaag  
 1440  
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 1560  
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 1620  
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 1680  
 cagtggaggg tgagggtgac cccatctgct atttttgtgc tcacccctcat acaaccattt  
 1740  
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 1800  
 gtgccccac acacagcctt cccttgacgc ctacatttct aggcacatgt gaggcattct  
 1860  
 tcttgagacc ccgagccagc cctgtccctc cccagtgcag catggcactc aggagataca  
 1920  
 ggctggacat ggggcagtcg ttctggggag gcctggccta gcagccaccc acctgagccc  
 1980  
 tcccgccag gcttcgtgct ggggtgggccc atgtgccagg acaggagggt cccggcgga  
 2040  
 agccagcccc ggactcatcg tgacattgag atcccactgg agggtagggg tggtaataaa  
 2100  
 cttctccaaa cgataaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  
 2160  
 aaaa  
 2164

<210> 2416

<211> 213

<212> PRT

<213> Homo sapiens

<400> 2416

Met	Glu	Val	Leu	Arg	Arg	Ser	Ser	Val	Phe	Ala	Ala	Glu	Ile	Met	Asp
1				5				10						15	
Ala	Phe	Asp	Arg	Trp	Pro	Thr	Asp	Lys	Glu	Leu	Val	Ala	Gln	Ala	Lys
			20				25						30		
Ala	Leu	Gly	Arg	Glu	Tyr	Val	His	Ala	Arg	Leu	Leu	Arg	Ala	Gly	Leu
		35				40						45			
Ser	Trp	Ser	Ala	Pro	Glu	Arg	Ala	Ser	Pro	Ala	Pro	Gly	Gly	Arg	Leu

```

      50              55              60
Ala Glu Val Cys Ala Val Leu Leu Arg Leu Gly Asp Glu Leu Glu Met
65              70              75              80
Ile Arg Pro Ser Val Tyr Arg Asn Val Ala Arg Gln Leu His Ile Ser
      85              90              95
Leu Gln Ser Glu Pro Val Val Thr Asp Ala Phe Leu Ala Val Ala Gly
      100              105              110
His Ile Phe Ser Ala Gly Ile Thr Trp Gly Lys Val Val Ser Leu Tyr
      115              120              125
Ala Val Ala Ala Gly Leu Ala Val Asp Cys Val Arg Gln Ala Gln Pro
      130              135              140
Ala Met Val His Ala Leu Val Asp Cys Leu Gly Glu Phe Val Arg Lys
145              150              155              160
Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly Trp Thr Asp Val Leu
      165              170              175
Lys Cys Val Val Ser Thr Asp Pro Gly Leu Arg Ser His Trp Leu Val
      180              185              190
Ala Ala Leu Cys Ser Phe Gly Arg Phe Leu Lys Ala Ala Phe Phe Val
      195              200              205
Leu Leu Pro Glu Arg
210

```

&lt;210&gt; 2417

&lt;211&gt; 615

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2417

```

nnagatcttt ggaatgggca gaactactaa atacagttaa tgcaccaaca agggtaagta
60
aagctgattt gattttcata ttgatacttc aatagttaag tgaaggacta gttattgctc
120
cagttgtag ttttcacact ttaaaaagg ctttcaatta taaaatcttt ctccattatt
180
acgttttttc acaactgtga tccacgccac agttgcaa atcaacata gaaaaattaa
240
ataacataat tgatgaaaag ttagtttttc acaaaaatac gaaaaatttc atcacctaga
300
gaggaaaatg ttatgacaac ctatttcgat aaaattgaaa aaatctcctt tgaggagaga
360
aaatccacaa atccttttgc tttcaaact tatgatgcta atcaagtaat tttaggtaaa
420
actatggctg aacatttacg cttaacggtg tgttattggc ataccttttg ctggaatggg
480
aatgatatgt ttgggctagg ttctttggaa cgaagtggc agaaaaattc aaatttgctt
540
gctggcgtag aacaaaaagc cgatattgct ttgagtttt tgaataagtt aggcgtgcct
600
tattattggt ttcatt
615

```

&lt;210&gt; 2418

&lt;211&gt; 101

&lt;212&gt; PRT

<213> Homo sapiens

<400> 2418

```

Met Thr Thr Tyr Phe Asp Lys Ile Glu Lys Ile Ser Phe Glu Gly Glu
 1           5           10           15
Lys Ser Thr Asn Pro Phe Ala Phe Lys His Tyr Asp Ala Asn Gln Val
          20           25           30
Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Thr Val Cys Tyr
          35           40           45
Trp His Thr Phe Cys Trp Asn Gly Asn Asp Met Phe Gly Leu Gly Ser
          50           55           60
Leu Glu Arg Ser Trp Gln Lys Asn Ser Asn Leu Leu Ala Gly Ala Glu
65           70           75           80
Gln Lys Ala Asp Ile Ala Phe Glu Phe Leu Asn Lys Leu Gly Val Pro
          85           90           95
Tyr Tyr Cys Phe His
          100

```

<210> 2419

<211> 318

<212> DNA

<213> Homo sapiens

<400> 2419

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aaattttcag aagtcctggt gttgcgcggt caaacagggg ccgaggaggg acgaccgcct
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ccccgtgacg ctgcttcttc ttcttgccctg cagctgaggg gtctgttttg tgcgcttcc
120
gtccttcct cactacaca gggggcagct tagcctctgg gatgggagtg gcttcataca
180
tgagacacat gcccgagtcg aggtagatgt cgctgtcgtc ctgcggcggg gtgggtgggg
240
tccagaacgg catgacttct gtctgcccac cgacatcttc gtagacatac tccatgttgt
300
aggcatcccc tcacgcgt
318

```

<210> 2420

<211> 98

<212> PRT

<213> Homo sapiens

<400> 2420

```

Met Glu Tyr Val Tyr Glu Asp Val Asp Gly Gln Thr Glu Val Met Pro
 1           5           10           15
Phe Trp Thr Pro Pro Thr Pro Pro Gln Asp Asp Ser Asp Ile Tyr Leu
          20           25           30
Asp Ser Gly Met Cys Leu Met Tyr Glu Ala Thr Pro Ile Pro Glu Ala
          35           40           45
Lys Leu Pro Pro Val Tyr Val Arg Lys Glu Arg Lys Arg His Lys Thr
          50           55           60
Asp Pro Ser Ala Ala Gly Arg Lys Lys Lys Gln Arg His Gly Glu Ala
65           70           75           80
Val Val Pro Pro Arg Ser Leu Phe Asp Arg Ala Thr Pro Gly Leu Leu

```

1751

gaatgcgag actgcaagtc aaagggctct cgatgggcaa gtgtgaatct aggtatcttt  
 180  
 atatgcatga catgttctgg cattcataga agcctggggg tgcacatatc taaggttaaga  
 240  
 tctgccaccc tggatacatg gctgccagag caagttgcat ttattcaatc aatgggaaac  
 300  
 gaaaaagcaa atagctattg ggaagcagag ctgcctccta actacgatag ggttgggaata  
 360  
 gagaatttga t  
 371

<210> 2424

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2424

Met	Asn	Glu	Lys	Ala	Ser	Val	Ser	Lys	Glu	Leu	Asn	Ala	Lys	His	Lys
1				5					10					15	
Lys	Ile	Leu	Glu	Gly	Leu	Leu	Arg	His	Pro	Glu	Asn	Arg	Glu	Cys	Ala
		20					25					30			
Asp	Cys	Lys	Ser	Lys	Gly	Pro	Arg	Trp	Ala	Ser	Val	Asn	Leu	Gly	Ile
	35					40				45					
Phe	Ile	Cys	Met	Thr	Cys	Ser	Gly	Ile	His	Arg	Ser	Leu	Gly	Val	His
	50				55				60						
Ile	Ser	Lys	Val	Arg	Ser	Ala	Thr	Leu	Asp	Thr	Trp	Leu	Pro	Glu	Gln
65				70				75					80		
Val	Ala	Phe	Ile	Gln	Ser	Met	Gly	Asn	Glu	Lys	Ala	Asn	Ser	Tyr	Trp
			85				90					95			
Glu	Ala	Glu	Leu	Pro	Pro	Asn	Tyr	Asp	Arg	Val	Gly	Ile	Glu	Asn	Leu
			100				105					110			

<210> 2425

<211> 411

<212> DNA

<213> Homo sapiens

<400> 2425

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 120  
 acctcccggc ctgcacgggg gtctgggttc accgcccacg cccagcccga ggaacgcccc  
 180  
 cgtgcaagg aagccggcat gaacgactgc ctgttcaagc ccatcagcct gaccaccctc  
 240  
 aaccagaaac tcgccgacgt cacgccgcgc ccgctccga gccaggccgc cttcagcctc  
 300  
 gacggcctgc acgcccagc cgggggagag ccgctgctga tgcgtcgctt gatcgacgag  
 360  
 ctgctgagca gttgccaggc ggcccgcgag gcaactgctc gactgcccac c  
 411

<210> 2426

<211> 137  
 <212> PRT  
 <213> Homo sapiens

<400> 2426  
 Thr Gly Leu Gln Ala Trp Lys Asp Gly His Phe Asp Leu Val Ile Val  
 1 5 10 15  
 Asp Cys Asn Met Pro Val Leu Asn Gly Tyr Glu Met Thr Arg Arg Leu  
 20 25 30  
 Arg Glu His Glu Ala Xaa Ala Met Thr Ser Arg Pro Ala Arg Gly Phe  
 35 40 45  
 Gly Phe Thr Ala His Ala Gln Pro Glu Glu Arg Pro Arg Cys Lys Glu  
 50 55 60  
 Ala Gly Met Asn Asp Cys Leu Phe Lys Pro Ile Ser Leu Thr Thr Leu  
 65 70 75 80  
 Asn Gln Lys Leu Ala Asp Val Thr Pro Arg Pro Arg Pro Ser Gln Ala  
 85 90 95  
 Ala Phe Ser Leu Asp Gly Leu His Ala Leu Thr Gly Gly Glu Pro Leu  
 100 105 110  
 Leu Met Arg Arg Leu Ile Asp Glu Leu Leu Ser Ser Cys Gln Ala Ala  
 115 120 125  
 Arg Glu Ala Leu Leu Gly Leu Pro Ile  
 130 135

<210> 2427  
 <211> 293  
 <212> DNA  
 <213> Homo sapiens

<400> 2427  
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 tggagcgtaa aatgttgcag agcccagcta gaagccagga ggagcagaca ccctgctgat  
 120  
 ggagcccaac aagaaagatg ttgtgtccct cctggtgagc gctgtcccag tgcacccgat  
 180  
 aatggcgaag aaaatgtgcc tctttcagga aaagtatagg aaatgagaga agactgtgac  
 240  
 aactcatgac ctgcatcctt aatatccagt gacttcatct ccccttcacg cgt  
 293

<210> 2428  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<400> 2428  
 His Asn Lys Gly Leu Gly Ile Leu Val Pro Cys Ala Ile Xaa Ala Ala  
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 Phe Leu Leu Ile Trp Ser Val Lys Cys Cys Arg Ala Gln Leu Glu Ala  
 20 25 30  
 Arg Arg Ser Arg His Pro Ala Asp Gly Ala Gln Gln Glu Arg Cys Cys  
 35 40 45  
 Val Pro Pro Gly Glu Arg Cys Pro Ser Ala Pro Asp Asn Gly Glu Glu



50 55 60  
 Asn Val Pro Leu Ser Gly Lys Val  
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<210> 2429  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<400> 2429  
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 gatgtcctgc tcaatgggggt agagacgtcg accggtcgcg agccgggtgc gcttgctttg  
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 ttggctgagc gcgcccgcga gatgtcgtat gacctcactg acctcgtctgc ttcggtcgtc  
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 428

<210> 2430  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 2430  
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 35 40 45  
 Thr Ser Thr Gly Pro Gln Pro Gly Ala Leu Ala Leu Leu Glu Gln Ala  
 50 55 60  
 Val His Glu Leu Asp Gly Thr Gly Asp Ala Asp Pro Arg Ala Ala Glu  
 65 70 75 80  
 Leu Ala Glu Arg Ala Arg Gln Met Ser Tyr Asp Leu Thr Asp Leu Ala  
 85 90 95  
 Ala Ser Val Ala Gly His Ala Ala Arg Ala Glu Ala Asp Pro Gln Arg  
 100 105 110  
 Leu Glu Glu Leu Gly Gly Arg Leu Ala Ala Ile Gln Arg Leu Leu Arg  
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 Ala Arg Thr Thr Thr Leu Asp Asp Leu Leu Asp Ser Thr Ala  
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<210> 2431  
 <211> 409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2431

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aatggcgagg taacaatttc tggggcaaaa aatgccgcat taccaatcct atttgctact
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240
actatcgagt tgtaaaaga gctgggtgct actgctactc agactcaaca ctgctgcat
300
attaatgcga aagaagttaa gaactatact gcttcttatg aattagttag aagtatgcgt
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gcttcaattt tggcattagg tccattgggt gctcgggttc gtgaagctt
409

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&lt;210&gt; 2432

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2432

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Met Gly Gln Phe Ile Ile Gln Gly Gly Cys Gln Leu Asn Gly Glu Val
 1           5           10          15
Thr Ile Ser Gly Ala Lys Asn Ala Ala Leu Pro Ile Leu Phe Ala Thr
 20          25          30
Leu Leu Ser Glu Gly Asp Ile Asn Leu Ser Asn Val Pro Leu Leu Lys
 35          40          45
Asp Ile Ala Thr Thr Ile Glu Leu Leu Lys Glu Leu Gly Ala Thr Ala
 50          55          60
Thr Gln Thr Gln His Cys Val His Ile Asn Ala Lys Glu Val Lys Asn
 65          70          75          80
Tyr Thr Ala Ser Tyr Glu Leu Val Arg Ser Met Arg Ala Ser Ile Leu
 85          90          95
Ala Leu Gly Pro Leu Val Ala Arg Phe Gly Glu Ala
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&lt;210&gt; 2433

&lt;211&gt; 655

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2433

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120
gctctatgat gctcacgtaa caatgaaatc acggaatctc tctctcagaa catttccccg
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ttgtgaagca gcacgtgact ataatctttt cccagggtt cccctgaagt tcaagtgc
240

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<210> 2434

<211> 137

<212> PRT

<213> Homo sapiens

<400> 2434

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Cys	Ser	Glu	Thr	Val	Pro	Phe	Ala	Lys	Pro	Pro	Ser	Leu	Gly	Phe	Cys
			20					25				30			
Lys	Ser	Lys	Gly	Cys	Val	Trp	Asn	Thr	Ala	Val	Thr	Glu	Lys	Val	Leu
		35					40				45				
Phe	Ala	Gln	Ser	Ala	Arg	Pro	Leu	Leu	Leu	Ser	Leu	Met	Ser	Pro	Asp
	50				55					60					
Trp	Ala	Phe	Ile	Val	Pro	Cys	Thr	Glu	Ala	Ser	Leu	Ser	Pro	Arg	Ser
65				70				75					80		
Cys	Leu	Phe	Gly	Arg	Gly	Ser	Thr	Asn	Gly	Ser	Thr	Leu	Pro	Pro	Thr
			85					90					95		
Pro	Thr	Ala	Arg	Pro	Ala	Gly	Pro	Val	Val	Gln	Leu	Glu	Lys	Ala	Arg
			100				105					110			
Leu	Leu	Ser	Ser	Pro	Ala	Leu	Cys	Cys	Ala	Gly	Ala	Leu	His	Leu	Asn
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Phe	Arg	Gly	Lys	Pro	Gly	Lys	Arg	Leu							
	130					135									

<210> 2435

<211> 401

<212> DNA

<213> Homo sapiens

<400> 2435

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aaactcgttg cggagtttga gaagctcaat ctgggcaatg gtatggacga aggtattacc  
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 401

<210> 2436

<211> 133

<212> PRT

<213> Homo sapiens

<400> 2436

Lys Leu Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Thr Leu Leu Lys  
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 Ala Pro Phe Ile Val Phe Glu Asp Ala Asp Ile Asp Gln Ala Val Gln  
 35 40 45  
 Gly Ala Met Gly Ala Lys Met Arg Asn Ile Gly Glu Ala Cys Thr Ala  
 50 55 60  
 Ala Asn Arg Phe Leu Val His Glu Ser Val Ala Glu Glu Phe Ser Glu  
 65 70 75 80  
 Lys Leu Val Ala Glu Phe Glu Lys Leu Asn Leu Gly Asn Gly Met Asp  
 85 90 95  
 Glu Gly Ile Thr Cys Gly Pro Leu Val Glu Ser Lys Ala Leu Glu Ser  
 100 105 110  
 Ile Ala Ala Leu Val Asp Asp Ala Ala Glu Lys Gly Ala Thr Ile Ser  
 115 120 125  
 Thr Gly Gly Lys Arg  
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<210> 2437

<211> 449

<212> DNA

<213> Homo sapiens

<400> 2437

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 180  
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<210> 2438  
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 <212> PRT  
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<400> 2438  
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 35 40 45  
 Glu Met Pro Met Tyr Gly Phe Gly Pro Met Pro Gln Pro Asp Leu Arg  
 50 55 60  
 Asp Leu Arg Gly Ser Ala Pro Arg Pro Pro Leu His Ile Cys Asp Pro  
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 Thr His Phe His Pro Ser Ala Thr Phe Lys Phe Gln Ser Phe His Phe  
 85 90 95  
 Ile Ala Val

<210> 2439  
 <211> 4425  
 <212> DNA  
 <213> Homo sapiens

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<211> 1306

<212> PRT

<213> Homo sapiens

<400> 2440

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Thr	Asp	Asn	Ile	Lys	Lys	Thr	Leu	His	Lys	Phe	Cys	Gly	Pro	Ser	Pro
		20					25					30			
Val	Val	Phe	Ser	Asp	Val	Asn	Ser	Met	Tyr	Leu	Ser	Ser	Thr	Glu	Pro
	35					40					45				
Pro	Ala	Ala	Ala	Glu	Trp	Ala	Cys	Leu	Leu	Arg	Pro	Leu	Arg	Gly	Arg
	50				55					60					
Glu	Pro	Glu	Gly	Val	Trp	Asn	Leu	Leu	Ser	Ile	Val	Arg	Glu	Met	Phe
65				70				75						80	
Lys	Arg	Arg	Asp	Ser	Asn	Ala	Ala	Pro	Leu	Leu	Glu	Ile	Leu	Thr	Asp
			85			90					95				
Gln	Cys	Leu	Thr	Tyr	Glu	Gln	Ile	Thr	Gly	Trp	Trp	Tyr	Ser	Val	Arg
	100					105					110				
Thr	Ser	Ala	Ser	His	Ser	Ser	Ala	Ser	Gly	His	Thr	Gly	Arg	Ser	Asn
	115					120					125				
Gly	Gln	Ser	Glu	Val	Ala	Ala	His	Ala	Cys	Ala	Ser	Met	Cys	Asp	Glu
	130				135					140					
Met	Val	Thr	Leu	Trp	Arg	Leu	Ala	Val	Leu	Asp	Pro	Ala	Leu	Ser	Pro
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Gln	Arg	Arg	Arg	Glu	Leu	Cys	Thr	Gln	Leu	Arg	Gln	Trp	Gln	Leu	Lys
			165			170					175				
Val	Ile	Glu	Asn	Val	Lys	Arg	Gly	Gln	His	Lys	Lys	Thr	Leu	Glu	Arg
	180				185						190				
Leu	Phe	Pro	Gly	Phe	Arg	Pro	Ala	Val	Glu	Ala	Cys	Tyr	Phe	Asn	Trp
	195				200						205				
Glu	Glu	Ala	Tyr	Pro	Leu	Pro	Gly	Val	Thr	Tyr	Ser	Gly	Thr	Asp	Arg
	210				215						220				
Lys	Leu	Ala	Leu	Cys	Trp	Ala	Arg	Ala	Leu	Pro	Ser	Arg	Pro	Gly	Ala
225				230				235						240	
Ser	Arg	Ser	Gly	Gly	Leu	Glu	Glu	Ser	Arg	Asp	Arg	Pro	Arg	Pro	Leu
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Pro	Thr	Glu	Pro	Ala	Val	Arg	Pro	Lys	Glu	Pro	Gly	Thr	Lys	Arg	Lys



	260		265		270										
Gly	Leu	Gly	Glu	Gly	Val	Pro	Ser	Ser	Gln	Arg	Gly	Pro	Arg	Arg	Leu
	275						280				285				
Ser	Ala	Glu	Gly	Gly	Asp	Lys	Ala	Leu	His	Lys	Met	Gly	Pro	Gly	Gly
	290					295					300				
Gly	Lys	Ala	Lys	Ala	Leu	Gly	Gly	Ala	Gly	Ser	Gly	Ser	Lys	Gly	Ser
305					310					315				320	
Ala	Gly	Gly	Gly	Ser	Lys	Arg	Arg	Leu	Ser	Ser	Glu	Asp	Ser	Ser	Leu
				325					330					335	
Glu	Pro	Asp	Leu	Ala	Glu	Met	Ser	Leu	Asp	Asp	Ser	Ser	Leu	Ala	Leu
			340						345					350	
Gly	Ala	Glu	Ala	Ser	Thr	Phe	Gly	Gly	Phe	Pro	Glu	Ser	Pro	Pro	Pro
	355						360					365			
Cys	Pro	Leu	His	Gly	Gly	Ser	Arg	Gly	Pro	Ser	Thr	Phe	Leu	Pro	Glu
	370					375					380				
Pro	Pro	Asp	Thr	Tyr	Glu	Glu	Asp	Gly	Gly	Val	Tyr	Phe	Ser	Glu	Gly
385					390					395				400	
Pro	Glu	Pro	Pro	Thr	Ala	Ser	Val	Gly	Pro	Pro	Gly	Leu	Leu	Pro	Gly
				405					410					415	
Asp	Val	Cys	Thr	Gln	Asp	Asp	Leu	Pro	Ser	Thr	Asp	Glu	Ser	Gly	Asn
			420					425						430	
Gly	Leu	Pro	Lys	Thr	Lys	Glu	Ala	Ala	Pro	Ala	Val	Gly	Glu	Glu	Asp
	435						440					445			
Asp	Asp	Tyr	Gln	Ala	Tyr	Tyr	Leu	Asn	Ala	Gln	Asp	Gly	Ala	Gly	Gly
	450					455				460					
Glu	Glu	Glu	Lys	Ala	Glu	Gly	Gly	Ala	Gly	Glu	Glu	His	Asp	Leu	Phe
465					470					475				480	
Ala	Gly	Leu	Lys	Pro	Leu	Glu	Gln	Glu	Ser	Arg	Met	Glu	Val	Leu	Phe
				485					490					495	
Ala	Cys	Ala	Glu	Ala	Leu	His	Ala	His	Gly	Tyr	Ser	Ser	Glu	Ala	Ser
			500					505					510		
Arg	Leu	Thr	Val	Glu	Leu	Ala	Gln	Asp	Leu	Leu	Ala	Asn	Pro	Pro	Asp
	515						520					525			
Leu	Lys	Gly	Lys	Lys	Asn	Lys	Val	Ser	Thr	Ser	Arg	Gln	Thr	Trp	Val
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Ala	Thr	Asn	Thr	Leu	Ser	Lys	Ala	Ala	Phe	Leu	Leu	Thr	Val	Leu	Ser
545						550				555				560	
Glu	Arg	Pro	Glu	Arg	His	Asn	Leu	Ala	Phe	Arg	Val	Gly	Met	Phe	Ala
				565					570					575	
Leu	Glu	Leu	Gln	Arg	Pro	Pro	Ala	Ser	Thr	Lys	Ala	Leu	Glu	Val	Lys
			580					585					590		
Leu	Ala	Tyr	Gln	Glu	Ser	Glu	Val	Ala	Ala	Leu	Leu	Lys	Lys	Ile	Pro
	595						600					605			
Leu	Gly	Pro	Ser	Glu	Met	Ser	Thr	Met	Arg	Cys	Arg	Ala	Glu	Glu	Leu
	610					615					620				
Arg	Glu	Gly	Thr	Leu	Cys	Asp	Tyr	Arg	Pro	Val	Leu	Pro	Leu	Met	Leu
625					630					635				640	
Ala	Ser	Phe	Ile	Phe	Asp	Val	Leu	Cys	Ala	Pro	Val	Val	Ser	Pro	Thr
			645						650					655	
Gly	Ser	Arg	Pro	Pro	Ser	Arg	Asn	Trp	Asn	Ser	Glu	Thr	Pro	Gly	Asp
			660				665					670			
Glu	Glu	Leu	Gly	Phe	Glu	Ala	Ala	Val	Ala	Ala	Leu	Gly	Met	Lys	Thr
	675					680					685				
Thr	Val	Ser	Glu	Ala	Glu	His	Pro	Leu	Leu	Cys	Glu	Gly	Thr	Arg	Arg

690	695	700
Glu Lys Gly Asp Leu	Ala Leu Ala Leu Met Ile Thr Tyr Lys Asp Asp	
705	710	715 720
Gln Ala Lys Leu Lys Lys Ile Leu Asp Lys Leu Leu Asp Arg Glu Ser		
725	730	735
Gln Thr His Lys Pro Gln Thr Leu Ser Ser Phe Tyr Ser Ser Ser Arg		
740	745	750
Pro Thr Thr Ala Ser Gln Arg Ser Pro Ser Lys His Gly Gly Pro Ser		
755	760	765
Ala Pro Gly Ala Leu Gln Pro Leu Thr Ser Gly Ser Ala Gly Pro Ala		
770	775	780
Gln Pro Gly Ser Val Ala Gly Ala Gly Pro Gly Pro Thr Glu Gly Phe		
785	790	795 800
Thr Glu Lys Asn Val Pro Glu Ser Ser Pro His Ser Pro Cys Glu Gly		
805	810	815
Leu Pro Ser Glu Ala Ala Leu Thr Pro Arg Pro Glu Gly Lys Val Pro		
820	825	830
Ser Arg Leu Ala Leu Gly Ser Arg Gly Gly Tyr Asn Gly Arg Gly Trp		
835	840	845
Gly Ser Ser Gly Arg Pro Lys Lys Lys His Thr Gly Met Ala Ser Ile		
850	855	860
Asp Ser Ser Ala Pro Glu Thr Thr Ser Asp Ser Ser Pro Thr Leu Ser		
865	870	875 880
Arg Arg Pro Leu Arg Gly Gly Trp Ala Pro Thr Ser Trp Gly Arg Gly		
885	890	895
Gln Asp Ser Asp Ser Ile Ser Ser Ser Ser Asp Ser Leu Gly Ser		
900	905	910
Ser Ser Ser Ser Gly Ser Arg Arg Ala Ser Ala Ser Gly Gly Ala Arg		
915	920	925
Ala Lys Thr Val Glu Val Gly Arg Tyr Lys Gly Arg Arg Pro Glu Ser		
930	935	940
His Ala Pro His Val Pro Asn Gln Pro Ser Glu Ala Ala Ala His Phe		
945	950	955 960
Tyr Phe Glu Leu Ala Lys Thr Val Leu Ile Lys Ala Gly Gly Asn Ser		
965	970	975
Ser Thr Ser Ile Phe Thr His Pro Ser Ser Ser Gly Gly His Gln Gly		
980	985	990
Pro His Arg Asn Leu His Leu Cys Ala Phe Glu Ile Gly Leu Tyr Ala		
995	1000	1005
Leu Gly Leu His Asn Phe Val Ser Pro Asn Trp Leu Ser Arg Thr Tyr		
1010	1015	1020
Ser Ser His Val Ser Trp Ile Thr Gly Gln Ala Met Glu Ile Gly Ser		
1025	1030	1035 1040
Ala Ala Leu Thr Ile Leu Val Glu Cys Trp Asp Gly His Leu Thr Pro		
1045	1050	1055
Pro Glu Val Ala Ser Leu Ala Asp Arg Ala Ser Arg Ala Arg Asp Ser		
1060	1065	1070
Asn Met Val Arg Ala Ala Ala Glu Leu Ala Leu Ser Cys Leu Pro His		
1075	1080	1085
Ala His Ala Leu Asn Pro Asn Glu Ile Gln Arg Ala Leu Val Gln Cys		
1090	1095	1100
Lys Glu Gln Asp Asn Leu Met Leu Glu Lys Ala Cys Met Ala Val Glu		
1105	1110	1115 1120
Glu Ala Ala Lys Gly Gly Gly Val Tyr Pro Glu Val Leu Phe Glu Val		

1125 1130 1135  
 Ala His Gln Trp Phe Trp Leu Tyr Glu Gln Thr Ala Gly Gly Ser Ser  
 1140 1145 1150  
 Thr Ala Arg Glu Gly Ala Thr Ser Cys Ser Ala Ser Gly Ile Arg Ala  
 1155 1160 1165  
 Gly Gly Glu Ala Gly Arg Gly Met Pro Glu Gly Arg Gly Gly Pro Gly  
 1170 1175 1180  
 Thr Glu Pro Val Thr Val Ala Ala Ala Val Thr Ala Ala Ala Thr  
 1185 1190 1195 1200  
 Val Val Pro Val Ile Ser Val Gly Ser Ser Leu Tyr Pro Gly Pro Gly  
 1205 1210 1215  
 Leu Gly His Gly His Ser Pro Gly Leu His Pro Tyr Thr Ala Leu Gln  
 1220 1225 1230  
 Pro His Leu Pro Cys Ser Pro Gln Tyr Leu Thr His Pro Ala His Pro  
 1235 1240 1245  
 Ala His Pro Met Pro His Met Pro Arg Pro Ala Val Phe Pro Val Pro  
 1250 1255 1260  
 Ser Ser Ala Tyr Pro Gln Val Arg Pro Val Phe Cys Trp Gly Val Arg  
 1265 1270 1275 1280  
 His Gly Lys Ile Leu Gly Ile His Arg Gly Leu Glu Trp Val Leu Trp  
 1285 1290 1295  
 Glu Tyr Asn Trp Ser Val Gly Glu Ser Trp  
 1300 1305

&lt;210&gt; 2441

&lt;211&gt; 2244

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2441

nacgcgtgtg tgtctgcatg catccatgtg tctgtacatg tatgtctcca tgtgtggtgt  
 60  
 ggaggacaca gaaggatgga gggaaaggca ccactcacag aggcggcgct ggagaatttt  
 120  
 ccatttggtta ttttgggttt ggtgaacatg cactttgcgt catgcaaatac aggtttctaa  
 180  
 acattaacaa ccggagagaa atgacatttt ggggccgccc gtgactcttg cgtgcctctg  
 240  
 ctgccccctg gtggcagccc cgagtcactt ccagcagggc cccccaccc caagggccca  
 300  
 gcctcgggca ggaaggttac aaagcccccg ccgtggttct gccacgaggt ctcttgga  
 360  
 tgaggggaac agcacagcga cgtccttgcg tcctaaatgc atcccctggt ggccgttttt  
 420  
 cgccacacag gcttggcaaa atctctgcgt cactgagcag cattttaacc tcttgaatga  
 480  
 gatgcctccg accttttgga tctcttttct gcacctctca ggggacaggt cccgtctgta  
 540  
 cggcgctgcc tacgagaaac ccaagttcat tactgcagcc aaaggaaagg tgcaggcggt  
 600  
 gggaggctcc tgcaaggtga tgcgtctggc cataagtcct actgccttct cccacctgct  
 660  
 ggccctgtgc cagcagttcc ggaagcagac ccaggcccag gtgtacagtg aggacatggc  
 720

cctgaacata ggctcggaa cagaaggcct gcaggtggaa gagaaggagc gccctgtgca  
780  
gaggctcagt agcgtcctgg ggcccctgga ggagcttctg cagccgctat tccccctgct  
840  
cagcctctcc aaggccagag tgcagacacc tgcggttgtt gccgattcag ggaagtcgaa  
900  
gggcaaagac aaggagagga aaacgtccac aggacaacac agcacagtcc agcctgaggt  
960  
tgccgataag atagtcctgg tcacagacag acatctcctg gagctgccac tggaaggtct  
1020  
ctctgtgttc gatgaaggga caatttcctc tgtgtcacga gaattttctc ttcaaagtct  
1080  
gtggaatcgc ctccataaag aagagacaga aggtggcgtg aaaaaggagg gaagaagcag  
1140  
agaccccaaa aagagaagcc tagcgaagaa gggcaggaag ggcagcatcc cccggaccat  
1200  
ccccctgac tgcattcatag tcgactcaga caatttcaag ttcgtcgtgg acccatacga  
1260  
ggaggccag ggcccagaaa tgctaactcc tgtctccatc acccaagaca ttttgaaag  
1320  
attccaagac acattcacgt cgcgatgggc gggacatctg ggaagcaagc actttcccag  
1380  
ccaggccag tgggagcagg ccctgggcag ctgcagcggc ttcttcttct atggaatgga  
1440  
gagcttctg tcccatatat tagtggagag attggtcgcc atgaacttgc aagagtgcc  
1500  
ggtggcagtc ctgctggacc tggcacggc ctaccagagc ttgaagaggc acatggagag  
1560  
cgtggagcac aggagatctg ttggccgttg ggaagccaat tggagaaacg gtgcgtctcc  
1620  
ttcagaagat gagtggcgac gaggcgtga accaaggcga ggcttctcag accttgaagg  
1680  
acaagctgct gctgctcaa agctccgagc tccttccac cacgctcaac ttggtcctgt  
1740  
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1800  
tggggcccca gcaattgcct ctgcccttgg ctctgcccct ctgccaacct atccccacct  
1860  
cccgtctcc atccccagct ccagctcgc tctcccctc ctgggcctct cccagccct  
1920  
tggtgcagcc tcagccaggg acctcccc agcgacttcc cgcaaggcag ccgcctggac  
1980  
ctcagactct gcctgcctgt gtgcgccatg gggctctcgt cggggctgga gctgcgtctc  
2040  
ttcccggggc caggacaagg gcgccctccc cttggcgggc ctggtgctga gttgcttaga  
2100  
ccagaagact attcagaccg tgagcctgtt tttgatttga gtgttccact aaacaaacaa  
2160  
caaaagccca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  
2220  
aaaaaaaaa aaaaaaaaaa aaaa  
2244

&lt;210&gt; 2442

<211> 168  
 <212> PRT  
 <213> Homo sapiens

<400> 2442  
 Met Gly Cys Arg Thr Lys Pro Ser Gly Ser Ala Gly Leu Asp Leu Pro  
 1 5 10 15  
 Pro Ile Ser Cys Trp Gly Pro Ser Thr Cys Leu Cys Pro Trp Leu Cys  
 20 25 30  
 Pro Ser Ala Asn Pro Ser Pro Pro Gly Ser His Pro Gln Leu Pro  
 35 40 45  
 Ala Arg Ser Pro Leu Pro Gly Pro Leu Pro Ser Pro Trp Cys Ser Leu  
 50 55 60  
 Ser Gln Gly Pro Ser Pro Ser Asp Phe Pro Gln Gly Ser Arg Leu Asp  
 65 70 75 80  
 Leu Glu Leu Cys Leu Pro Val Cys Ala Met Gly Ser Ala Ser Gly Leu  
 85 90 95  
 Glu Leu Arg Leu Phe Pro Gly Pro Gly Gln Gly Arg Pro Pro Leu Gly  
 100 105 110  
 Gly Ala Gly Ala Glu Leu Leu Arg Pro Glu Asp Tyr Ser Asp Arg Glu  
 115 120 125  
 Pro Val Phe Asp Leu Ser Val Pro Leu Asn Lys Gln Gln Lys Pro Lys  
 130 135 140  
 Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
 145 150 155 160  
 Lys Lys Lys Lys Lys Lys Lys Lys  
 165

<210> 2443  
 <211> 361  
 <212> DNA  
 <213> Homo sapiens

<400> 2443  
 nccgtgcgcg ctatcttgcg tcgtacgcgcg tccagggaag atgaaaaaat gctacaaacg  
 60  
 gccgatggac gattgcgcgcat tgatatcgaa tccatgcgca cctttgtaga gggcaaagaa  
 120  
 gtccatttga cgaaaaacga atttttaatt gtgcagactt tgtttacgca cccaataag  
 180  
 atctatacgc gcgatgaaat tatcgaagtc accttcggaa tggattatga ggcctttgac  
 240  
 cgtgccattg atacccatat caaaaacatt cgccagaaga ttgaagcggg tccgaaaaac  
 300  
 cccgtctata tccgcacggg ttatggtgtc gggtatctgc ccggaggctt tgatgaagct  
 360  
 t  
 361

<210> 2444  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 2444

```

Xaa Val Arg Ala Ile Leu Arg Arg Thr Pro Ser Arg Glu Asp Glu Lys
 1           5           10           15
Met Leu Gln Thr Ala Asp Gly Arg Leu Arg Ile Asp Ile Glu Ser Met
          20           25           30
Arg Thr Phe Val Glu Gly Lys Glu Val His Leu Thr Lys Asn Glu Phe
      35           40           45
Leu Ile Val Gln Thr Leu Phe Thr His Pro Asn Lys Ile Tyr Thr Arg
    50           55           60
Asp Glu Ile Ile Glu Val Thr Phe Gly Met Asp Tyr Glu Ala Phe Asp
65           70           75           80
Arg Ala Ile Asp Thr His Ile Lys Asn Ile Arg Gln Lys Ile Glu Ala
      85           90           95
Asp Pro Lys Asn Pro Val Tyr Ile Arg Thr Val Tyr Gly Val Gly Tyr
    100           105           110
Leu Pro Gly Gly Phe Asp Glu Ala
      115           120

```

&lt;210&gt; 2445

&lt;211&gt; 403

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2445

```

agatctgttg aatgaagcag gtgccactta gacattcact tcactgactc caaccacaac
60
ctcccccttca tttgatatcc tgctcttggc agaaggatgg agaaagagca tcgcacaaaag
120
aggaagcatg tttatcctgt tcagattact gcttctgccca ggctgctgct gctgttgggt
180
tctgcacatt tgctctttat taagcaaagt tcagagctgg gtgctggcaa gggaatcccc
240
tgtattttaca caggttaaacc tgagagccag agggcccaa accatcctgg ctgagagga
300
caagctatta gagttaataa cagtgcactg gcattccttc aaaatcctaa tggaagcata
360
aataaaaaga ggaaagtcct ctttaccaa gaacctgaaa aan
403

```

&lt;210&gt; 2446

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2446

```

Met Glu Lys Glu His Arg Thr Lys Arg Lys His Val Tyr Pro Val Gln
 1           5           10           15
Ile Thr Ala Ser Ala Arg Leu Leu Leu Leu Gly Ser Ala His Leu
      20           25           30
Leu Phe Ile Lys Gln Met Ser Glu Leu Gly Ala Gly Lys Gly Ile Pro
    35           40           45
Cys Ile Tyr Thr Gly Lys Pro Glu Ser Gln Arg Ala Pro Asn His Pro
    50           55           60
Gly Cys Glu Gly Gln Ala Ile Arg Val Asn Asn Ser Ala Leu Ala Phe

```

65                                      70                                      75                                      80  
 Leu Gln Asn Pro Asn Gly Ser Ile Asn Lys Lys Arg Lys Val Pro Phe  
    85                                      90                                      95  
 Thr Gln Glu Pro Glu Lys  
    100

<210> 2447  
 <211> 744  
 <212> DNA  
 <213> Homo sapiens

<400> 2447  
 nacgcgtcga ggtttgccag tcacgggttg cgggtggggc aggtactact caccgtcaat  
 60  
 gacctggtgc ggcccacttc gtaccgcaat gcctgggtcaa ccctcgacac ttgctggggg  
 120  
 ttgggcgtcg tgccgatcgt caacgagaac gacacggtcg ccaccggaga aattcggttt  
 180  
 ggcgataatg atcgggttgc tgccctggta gccgagctgg tgccgctca agccctcatt  
 240  
 ctgctctctg acgttgacgc cttgtacacc gcccatccgg attcaccgga tgctcgtcgc  
 300  
 gtggagggttg tggaggacat cgatgcattg gatgtcgata ccataaaagc tggttcgggg  
 360  
 gtggggaaccg gcggcatgac caggaactt gaagccgcc gaatggccac ctgtgccggg  
 420  
 gtaccggttg tactcgcagc ggcggtggat gcccggacg ttctggctgg tgccccctg  
 480  
 ggtacctact tccgcccgct ggcgacgcga cggccccgac ggttgctgtg gttggccgac  
 540  
 gctgccaccc cgcagggaca gatcgtcatc gacgacggag ctgtcgaagc ttgacacag  
 600  
 cgtcattcct cgttgttggc ggtgggtgtg actcgggtac acggggattt ccaagcaggc  
 660  
 gacccagtga cgatcctggc ctccgacggt cgagttgttg gtcgcggtat cgcacagttc  
 720  
 tcccatgatg aggtgcgcgt catg  
 744

<210> 2448  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 2448  
 Xaa Ala Ser Arg Phe Ala Ser His Gly Leu Arg Val Gly Gln Val Leu  
 1                                      5                                      10                                      15  
 Leu Thr Val Asn Asp Leu Val Arg Pro Thr Ser Tyr Arg Asn Ala Trp  
    20                                      25                                      30  
 Ser Thr Leu Asp Thr Leu Leu Gly Leu Gly Val Val Pro Ile Val Asn  
    35                                      40                                      45  
 Glu Asn Asp Thr Val Ala Thr Gly Glu Ile Arg Phe Gly Asp Asn Asp  
    50                                      55                                      60  
 Arg Leu Ala Ala Leu Val Ala Glu Leu Val Arg Ala Gln Ala Leu Ile

```

65          70          75          80
Leu Leu Ser Asp Val Asp Ala Leu Tyr Thr Ala His Pro Asp Ser Pro
      85          90          95
Asp Ala Arg Arg Val Glu Val Val Glu Asp Ile Asp Ala Leu Asp Val
      100        105        110
Asp Thr His Lys Ala Gly Ser Gly Val Gly Thr Gly Gly Met Thr Thr
      115        120        125
Lys Leu Glu Ala Ala Arg Met Ala Thr Cys Ala Gly Val Pro Val Val
      130        135        140
Leu Ala Ala Ala Val Asp Ala Pro Asp Val Leu Ala Gly Ala Pro Val
      145        150        155        160
Gly Thr Tyr Phe Arg Pro Leu Ala Thr Arg Arg Pro Arg Arg Leu Leu
      165        170        175
Trp Leu Ala Asp Ala Ala Thr Pro Gln Gly Gln Ile Val Ile Asp Asp
      180        185        190
Gly Ala Val Glu Ala Leu Thr Gln Arg His Ser Ser Leu Leu Ala Val
      195        200        205
Gly Val Thr Arg Val His Gly Asp Phe Gln Ala Gly Asp Pro Val Thr
      210        215        220
Ile Leu Ala Ser Asp Gly Arg Val Val Gly Arg Gly Ile Ala Gln Phe
      225        230        235        240
Ser His Asp Glu Val Arg Val Met
      245

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&lt;210&gt; 2449

&lt;211&gt; 296

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2449

```

gtgcactttg ttacagccct ggaacatgaa cacatgccgt catcaactcc ccaaaatctc
60
ctactgtctt cccctctctc ctgggccctg tctatcccc agaggccaga caggccttcc
120
tcgcatgcaa gagtctccct cgcctgccg gacagtggcc tccatctacc tgctgtctt
180
gctggactcc agaactctcc agtcctttcc cccttggggg ttgggggggg ccccccttt
240
ttttccccc ctttccctt tcatccaca ggaggccagc ctcaacatcc cncccc
296

```

&lt;210&gt; 2450

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2450

```

Met Asn Thr Cys Arg His Gln Leu Pro Lys Ile Ser Tyr Cys Ser Pro
  1          5          10         15
Leu Leu Pro Gly Pro Cys Pro Ile Pro Arg Gly Gln Thr Gly Leu Pro
      20        25        30
Arg Met Gln Glu Ser Pro Ser Pro Cys Arg Thr Val Ala Ser Ile Tyr
      35        40        45
Leu Pro Val Leu Leu Asp Ser Arg Thr Leu Gln Ser Phe Pro Pro Trp

```



50                      55                      60  
 Gly Leu Gly Gly Ala Pro Pro Phe Phe Pro Pro Leu Ser Leu Phe Ile  
 65                      70                      75                      80  
 Pro Gln Glu Ala Ser Leu Asn Ile Pro Xaa  
                     85                      90

<210> 2451  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens

<400> 2451  
 nacgcgtgac tggattgctc aacgggtgag gaatcgagcg gttacgatgt cgggccgatc  
 60  
 tgcaacgatg atcttgtagag cgatgtattg accggtgtgt gggccgatct tgtgggccag  
 120  
 gagaaggctg tcggggctct gcgtcgtgcc gccgaatcgc agccggggcg ctgcgtccat  
 180acgcattggt cattacgggt ccgcctggat caggctcggtc gaatgctgcg 240  
 aaggcctttg cagcggcgct acagtgcgtc gaccatggat gcgggcagtg caatgcctgt  
 300  
 cgaaccngcc tgtcaggcgc ccatcctgac gtcaccctcg tgcgtactga ggcgctgtct  
 360  
 attggcgtcg attgaggtcg tgaaatgggt ttgttcgagc gggcgatgaa ttcgggtccc  
 420  
 cggggcgctc ccagggttgt cgtcgtcgaa gatgccgacc gcatcactga acgcggagct  
 480  
 gacgccttgc ttaaagctat cgaggagcct gcgccgaaaa ccgtctgggt gctgtgtgcc  
 540  
 cctactccag aggacgtcat cgtcacgacg aggtcgagat gtcggcgcc  
 589

<210> 2452  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 2452  
 Leu Asp Cys Ser Thr Gly Glu Glu Ser Ser Gly Tyr Asp Val Gly Pro  
 1                      5                      10                      15  
 Ile Cys Asn Asp Asp Leu Val Ser Asp Val Leu Thr Gly Val Trp Ala  
                     20                      25                      30  
 Asp Leu Val Gly Gln Glu Lys Ala Val Gly Val Leu Arg Arg Ala Ala  
                     35                      40                      45  
 Glu Ser Gln Pro Gly Arg Ser Ser His Ala Met Ser His Ala Trp Leu  
                     50                      55                      60  
 Ile Thr Gly Pro Pro Gly Ser Gly Arg Ser Asn Ala Ala Lys Ala Phe  
 65                      70                      75                      80  
 Ala Ala Ala Leu Gln Cys Val Asp His Gly Cys Gly Gln Cys Asn Ala  
                     85                      90                      95  
 Cys Arg Thr Xaa Leu Ser Gly Ala His Pro Asp Val Thr Leu Val Arg  
                     100                      105                      110  
 Thr Glu Ala Leu Ser Ile Gly Val Asp  
                     115                      120

<210> 2453  
 <211> 695  
 <212> DNA  
 <213> Homo sapiens

<400> 2453  
 nnacgcgtca gccatctgtg agtgctcaca ctatacacac atccccgggc acactcaggg  
 60  
 agattcacac attcctacga gcacacatgt gcctgcatga gttattcccc atgtgaacac  
 120  
 acagggttggc acacgcacat gcccctgggt atgtctatgt ccattcatcc atcccagcct  
 180  
 gtgcacgtcc tctcactcct gtgttcacac ctatgcccaa atgaaccaag ggacacacat  
 240  
 gcacaccctt atgtggtgca cacacactcg tgcacacgga gccacaccag cacatgctca  
 300  
 gaggcatttg tgtgctgagg catttgacgc atgactcaga acggagtatg ggggtggcgcg  
 360  
 gcgtggctgg ggagggtccca tcagcccgcc tctgaaaccc tcccaacctg cccatcctgg  
 420  
 cccaggcact gtgtctccgg cttgggcttc agccccggac cccaggacac cccggacaaa  
 480  
 gaggagctgc tctcgtctga agcctgctac gaatgcagga tcaatggcct ctcccctcgg  
 540  
 gaccggccac gacgcagtgc ccacaggga caccagggtga catgggtgct gcactaggca  
 600  
 ggggtggcca gggaatgggt gagggtggga aaggaggctgt ggacccgact tagtcatgtc  
 660  
 agccccccga agaaggagca ccagggtcca gatct  
 695

<210> 2454  
 <211> 166  
 <212> PRT  
 <213> Homo sapiens

<400> 2454  
 Met Ser Tyr Ser Pro Cys Glu His Thr Gly Trp His Thr His Met Pro  
 1 5 10 15  
 Leu Gly Met Leu Met Ser Ile His Pro Ser Gln Pro Val His Val Leu  
 20 25 30  
 Ser Leu Leu Cys Ser His Leu Cys Pro Asn Glu Pro Arg Asp Thr His  
 35 40 45  
 Ala His Pro Tyr Val Val His Thr His Ser Cys Thr Arg Ser His Thr  
 50 55 60  
 Ser Thr Cys Ser Glu Ala Phe Val Cys Val Gly Ile Cys Ser Met Thr  
 65 70 75 80  
 Gln Asn Gly Val Trp Gly Gly Ala Ala Trp Leu Gly Arg Ser His Gln  
 85 90 95  
 Pro Ala Ser Glu Thr Leu Pro Thr Cys Pro Ser Trp Pro Arg His Cys  
 100 105 110  
 Val Ser Gly Leu Gly Phe Ser Pro Gly Pro Gln Asp Thr Pro Asp Lys  
 115 120 125  
 Glu Glu Leu Leu Ser Ser Glu Ala Cys Tyr Glu Cys Arg Ile Asn Gly

130		135		140
Leu Ser Pro Arg Asp Arg	Pro Arg Arg Ser	Ala His Arg Asp His Gln		
145	150	155	160	
Val Thr Trp Val Leu His				
	165			

<210> 2455  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<400> 2455  
 acgcgtcggc agaagcgtca gctgaccgtc ggagccgata tgtcccagc cgctcgcagc  
 60  
 ggaaccgcgc agaaggaaat ccacgcgctg ccgatcatga aggcgctccc catgggcgctc  
 120  
 aaagaactcg ttctggggcga atcgaagtgg caggacgagt tgatcaacaa cttcatcgctc  
 180  
 gcgctgtttg caggcgtggt gttgctgttc gcggtgctgg tgctgtgta ccggcgcttg  
 240  
 ctgccgcgct tcatcaacgt gatgtcgctg gcggtggcac cgctgggcgg gttgatcggc  
 300  
 ctgtggctga ccaacacgcc gatctcgatg ccggtctata tcggcttgat catgctgctc  
 360  
 ggcacgtcgc ccaagaat  
 378

<210> 2456  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 2456  
 Thr Arg Arg Gln Lys Arg Gln Leu Thr Val Gly Ala Asp Leu Ser Pro  
 1 5 10 15  
 Gly Val Val Ser Gly Thr Ala Gln Lys Glu Ile His Ala Leu Pro Ile  
 20 25 30  
 Met Lys Ala Leu Pro Met Gly Val Lys Glu Leu Val Leu Gly Glu Ser  
 35 40 45  
 Lys Trp Gln Asp Glu Leu Ile Asn Asn Phe Ile Val Ala Leu Phe Ala  
 50 55 60  
 Gly Val Val Leu Leu Phe Ala Val Leu Val Leu Tyr Arg Arg Leu  
 65 70 75 80  
 Leu Pro Pro Phe Ile Asn Val Met Ser Leu Ala Val Ala Pro Leu Gly  
 85 90 95  
 Gly Leu Ile Gly Leu Trp Leu Thr Asn Thr Pro Ile Ser Met Pro Val  
 100 105 110  
 Tyr Ile Gly Leu Ile Met Leu Leu Gly Ile Val Ala Lys Asn  
 115 120 125

<210> 2457  
 <211> 754  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 2457

cctaggaatt taccaccatc aaagacttac attaaccagc tatccatgaa ctcacctgag  
 60  
 atgagcgaat gtgacatctt gcacactctg cgatggctct ctcggctccg gatcagctcc  
 120  
 tatgtcaact ggataaagga tcaccttata aaacagggaa tgaaggctga gcatgctagc  
 180  
 tcgcttctag aactggcatc caccactaag tgtagctcag tgaaatatga tgttgaaata  
 240  
 gtagaggaat acttcgctcg acagatctca tccttctgta gtatcgactg tgccaccatc  
 300  
 ttgcagctgc atgaaattcc cagtctgcag tccatctaca cccttgatgc cgcgattcta  
 360  
 aaaggccag gtcttttttg gatgagcatt tttctaagat ggctgctgag actgatcctc  
 420  
 ataagtcgtc tgagattacc aagaacctac ttccagccac gctgcaactc attgacacct  
 480  
 atgcatcggt caccagagcc tatttgctgc aaaactttaa tgaagagggg acaactgaga  
 540  
 aaccttccaa ggagaaactg caaggctttg ctgctgtttt ggctattggc tctagcaggt  
 600  
 gcaaggcaaa tactctgggt ccgacactgg ttcagaattt gccatcgta gtgcagactg  
 660  
 tgtgtgagtc ctggaacaac atcaatacca atgaatttcc caatattgga tcctggcgca  
 720  
 atgcctttgc caatgacacc atcccttcac gcgt  
 754

&lt;210&gt; 2458

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2458

Met	Asn	Ser	Pro	Glu	Met	Ser	Glu	Cys	Asp	Ile	Leu	His	Thr	Leu	Arg
1				5				10						15	
Trp	Ser	Ser	Arg	Leu	Arg	Ile	Ser	Ser	Tyr	Val	Asn	Trp	Ile	Lys	Asp
			20				25						30		
His	Leu	Ile	Lys	Gln	Gly	Met	Lys	Ala	Glu	His	Ala	Ser	Ser	Leu	Leu
			35				40					45			
Glu	Leu	Ala	Ser	Thr	Thr	Lys	Cys	Ser	Ser	Val	Lys	Tyr	Asp	Val	Glu
			50				55					60			
Ile	Val	Glu	Glu	Tyr	Phe	Ala	Arg	Gln	Ile	Ser	Ser	Phe	Cys	Ser	Ile
					70					75				80	
Asp	Cys	Ala	Thr	Ile	Leu	Gln	Leu	His	Glu	Ile	Pro	Ser	Leu	Gln	Ser
				85					90					95	
Ile	Tyr	Thr	Leu	Asp	Ala	Ala	Ile	Leu	Lys	Gly	Pro	Gly	Leu	Phe	Gly
			100					105					110		
Met	Ser	Ile	Phe	Leu	Arg	Trp	Leu	Leu	Arg	Leu	Ile	Leu	Ile	Ser	Arg
			115					120					125		
Leu	Arg	Leu	Pro	Arg	Thr	Tyr	Phe	Gln	Pro	Arg	Cys	Asn	Ser	Leu	Thr
			130					135				140			
Pro	Met	His	Arg	Ser	Pro	Glu	Pro	Ile	Cys	Cys	Lys	Thr	Leu	Met	Lys

```

145          150          155          160
Arg Glu Gln Leu Arg Asn Leu Pro Arg Arg Asn Cys Lys Ala Leu Leu
          165          170          175
Leu Phe Trp Leu Leu Ala Leu Ala Gly Ala Arg Gln Ile Leu Trp Val
          180          185          190
Arg His Trp Phe Arg Ile Cys His Arg Gln Cys Arg Leu Cys Val Ser
          195          200          205
Pro Gly Thr Thr Ser Ile Pro Met Asn Phe Pro Ile Leu Asp Pro Gly
          210          215          220
Ala Met Pro Leu Pro Met Thr Pro Ser Leu His Ala
225          230          235

```

&lt;210&gt; 2459

&lt;211&gt; 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2459

```

accggtgcac agatcgttct ggccgcgtgc actgccccgc tcaagcaa at cgctatcaac
60
gctggtcttt agggcggcgt cgtggctgag aaggctcgtg gtctgcccgc aggacagggc
120
ctcaacgcgg ccaatgacga gtatgtcgac atggtagagg ccggcatcat tgaccgggcc
180
aaggtagacc gttcggctct gcagaacgcc gcgtccatcg cgccctgtt cctcaccact
240
gaagccgtca tcgctgacaa gcccgagcct gttaaggctc ccgctggcgg cggtgatatg
300
gacggtatgg gtggcatggg cggcatgatg tgatcgtgta ttgccttcgc tgatttgagt
360
gggatgccac tttgccccag gc
382

```

&lt;210&gt; 2460

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2460

```

Thr Gly Ala Gln Ile Val Leu Ala Ala Cys Thr Ala Pro Leu Lys Gln
1      5      10      15
Ile Ala Ile Asn Ala Gly Leu Glu Gly Gly Val Val Ala Glu Lys Val
20     25     30
Ala Gly Leu Pro Ala Gly Gln Gly Leu Asn Ala Ala Asn Asp Glu Tyr
35     40     45
Val Asp Met Val Glu Ala Gly Ile Ile Asp Pro Ala Lys Val Thr Arg
50     55     60
Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Ala Leu Phe Leu Thr Thr
65     70     75     80
Glu Ala Val Ile Ala Asp Lys Pro Glu Pro Val Lys Ala Pro Ala Gly
85     90     95
Gly Gly Asp Met Asp Gly Met Gly Gly Met Gly Gly Met Met
100    105    110

```

<210> 2461  
 <211> 558  
 <212> DNA  
 <213> Homo sapiens

<400> 2461  
 tccggacaaa aggggttcaat cgaagtatgg ttagcctttt ccaagtcgcc aggacggacc  
 60  
 tgcaatgctg tttgtcgtca tgctcggggg caagcaccca cgggctaaaa tcgaaattca  
 120  
 cgatgtggta ttgcagtcg cggatacgt gcaacacacc tacaccaat tgcgcgacgg  
 180  
 ctggttcggc agccctaagg tgtgcatatc gatgcgtgga tggccgtcga tggcgtcgac  
 240  
 ggctggaaag tcgaactcag ccagatggcg ccgcctgccg acgcgcatca cctgtacttc  
 300  
 atcaacctcg ggggctacga ggccaacgct tttggcgagg cccatcatta cctgctggtg  
 360  
 gtcgcccggg acaaacagga agccaagcgc aaggggcagc ggcaaatgtt gcaacactgg  
 420  
 tcccaggccc acaccgatgg cgtaatggat atcgacgact gcttgccgat tgatctggtg  
 480  
 gacggtcgct atgttcacct ggtgcaaggc ccgcaccagc cgatcatcca gcacaacgac  
 540  
 tacatcatcc tgccgcga  
 558

<210> 2462  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 2462  
 Met Val Ser Leu Phe Gln Val Ala Arg Thr Asp Leu Gln Cys Cys Leu  
 1 5 10 15  
 Ser Ser Cys Ser Gly Ala Ser Thr His Gly Leu Lys Ser Lys Phe Thr  
 20 25 30  
 Met Trp Tyr Ser Gln Ser Arg Ile Arg Cys Asn Thr Pro Thr Pro Asn  
 35 40 45  
 Cys Ala Thr Ala Gly Ser Ala Ala Leu Arg Cys Ala Tyr Arg Cys Val  
 50 55 60  
 Asp Gly Arg Arg Trp Arg Arg Arg Leu Glu Ser Arg Thr Gln Pro Asp  
 65 70 75 80  
 Gly Ala Ala Cys Arg Arg Ala Ser Pro Val Leu His Gln Pro Arg Arg  
 85 90 95  
 Leu Arg Gly Gln Arg Phe Trp Arg Gly Pro Ser Leu Pro Ala Gly Gly  
 100 105 110  
 Arg Pro Gly Gln Thr Gly Ser Gln Ala Gln Gly Ala Ala Asn Val  
 115 120 125  
 Ala Thr Leu Val Pro Gly Pro His Arg Trp Arg Asn Gly Tyr Arg Arg  
 130 135 140  
 Leu Leu Ala Asp  
 145

&lt;210&gt; 2463

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2463

```

cccagggggt aagccatgag cctgttgagc caagtggccc gggcgccgtt gagcgccaag
60
ttcggcctgc tgattattct gttatacgtc gcgctggcgc tgtgngcgcc gctgctggcg
120
ccctatggcg aaaccaggt ggtgggtgaa ggcttcgcgc cgtggagcgg ccagtttttg
180
ctgggcaccg ataacctggg gcgcgacatg ttcagccgcc tgatgtacgg cgcgcgcaat
240
accttgggca ttgccttctt gacgacgacg ctggcgtttc tgctcgggtg tttgagcggg
300
ttggtcgcgg cgatcaaggg cggttgggtc gac
333

```

&lt;210&gt; 2464

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2464

```

Met Ser Leu Leu Ser Gln Val Ala Arg Ala Pro Leu Ser Ala Lys Phe
 1             5             10             15
Gly Leu Leu Ile Ile Leu Leu Tyr Val Ala Leu Ala Leu Xaa Ala Pro
      20             25             30
Leu Leu Ala Pro Tyr Gly Glu Thr Gln Val Val Gly Glu Gly Phe Ala
      35             40             45
Pro Trp Ser Gly Gln Phe Leu Leu Gly Thr Asp Asn Leu Gly Arg Asp
      50             55             60
Met Phe Ser Arg Leu Met Tyr Gly Ala Arg Asn Thr Leu Gly Ile Ala
      65             70             75             80
Phe Leu Thr Thr Thr Leu Ala Phe Leu Leu Gly Gly Leu Ser Gly Leu
      85             90             95
Val Ala Ala Ile Lys Gly Gly Trp Val Asp
      100             105

```

&lt;210&gt; 2465

&lt;211&gt; 434

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2465

```

nntcatgagg acatttcctt catatttggt ggtggtaaatt ccctcctggg acacggggaa
60
atgaccagag gctggcgccc cacctggcag gaacagatgc cagctctgct gcagccatcg
120
cccttgagc ggggtggctct gtgcctcttt ctgcactgct ggtgggtggt gctgttggt
180
gggtgatgga taccggctgc cagagatggc tcaggtgccca gctgctgggc tatctcagge
240

```

actggctgct gggctatctc gggcgccggc tgctgggcta tctcaggcgc tggtgctgc  
 300  
 tgggctgtct cgggtgctgg ctgttgggac gtctcctgtc ctggcactgg gctctcgggt  
 360  
 gctgggtgcc agctgctgcc taccttgac tgggctctgg gcactcactg cactcgggct  
 420  
 tttccatctc cgac  
 434

<210> 2466  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 2466  
 Trp Ile Pro Ala Ala Arg Asp Gly Ser Gly Ala Ser Cys Trp Ala Ile  
 1 5 10 15  
 Ser Gly Thr Gly Cys Trp Ala Ile Ser Gly Ala Gly Cys Trp Ala Ile  
 20 25 30  
 Ser Gly Ala Gly Cys Cys Trp Ala Val Ser Gly Ala Gly Cys Trp Asp  
 35 40 45  
 Val Ser Cys Pro Gly Thr Gly Leu Ser Gly Ala Gly Cys Gln Leu Leu  
 50 55 60  
 Pro Thr Leu His Trp Ala Leu Gly Thr His Cys Thr Arg Ala Phe Pro  
 65 70 75 80  
 Ser Pro

<210> 2467  
 <211> 306  
 <212> DNA  
 <213> Homo sapiens

<400> 2467  
 atggactcca ccggcaccgg agcagggggg aaggggaaga agggagcggc cgggcgcaag  
 60  
 gtcggcgggc caaggaagaa gtcggtgtcg aggtccgtga aggccggtct ccagttcccc  
 120  
 gtcggccgca tcgggcgcta cttgaagaag ggccgctacg cgcagcgtgt cggcaccggc  
 180  
 gccccgtct acctcgccgc tgtcctcgaa tacctcgccg ctgaggttct ggagctcgcc  
 240  
 ggtaatgctg ccagggacaa caagaagact cgcattatct cgcgccacgt gcttctggcg  
 300  
 atccgg  
 306

<210> 2468  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 2468  
 Met Asp Ser Thr Gly Thr Gly Ala Gly Gly Lys Gly Lys Lys Gly Ala



```

      1           5           10           15
Ala Gly Arg Lys Val Gly Gly Pro Arg Lys Lys Ser Val Ser Arg Ser
      20           25           30
Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Gly Arg Tyr Leu
      35           40           45
Lys Lys Gly Arg Tyr Ala Gln Arg Val Gly Thr Gly Ala Pro Val Tyr
      50           55           60
Leu Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val Leu Glu Leu Ala
      65           70           75           80
Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile Ile Pro Arg His
      85           90           95
Val Leu Leu Ala Ile Arg
      100

```

&lt;210&gt; 2469

&lt;211&gt; 489

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2469

```

gccggcgtgg cacatggctt ccctgaagcc agcattgccc tggccaagga agctttgcag
60
aacagatgag atttcagctg ggacttgcag ccaagtggga tttggccttt tggggagaag
120
ggaaaggcca ttcaaaggcc agggacagag tatggtcaaa ggcattggaga tgaggaagag
180
gggaccagag cagagggtca ggttggaag cgagttgggg tcaatctgca aaggggctga
240
cgtgccaggt aaaaaacagg agcacagttt agttttgtcg gatcatttca ggtggaaggg
300
cagtgggaat gttggagaaa acactttttg gtgtcgttac attgaatctg ctcatctata
360
agaataaaac tttatttcat agagttattg tatggctcaa aataggtatg aagaattaag
420
aaaaagaatt ttagatttaa aatgaaaagg cacctacaaa agtagagtgg tagagttacc
480
aacgtggag
489

```

&lt;210&gt; 2470

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2470

```

Met Ala Ser Leu Lys Pro Ala Leu Pro Trp Pro Arg Lys Leu Cys Arg
      1           5           10           15
Thr Asp Glu Ile Ser Ala Gly Thr Cys Ser Gln Val Gly Phe Gly Leu
      20           25           30
Leu Gly Arg Arg Glu Arg Ala Phe Lys Gly Gln Gly Gln Ser Met Val
      35           40           45
Lys Gly Met Glu Met Arg Lys Arg Gly Pro Glu Gln Arg Val Arg Leu
      50           55           60
Glu Ser Glu Leu Gly Ser Ile Cys Lys Gly Ala Asp Val Pro Gly Lys

```

65		70		75		80									
Lys	Gln	Glu	His	Ser	Leu	Val	Leu	Ser	Asp	His	Phe	Arg	Trp	Lys	Gly
				85					90					95	
Ser	Gly	Asn	Val	Gly	Glu	Asn	Thr	Phe	Trp	Cys	Arg	Tyr	Ile	Glu	Ser
			100					105					110		
Ala	His	Leu													
		115													

&lt;210&gt; 2471

&lt;211&gt; 779

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2471

```

tggccatcct ccgtgacatg tacacttcca atatgccggt gtttgagccg ttcatagatc
60
ctcacatggt ggcccttgac ttctttcaca gtgaggacct ctgcttcatg aggctcataa
120
gaagaggagc taaggactat tttgtcatgg gggcgccaat ccaactgcac ttctactata
180
attctctcat ttcttgaggc aatatcagct ccaagatgtg tccaggagtt cttaggataa
240
gcactgtaaa gatgaacttt ccataaaacc ccaattgttc ctgggtcaat atgaattcca
300
ttcatacggg caaaaagac tccctctgag gctctaagga gaatcagaag cttttgttcc
360
ttttctaagg gattttctaa agtaccact ttcagctccc cgctgcaat gaccatgcat
420
gccacactca gaacattgct tctgtccaca ggaagtcta aggtcccat cacatacagc
480
cctttgaaga attggaaaat ctgtatccac aaggacagtt ctgttgggta aaatgagaac
540
gtcatcccca gggcctggaa tggattgtt gtatcctccc cagccttctt caacaccttg
600
ccatgtttca gggagggacc attttaaagc tgattcaggg gcagaggtag aagctgaaat
660
agttgggggc ataccttctt tcaccggag aatgacttga acttggcctt cacctaaaac
720
cagataggtg agttgcctca gctggctatt gaagaaccag tcacagcctt ggttctggc
779

```

&lt;210&gt; 2472

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2472

Met	Thr	Phe	Ser	Phe	Tyr	Pro	Thr	Glu	Leu	Ser	Leu	Trp	Ile	Gln	Ile
1				5				10				15			
Phe	Gln	Phe	Phe	Lys	Gly	Leu	Tyr	Val	Met	Gly	Thr	Leu	Asp	Phe	Pro
			20				25					30			
Val	Asp	Arg	Ser	Asn	Val	Leu	Ser	Val	Ala	Cys	Met	Val	Ile	Ala	Gly
		35				40					45				
Gly	Glu	Leu	Lys	Val	Gly	Thr	Leu	Glu	Asn	Pro	Leu	Glu	Lys	Glu	Gln

```

      50      55      60
Lys Leu Leu Ile Leu Leu Arg Ala Ser Glu Gly Val Phe Cys Asp Arg
65      70      75      80
Met Asn Gly Ile His Ile Asp Pro Gly Thr Ile Gly Val Tyr Gly Lys
      85      90      95
Val His Leu Tyr Ser Ala Tyr Pro Lys Asn Ser Trp Thr His Leu Gly
      100      105      110
Ala Asp Ile Ala Ser Gly Asn Glu Arg Ile Ile Val Glu Asp Ala Val
      115      120      125
Asp Trp Arg Pro His Asp Lys Ile Val Leu Ser Ser Ser Ser Tyr Glu
      130      135      140
Pro His Glu Ala Glu Val Leu Thr Val Lys Glu Val Lys Gly His His
145      150      155      160
Val Arg Ile Tyr Glu Arg Leu Lys His Arg His Ile Gly Ser Val His
      165      170      175
Val Thr Glu Asp Gly
      180

```

&lt;210&gt; 2473

&lt;211&gt; 698

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2473

```

nngtgcacca agaaatggca gcctgacaag ctggtggtgg tatggactcg gcggaaccga
60
cgcattctgct ccaaggccca cagctggcag ccgnnggcatt ccagaaccca taccggggga
120
ccgtggtgtg gatggtacnc tgagaatgtg gacattctctg tgaccctcta cagggacccc
180
cacgtggacc agtatgaggc caaagagtgg acatttatta ttgaaaatga gtctaagggg
240
cagcggaagg tgctggccac ggccgaggtg gacctggccc gccatgccag ggcccgtgcc
300
ntgtccaagt ccnactgag gctgcggtg aagccaaagt cagtgaagac ggtgcaggct
360
gagctgagcc tcaactcttc cggggtgctg ctgcgggagg gccgtgccac ggacgatgac
420
atgcagagtc tcgcaagcct catgagtgtg aagcctagt atgtgggcaa cttggatgac
480
tttgctgaga gtgatgaaga tgaggctcat ggcccaggag ccccggaggc ccgggctcga
540
gtcccccagc caggtgggct cacagcctgc tgtggatcga gactgccaag acctggggag
600
ggagggttac ccgggccacc agccacttgc tgtgcccggc ctgtgatggg aactcattac
660
tgcccaggca gtcccaacca acccagcagc ctcaattg
698

```

&lt;210&gt; 2474

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2474

Xaa Cys Thr Lys Lys Trp Gln Pro Asp Lys Leu Val Val Val Trp Thr  
 1 5 10 15  
 Arg Arg Asn Arg Arg Ile Cys Ser Lys Ala His Ser Trp Gln Pro Xaa  
 20 25 30  
 Ala Ser Arg Thr His Thr Gly Ala Pro Trp Cys Gly Trp Tyr Xaa Glu  
 35 40 45  
 Asn Val Asp Ile Ser Val Thr Leu Tyr Arg Asp Pro His Val Asp Gln  
 50 55 60  
 Tyr Glu Ala Lys Glu Trp Thr Phe Ile Ile Glu Asn Glu Ser Lys Gly  
 65 70 75 80  
 Gln Arg Lys Val Leu Ala Thr Ala Glu Val Asp Leu Ala Arg His Ala  
 85 90 95  
 Arg Ala Arg Ala Xaa Ser Lys Ser Xaa Leu Arg Leu Arg Leu Lys Pro  
 100 105 110  
 Lys Ser Val Lys Thr Val Gln Ala Glu Leu Ser Leu Thr Leu Ser Gly  
 115 120 125  
 Val Leu Leu Arg Glu Gly Arg Ala Thr Asp Asp Asp Met Gln Ser Leu  
 130 135 140  
 Ala Ser Leu Met Ser Val Lys Pro Ser Asp Val Gly Asn Leu Asp Asp  
 145 150 155 160  
 Phe Ala Glu Ser Asp Glu Asp Glu Ala His Gly Pro Gly Ala Pro Glu  
 165 170 175  
 Ala Arg Ala Arg Val Pro Gln Pro Gly Gly Leu Thr Ala Cys Cys Gly  
 180 185 190  
 Ser Arg Leu Pro Arg Pro Gly Glu Gly Gly Leu Pro Gly Pro Pro Ala  
 195 200 205  
 Thr Cys Cys Ala Arg Pro Val Met Gly Thr His Tyr Cys Pro Gly Ser  
 210 215 220  
 Pro Asn Gln Pro Ser Ser Leu Asn  
 225 230

&lt;210&gt; 2475

&lt;211&gt; 1251

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2475

ngcgcgcccc agatgcaggt gagcaagagg atgctggcgg ggggcgtgag gagcatgccc  
 60  
 agccccctcc tggcctgctg gcagcccatc ctctgctggtg tgctgggctc agtgcgtgta  
 120  
 ggctcggcca cgggctgccc gccccgctgc gactgctccg cccaggaccg cgctgtgctg  
 180  
 tgccaccgca agcgctttgt ggcagtcccc gagggcatcc ccaccgagac gcgcctgctg  
 240  
 gacctaggca agaaccgcat caaaacgctc aaccaggacg agttcgccag cttcccgcac  
 300  
 ctggaggagc tggagctcaa cgagaacatc gtgagcgccg tggagcccgg cgccttcaac  
 360  
 aacctcttca acctccggac gctgggtctc cgcagcaacc gcctgaagct catccccgta  
 420  
 ggcgtcttca ctggcctcag caacctgacc aagctggaca tcagcgagaa caagatcggt  
 480

atcctactgg actacatggt tcaggacctg tacaacctca agtcactgga ggttggcgac  
 540  
 aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc tcaacagcct ggagcagctg  
 600  
 acgctggaga aatgcaacct gacctccatc cccaccgagg cgctgtcca cctgcacggc  
 660  
 ctcacgtgcc tgaggctccg gcacctcaac atcaatgcca tccgggacta ctccttcaag  
 720  
 aggctgtacc gactcaaggt cttggagatc tccactggc cctacttgga caccatgaca  
 780  
 cccaactgcc tctacggcct caacctgacg tccctgtcca tcacacactg caatctgacc  
 840  
 gctgtgccct acctggcctg ccgccaccta gtctatctcc gcttccctcaa cctctcctac  
 900  
 aaccccatca gcaccattga gggctccatg ttgcatgagc tgctccggct gcaggagatc  
 960  
 cagctgggtg gcgggcagct ggccgggtgg agccctgcct tccgcggcct caactacctg  
 1020  
 cgcgtgctca atgtctctgg caaccagctg accacactgg aggaatcagt cttccactcg  
 1080  
 gtgggcaacc tggagacact catcctggac tccaacccgc tggcctgcga ctgtcggctc  
 1140  
 ctgtgggtgt tccggcgccg tggcctacaa acttcaaccg gcagcagccc acgtgcgcca  
 1200  
 cgcccagatt tgtccagggg caaggagtcc aaggacttcc ctgatgtgct a  
 1251

<210> 2476

<211> 417

<212> PRT

<213> Homo sapiens

<400> 2476

Xaa	Ala	Pro	Glu	Met	Gln	Val	Ser	Lys	Arg	Met	Leu	Ala	Gly	Gly	Val
1				5					10					15	
Arg	Ser	Met	Pro	Ser	Pro	Leu	Leu	Ala	Cys	Trp	Gln	Pro	Ile	Leu	Leu
			20					25					30		
Leu	Val	Leu	Gly	Ser	Val	Leu	Ser	Gly	Ser	Ala	Thr	Gly	Cys	Pro	Pro
			35					40					45		
Arg	Cys	Glu	Cys	Ser	Ala	Gln	Asp	Arg	Ala	Val	Leu	Cys	His	Arg	Lys
			50				55					60			
Arg	Phe	Val	Ala	Val	Pro	Glu	Gly	Ile	Pro	Thr	Glu	Thr	Arg	Leu	Leu
					70					75				80	
Asp	Leu	Gly	Lys	Asn	Arg	Ile	Lys	Thr	Leu	Asn	Gln	Asp	Glu	Phe	Ala
				85					90					95	
Ser	Phe	Pro	His	Leu	Glu	Glu	Leu	Glu	Leu	Asn	Glu	Asn	Ile	Val	Ser
				100				105					110		
Ala	Val	Glu	Pro	Gly	Ala	Phe	Asn	Asn	Leu	Phe	Asn	Leu	Arg	Thr	Leu
			115				120					125			
Gly	Leu	Arg	Ser	Asn	Arg	Leu	Lys	Leu	Ile	Pro	Leu	Gly	Val	Phe	Thr
			130				135					140			
Gly	Leu	Ser	Asn	Leu	Thr	Lys	Leu	Asp	Ile	Ser	Glu	Asn	Lys	Ile	Val
				145			150			155				160	
Ile	Leu	Leu	Asp	Tyr	Met	Phe	Gln	Asp	Leu	Tyr	Asn	Leu	Lys	Ser	Leu

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<210> 2477
<211> 548
<212> DNA
<213> Homo sapiens
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<400> 2477
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60
gtggccgggg gctccctcca gctgtctctg gacggaggga cgggaagtgg ccagaagggg
120
aagtgtgagg agttcccgtc cagcctgtca tcagtctccc caggtcttga agcggcgggc
180
ctgctcctgg ccgtgaccat ggaccctctg gagacccta tcaaggatgg catcctctac
240
cagcagcatg tcaagtttgg caagaagtgc tggcggaagg tgtgggctct gctgtatgca
300
ggaggcccat caggcgtggc acggctggag aactgggagg tccgggatgg tggcctggga
360
gcagcgggtg acaggtcggc ggggcctggc cggcgagggg agcgacgggt catccgcctg
420
```

gctgactgtg tgtccgtgct gccggctgac ggcgagagct gccccggga caccggtgcc  
 480  
 ttctgtctca ccaccaccga gcgaagccat ctactggctg ctcagcaccg ccaggcctgg  
 540  
 atggggccc  
 548

<210> 2478<211> 113

<212> PRT

<213> Homo sapiens

<400> 2478

Leu	Glu	Thr	Pro	Ile	Lys	Asp	Gly	Ile	Leu	Tyr	Gln	Gln	His	Val	Lys
1				5				10					15		
Phe	Gly	Lys	Lys	Cys	Trp	Arg	Lys	Val	Trp	Ala	Leu	Leu	Tyr	Ala	Gly
			20				25					30			
Gly	Pro	Ser	Gly	Val	Ala	Arg	Leu	Glu	Asn	Trp	Glu	Val	Arg	Asp	Gly
		35					40					45			
Gly	Leu	Gly	Ala	Ala	Gly	Asp	Arg	Ser	Ala	Gly	Pro	Gly	Arg	Arg	Gly
	50					55					60				
Glu	Arg	Arg	Val	Ile	Arg	Leu	Ala	Asp	Cys	Val	Ser	Val	Leu	Pro	Ala
65					70				75					80	
Asp	Gly	Glu	Ser	Cys	Pro	Arg	Asp	Thr	Gly	Ala	Phe	Leu	Leu	Thr	Thr
			85					90					95		
Thr	Glu	Arg	Ser	His	Leu	Leu	Ala	Ala	Gln	His	Arg	Gln	Ala	Trp	Met
			100					105					110		

Gly

<210> 2479

<211> 324

<212> DNA

<213> Homo sapiens

<400> 2479

gaattcatgg aggtctatga ggaggatgaa gaatatgcgt atgaaaaata tgaaacccat  
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 ttccggcacga gctggatgga ggagaccgca ggcaccttct cactgaactg gtatcgcagc  
 120  
 aggtactgga atgacaatga agcagcagaa aggcttgcgt tgatgtgggc taaaaccttc  
 180  
 aaatatgcgt cgataaacgt ctctggcag accgggatta gcaatagcga cgacgagggc  
 240  
 aatgaagatg aagacatgtt ctacgccggt atctccattc cgctgggagg cggggcgctac  
 300  
 tctaactcct ggtatcgtga atat  
 324

<210> 2480

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2480

Glu Phe Met Glu Val Tyr Glu Glu Asp Glu Glu Tyr Ala Tyr Glu Lys  
 1 5 10 15  
 Tyr Glu Thr His Phe Gly Thr Ser Trp Met Glu Glu Thr Ala Gly Thr  
 20 25 30  
 Phe Ser Leu Asn Trp Tyr Arg Ser Arg Tyr Trp Asn Asp Asn Glu Ala  
 35 40 45  
 Ala Glu Arg Leu Ala Leu Met Trp Ala Lys Thr Phe Lys Tyr Ala Ser  
 50 55 60  
 Ile Asn Val Ser Trp Gln Thr Gly Ile Ser Asn Ser Asp Asp Glu Gly  
 65 70 75 80  
 Asn Glu Asp Glu Asp Met Phe Tyr Ala Gly Ile Ser Ile Pro Leu Gly  
 85 90 95  
 Gly Gly Ala Tyr Ser Asn Ser Trp Tyr Arg Glu Tyr  
 100 105

&lt;210&gt; 2481

&lt;211&gt; 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2481

gcgttcacta acgcttcaac aaactcttac aagcgtcttg ttcttggttt cgaagcacct  
 60  
 gttatgttggttt cttactcagc tcgtaaccgt tctgcttcta tccgtatccc atacgttgca  
 120  
 agccctaaag gcaagcgtat tgaagctcgt ttccctgatc caaccgctaa cccataccta  
 180  
 gcattttcag ctatgttgat ggctgggtatc gatgggtatca aaaacaagat tcaccctggc  
 240  
 gatgcagcag acaaagattt gtacgacctt ccagctgaag aagcagccgc tatecctcaa  
 300  
 gttgctagca gcttagaaga agcgtttaag tgcctagatc aagaccgtga gttcttgact  
 360  
 caaggtggcg ttttctctga cgacatgatc gatgcttaca tcgctcttaa agcagaagaa  
 420  
 gcacagcgtg ttgcaatgac aacaacacca cttgagttcg aactttacta cagcctataa  
 480  
 gctt  
 484

&lt;210&gt; 2482

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2482

Ala Phe Thr Asn Ala Ser Thr Asn Ser Tyr Lys Arg Leu Val Pro Gly  
 1 5 10 15  
 Phe Glu Ala Pro Val Met Leu Ala Tyr Ser Ala Arg Asn Arg Ser Ala  
 20 25 30  
 Ser Ile Arg Ile Pro Tyr Val Ala Ser Pro Lys Gly Lys Arg Ile Glu  
 35 40 45  
 Ala Arg Phe Pro Asp Pro Thr Ala Asn Pro Tyr Leu Ala Phe Ser Ala  
 50 55 60



```

Met Leu Met Ala Gly Ile Asp Gly Ile Lys Asn Lys Ile His Pro Gly
65          70          75          80
Asp Ala Ala Asp Lys Asp Leu Tyr Asp Leu Pro Ala Glu Glu Ala Ala
      85          90          95
Ala Ile Pro Gln Val Ala Ser Ser Leu Glu Glu Ala Leu Lys Cys Leu
      100         105         110
Asp Gln Asp Arg Glu Phe Leu Thr Gln Gly Gly Val Phe Ser Asp Asp
      115         120         125
Met Ile Asp Ala Tyr Ile Ala Leu Lys Ala Glu Glu Ala Gln Arg Val
      130         135         140
Ala Met Thr Thr Thr Pro Leu Glu Phe Glu Leu Tyr Tyr Ser Leu
145          150          155

```

&lt;210&gt; 2483

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2483

```

acgcgtgtta gccaaatctt ggttcctccc gttctctcct taccgagcc tgaggccctt
60
ctggagaaca ggcagcctct gaggaacct ctgatccccg atcagccacc ccacgcctg
120
cgccccagc cgcttctcc tggccttggt ccccttccc tgtgaaggag agaacagttt
180
cggctggccc tgagatgctg gcaggcctgc agtcagggca gtgggcgcct cccaccttga
240
aatggtcctt cgtggtgcag ttctgcttac ggggtagact ttgttgctt ccacagagga
300
cagttagggg gggcaggaag gaagtctctg ccacaagtct gcattccagg ctgtttccag
360
aagtgggaat tctctcgtgc cctggagtct gggaatgcat ttttagtttc ccagcttcag
420
gtagaattga aattgagtga gccaaacccac cacatccatc tggagccagg aactagt
477

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&lt;210&gt; 2484

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2484

```

Met His Ser Gln Thr Pro Gly His Glu Arg Ile Pro Thr Ser Gly Asn
1          5          10          15
Ser Leu Glu Cys Arg Leu Val Ala Glu Thr Ser Phe Leu Pro Thr Leu
      20          25          30
Thr Val Leu Cys Gly Arg Gln Gln Ser Leu Pro Arg Lys Gln Asn Cys
      35          40          45
Thr Thr Lys Asp His Phe Lys Val Gly Gly Ala His Cys Pro Asp Cys
      50          55          60
Arg Pro Ala Ser Ile Ser Gly Pro Ala Glu Thr Val Leu Ser Phe Thr
65          70          75          80
Gly Lys Gly Glu Gln Gly Gln Glu Glu Ala Ala Gly Asp Ala Gly Asp
      85          90          95

```

Gly Val Ala Asp Arg Gly Ser Glu Val Ser Ser Glu Ala Ala Cys Ser  
                   100                  105                  110  
 Pro Glu Gly Pro Gln Ala Arg Val Arg Arg Glu Arg Glu Glu Pro Arg  
                   115                  120                  125  
 Phe Gly  
           130

&lt;210&gt; 2485

&lt;211&gt; 608

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2485

accggtgagg cgaagtgcgg tggcaattac gcagcttcgc tgcgttccca gatcgatgcc  
 60  
 aagaccgcg actgcaacga ggtgctcttt gtcgatgcag ttgaacatcg ctggatcgag  
 120  
 gagctgggtg gtatgaactt catggccatc agcaaagacg gtcagctcgt caccctcgag  
 180  
 ctagctggca ccatactgcg tggcgtgacc cgcaagtcca ttctggaagt tgccccgac  
 240  
 ctcggtcttg aaccagtgga gcgcaagatc gatgttgacg agctccttga tggcgttcgc  
 300  
 tctggcgagt tcccggaagt cttcgctgtt ggtaccgccg cggttgtcac accgatcggc  
 360  
 tctttcctag atggagatac cgacgtgaag gtctctgagc ccaccggaaa gaccacgatg  
 420  
 gagatccgtc gccgtctgct ggatatccag ttcgacgcg ctgaggacac ccatggctgg  
 480  
 ttgaagcgag tctgctgacg gcgtcgacga ccattggggc cggccccaat gatgtgttca  
 540  
 cgatcgggct acgacggtgt cgatgacaat gtcttcgggc tggaagggtt gcccgacggt  
 600  
 gaacgcgt  
 608

&lt;210&gt; 2486

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2486

Thr Gly Glu Ala Lys Cys Gly Gly Asn Tyr Ala Ala Ser Leu Arg Ser  
   1                  5                  10                  15  
 Gln Ile Asp Ala Lys Thr Arg Asp Cys Asn Glu Val Leu Phe Val Asp  
           20                  25                  30  
 Ala Val Glu His Arg Trp Ile Glu Leu Gly Gly Met Asn Phe Met  
           35                  40                  45  
 Ala Ile Ser Lys Asp Gly Gln Leu Val Thr Pro Glu Leu Ala Gly Thr  
           50                  55                  60  
 Ile Leu Arg Gly Val Thr Arg Lys Ser Ile Leu Glu Val Ala Pro Asp  
   65                  70                  75                  80  
 Leu Gly Leu Glu Pro Val Glu Arg Lys Ile Asp Val Asp Glu Leu Leu  
                   85                  90                  95

Asp Gly Val Arg Ser Gly Glu Phe Pro Glu Val Phe Ala Cys Gly Thr  
 100 105 110  
 Ala Ala Val Val Thr Pro Ile Gly Ser Phe Leu Asp Gly Asp Thr Asp  
 115 120 125  
 Val Lys Val Ser Glu Pro Thr Gly Lys Thr Thr Met Glu Ile Arg Arg  
 130 135 140  
 Arg Leu Leu Asp Ile Gln Phe Gly Arg Ala Glu Asp Thr His Gly Trp  
 145 150 155 160  
 Leu Lys Arg Val Cys  
 165

&lt;210&gt; 2487

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2487

nnccctcag gagagcagcc catggaaggt ccccccaag gggccctga gagccctgac  
 60  
 agtctgcaaa gaaaccagaa agagctccag ggcctcctga cccaggtgca agccctggag  
 120  
 aaggaggccg caagcagtgt ggacgtgcag gccctgcgga ggctctttga ggccgtgccc  
 180  
 cagctgggag gggctgctcc tcaggctcct gctgcccacc aaaagcccg ggcctcagtg  
 240  
 gagcaggcct ttggggagct gacacgggtc agcacggaag ttgctcaact gaaggaacag  
 300  
 accttggtaa ggctgctgga cattgaagag gctgtgcac  
 339

&lt;210&gt; 2488

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2488

Xaa Pro Ser Gly Glu Gln Pro Met Glu Gly Pro Pro Gln Gly Ala Pro  
 1 5 10 15  
 Glu Ser Pro Asp Ser Leu Gln Arg Asn Gln Lys Glu Leu Gln Gly Leu  
 20 25 30  
 Leu Thr Gln Val Gln Ala Leu Glu Lys Glu Ala Ala Ser Ser Val Asp  
 35 40 45  
 Val Gln Ala Leu Arg Arg Leu Phe Glu Ala Val Pro Gln Leu Gly Gly  
 50 55 60  
 Ala Ala Pro Gln Ala Pro Ala Ala His Gln Lys Pro Glu Ala Ser Val  
 65 70 75 80  
 Glu Gln Ala Phe Gly Glu Leu Thr Arg Val Ser Thr Glu Val Ala Gln  
 85 90 95  
 Leu Lys Glu Gln Thr Leu Val Arg Leu Leu Asp Ile Glu Glu Ala Val  
 100 105 110  
 His

&lt;210&gt; 2489

&lt;211&gt; 594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2489

nacgcgttct tcggactggc gacgatgctg atttctatcc cgacgggggt gaagctatatt  
 60  
 aactggctgg tcaccatcta tcacggccgg gtgcgtatca ccagccaggt tctttggacc  
 120  
 ctgggcttca tggtagacct cgcgatcgga ggcgatgacc gcgtactgct ggccatcccc  
 180  
 ggtgctgact tcgtactgca caacagcctg ttcggaattg ctcacttcca caacgtgatc  
 240  
 atcggcggcg cagtattcgg ctacatcgca ggtttcagct tctacttccc gaaagcggtc  
 300  
 ggcttcaagc tgcaagaaag ctggggcaag gctgcattct ggttctggat ctcgggcttc  
 360  
 ttcgtcgcgt tcatgccgct ctatgcactg ggtttcatgg gcatgaccgg ttgtttgaac  
 420  
 gcccccccca cccctgagtg ggtcccgtag ctgtacgttg ccatggtcgg tgactgatg  
 480  
 atcgtgtcgc gtatcgctg ccagttgatt cagctgtatg tcagcgtgcg tgatcgcaag  
 540  
 cagaacatgt gcgaatccgg cgacccatgg aatgcacaca ccctggaatg gtcg  
 594

&lt;210&gt; 2490

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2490

Xaa	Ala	Phe	Phe	Gly	Leu	Ala	Thr	Met	Leu	Ile	Ser	Ile	Pro	Thr	Gly	1	5	10	15
Val	Lys	Leu	Phe	Asn	Trp	Leu	Val	Thr	Ile	Tyr	His	Gly	Arg	Val	Arg	20	25	30	
Ile	Thr	Ser	Gln	Val	Leu	Trp	Thr	Leu	Gly	Phe	Met	Val	Thr	Phe	Ala	35	40	45	
Ile	Gly	Gly	Met	Thr	Gly	Val	Leu	Leu	Ala	Ile	Pro	Gly	Ala	Asp	Phe	50	55	60	
Val	Leu	His	Asn	Ser	Leu	Phe	Gly	Ile	Ala	His	Phe	His	Asn	Val	Ile	65	70	75	80
Ile	Gly	Gly	Ala	Val	Phe	Gly	Tyr	Ile	Ala	Gly	Phe	Ser	Phe	Tyr	Phe	85	90	95	
Pro	Lys	Ala	Phe	Gly	Phe	Lys	Leu	His	Glu	Ser	Trp	Gly	Lys	Ala	Ala	100	105	110	
Phe	Trp	Phe	Trp	Ile	Ser	Gly	Phe	Val	Ala	Phe	Met	Pro	Leu	Tyr		115	120	125	
Ala	Leu	Gly	Phe	Met	Gly	Met	Thr	Arg	Cys	Leu	Asn	Ala	Pro	Pro	Thr	130	135	140	
Pro	Glu	Trp	Val	Pro	Tyr	Leu	Tyr	Val	Ala	Met	Val	Gly	Ala	Leu	Met	145	150	155	160
Ile	Ala	Val	Gly	Ile	Ala	Cys	Gln	Leu	Ile	Gln	Leu	Tyr	Val	Ser	Val	165	170	175	

Arg Asp Arg Lys Gln Asn Met Cys Glu Ser Gly Asp Pro Trp Asn Ala  
                   180                  185                  190  
 His Thr Leu Glu Trp Ser  
                   195

<210> 2491  
 <211> 592  
 <212> DNA  
 <213> Homo sapiens

<400> 2491  
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 actacgttgt tgcctggtct attccatgca gtaacgacga atatgtcgcg atctcaggat  
 120  
 gatcttgcag tgttcgaaag cggaactgta ttccgcgcgc tcaactccggc tgcggcaccg  
 180  
 cgtcccggcg tgcagcagcg cccctccgat gaagtccttg ccgagatcga cgccgccttg  
 240  
 ccagcccagc cgcgcatgct cgcggccgtg atctgtggca gctggctgcc cgatcgctgg  
 300  
 gatggagagt cgggtcaaggc tgactggcga cacgctgtgc tggtcgcccga gaaggctgct  
 360  
 gatgctcttg gcgtgaggct ggtgcgcaag gctgaccgtc aggctccatg gcatcccggc  
 420  
 cgttgtgcgg ctctcatcgt cgatgggaag gtcattggcc atgctggtga gttgcacccc  
 480  
 acagtagtgt cgaaggctgg tctgcctcag cgcacctgtg cggtcgagtt caatctagat  
 540  
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 592

<210> 2492  
 <211> 197  
 <212> PRT  
 <213> Homo sapiens

<400> 2492  
 Thr Arg His Ala Thr Val Lys Leu Ala Asn Pro Leu Asp Asp Thr Arg  
   1                  5                  10                  15  
 Pro Tyr Leu Arg Thr Thr Leu Leu Pro Gly Leu Phe His Ala Val Thr  
                   20                  25                  30  
 Thr Asn Met Ser Arg Ser Gln Asp Asp Leu Ala Val Phe Glu Ser Gly  
                   35                  40                  45  
 Thr Val Phe Arg Ala Val Thr Pro Ala Ala Ala Pro Arg Pro Gly Val  
                   50                  55                  60  
 Asp Glu Arg Pro Ser Asp Glu Val Leu Ala Glu Ile Asp Ala Ala Leu  
   65                  70                  75                  80  
 Pro Ala Gln Pro Arg Met Leu Ala Ala Val Ile Cys Gly Ser Trp Leu  
                   85                  90                  95  
 Pro Asp Arg Trp Asp Gly Glu Ser Val Lys Ala Asp Trp Arg His Ala  
                   100                  105                  110  
 Val Leu Val Ala Gln Lys Ala Ala Asp Ala Leu Gly Val Arg Leu Val  
                   115                  120                  125

Arg Lys Ala Asp Arg Gln Ala Pro Trp His Pro Gly Arg Cys Ala Ala  
 130 135 140  
 Leu Ile Val Asp Gly Lys Val Ile Gly His Ala Gly Glu Leu His Pro  
 145 150 155 160  
 Thr Val Val Ser Lys Ala Gly Leu Pro Gln Arg Thr Cys Ala Val Glu  
 165 170 175  
 Phe Asn Leu Asp Ala Leu Val Ala Cys Ala Pro Ser Gly Gly Glu Val  
 180 185 190  
 Met Val Ile Ser Arg  
 195

&lt;210&gt; 2493

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2493

acgcgtcagg ttgccggtga tcgtgccacc gtcacctcca tgggtgccttc aggagcagac  
 60  
 cccacacact atgagccgtc gctgcgtgac gttcggaccg tcgtgtattc gagagtcgcg  
 120  
 ctatcgaact acctcatgct cgaacctcat tcggtcatca agaccatcga ctcttcccta  
 180  
 cctacgggat ctatcaatgt ctccctggct gaggaagccc aaaagtacgg cgcacaagtg  
 240  
 atccccgtgg ttgaaaatgc caacctagac accgtgtggc tgggggttgcg cgtcattggc  
 300  
 aaggcgcca ggcggggagc cgaccgtct tctcgggtct acctccagct gacgtcggtg  
 360  
 gaggggctg gggacttcac tgcctatata actgggacct ttggtcgacc tcagatct  
 418

&lt;210&gt; 2494

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2494

Thr Arg Gln Val Ala Gly Asp Arg Ala Thr Val Thr Ser Met Val Pro  
 1 5 10 15  
 Ser Gly Ala Asp Pro His Thr Tyr Glu Pro Ser Leu Arg Asp Val Arg  
 20 25 30  
 Thr Val Val Tyr Ser Arg Val Ala Leu Ser Asn Tyr Leu Met Leu Glu  
 35 40 45  
 Pro His Ser Val Ile Lys Thr Ile Asp Ser Ser Leu Pro Thr Gly Ser  
 50 55 60  
 Ile Asn Val Ser Leu Ala Glu Glu Ala Gln Lys Tyr Gly Ala Gln Val  
 65 70 75 80  
 Ile Pro Leu Val Glu Asn Ala Asn Leu Asp Thr Val Trp Leu Gly Leu  
 85 90 95  
 Arg Val Ile Gly Lys Gly Ala Arg Arg Gly Ala Asp Arg Ser Ser Ser  
 100 105 110  
 Val Tyr Leu Gln Leu Thr Ser Val Glu Gly Pro Gly Asp Phe Thr Ala  
 115 120 125

Tyr Ile Thr Gly Thr Phe Gly Arg Pro Gln Ile  
 130 135

<210> 2495

<211> 1478

<212> DNA

<213> Homo sapiens

<400> 2495

nnggcctggc ccagttgcac cacgagcgct gcggacactc ggggcggcag tcggtctgtc  
 60  
 agtcctcccg ccaggtcccg cgccccgcac ctgccgcccg cacctgcagc tccgcacctg  
 120  
 cggccagtgc ctactgcctt ctcttgccgc ccgcacctgc agccccgcac ctgccgcttg  
 180  
 cacctgcagc cccgcgctct acccggttca agcatggctg accaggcgcc cttcgacacg  
 240  
 gacgtcaaca ccctgacctg ctctgctatg gaggagggca ggaaggcccg cggcacgggc  
 300  
 gagttgacct agctgctcaa ctgctctgac acagcagtca aagccatctc ttcggcggtg  
 360  
 cgcaaggcgg gcctcgcgca cctctatggc attgctgggt ctaccaacgt gacaggtgat  
 420  
 caagttaaga agctggacgt cctctccaac gacctgggta tgaacatgtt aaagtcattc  
 480  
 tttgccacgt gtgttctcgt gtcagaagaa gataaacacg ccatcatagt ggaaccggag  
 540  
 aaaaggggta aatatgtggt ctgttttgat ccccttgatg gatcttccaa catcgattgc  
 600  
 cttgtgtccg ttggaaccat ttttggcatc tatagaaaga aatcaactga tgagccttct  
 660  
 gagaaggatg ctctgcaacc aggccggaac ctggtggcag ccggtacgc actgtatggc  
 720  
 agtgccacca tgctggctct tgccatggac tgtggggcca actgcttcat gctggacctg  
 780  
 gccatcgggg agttcatttt ggtggacaag gatgtgaaga taaaaaagaa aggtaaaatc  
 840  
 tacagcctta acgagggcta cgccaaggac tttgacctg ccgtcactga gtacatccag  
 900  
 aggaagaagt tccccccaga taattcagct ctttatgggg cccggtatgt gggctccatg  
 960  
 gtggctgatg ttcctgcac tctggtctac ggagggatat ttctgtacct cgctaacaag  
 1020  
 aagagcccca atggaaagct gagactgctg tacgaatgca accccatggc ctacgtcatg  
 1080  
 gagaaggctg ggggaatggc caccactggg aaggaggccg tgttagacgt cattcccaca  
 1140  
 gacattcacc agagggcgcc ggtgatcttg ggggtccccg acgacgtgct cgagttcctg  
 1200  
 aaggtgtatg agaagcactc tgcccagtga gcacctgccc tgctgcac cggagaattg  
 1260  
 cctctacctg gaccttttgt ctcacacagc agtacctga cctgctgtgc accttacatt  
 1320

cctagagagc agaaataaaa agcatgacta tttccacccat caaatgctgt agaattgcttg  
 1380  
 gcactcccta accaaatgct gtctccataa tgccactggg gtttaagatat attttgagtg  
 1440  
 gatggaggag aaataaaactt attcctcctt aaaaaaaaa  
 1478

<210> 2496

<211> 338

<212> PRT

<213> Homo sapiens

<400> 2496

Met	Ala	Asp	Gln	Ala	Pro	Phe	Asp	Thr	Asp	Val	Asn	Thr	Leu	Thr	Arg
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Phe	Val	Met	Glu	Gly	Arg	Lys	Ala	Arg	Gly	Thr	Gly	Glu	Leu	Thr	
		20				25						30			
Gln	Leu	Leu	Asn	Ser	Leu	Cys	Thr	Ala	Val	Lys	Ala	Ile	Ser	Ser	Ala
	35					40					45				
Val	Arg	Lys	Ala	Gly	Ile	Ala	His	Leu	Tyr	Gly	Ile	Ala	Gly	Ser	Thr
	50					55				60					
Asn	Val	Thr	Gly	Asp	Gln	Val	Lys	Lys	Leu	Asp	Val	Leu	Ser	Asn	Asp
65					70					75				80	
Leu	Val	Met	Asn	Met	Leu	Lys	Ser	Ser	Phe	Ala	Thr	Cys	Val	Leu	Val
		85				90						95			
Ser	Glu	Glu	Asp	Lys	His	Ala	Ile	Ile	Val	Glu	Pro	Glu	Lys	Arg	Gly
		100					105					110			
Lys	Tyr	Val	Val	Cys	Phe	Asp	Pro	Leu	Asp	Gly	Ser	Ser	Asn	Ile	Asp
	115					120						125			
Cys	Leu	Val	Ser	Val	Gly	Thr	Ile	Phe	Gly	Ile	Tyr	Arg	Lys	Lys	Ser
	130					135				140					
Thr	Asp	Glu	Pro	Ser	Glu	Lys	Asp	Ala	Leu	Gln	Pro	Gly	Arg	Asn	Leu
145					150					155				160	
Val	Ala	Ala	Gly	Tyr	Ala	Leu	Tyr	Gly	Ser	Ala	Thr	Met	Leu	Val	Leu
		165				170						175			
Ala	Met	Asp	Cys	Gly	Val	Asn	Cys	Phe	Met	Leu	Asp	Pro	Ala	Ile	Gly
		180				185						190			
Glu	Phe	Ile	Leu	Val	Asp	Lys	Asp	Val	Lys	Ile	Lys	Lys	Lys	Gly	Lys
	195					200					205				
Ile	Tyr	Ser	Leu	Asn	Glu	Gly	Tyr	Ala	Lys	Asp	Phe	Asp	Pro	Ala	Val
	210					215				220					
Thr	Glu	Tyr	Ile	Gln	Arg	Lys	Lys	Phe	Pro	Pro	Asp	Asn	Ser	Ala	Pro
225				230					235					240	
Tyr	Gly	Ala	Arg	Tyr	Val	Gly	Ser	Met	Val	Ala	Asp	Val	His	Arg	Thr
		245				250						255			
Leu	Val	Tyr	Gly	Gly	Ile	Phe	Leu	Tyr	Pro	Ala	Asn	Lys	Lys	Ser	Pro
		260				265						270			
Asn	Gly	Lys	Leu	Arg	Leu	Leu	Tyr	Glu	Cys	Asn	Pro	Met	Ala	Tyr	Val
	275					280					285				
Met	Glu	Lys	Ala	Gly	Gly	Met	Ala	Thr	Thr	Gly	Lys	Glu	Ala	Val	Leu
295				300											290
Asp	Val	Ile	Pro	Thr	Asp	Ile	His	Gln	Arg	Ala	Pro	Val	Ile	Leu	Gly
305				310					315					320	
Ser	Pro	Asp	Asp	Val	Leu	Glu	Phe	Leu	Lys	Val	Tyr	Glu	Lys	His	Ser



325 330 335

Ala Gln

<210> 2497  
 <211> 399  
 <212> DNA  
 <213> Homo sapiens

<400> 2497  
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 60  
 cttggctacc tgccacagga tccccgcgac ccagacatgg aaatgatcgc gagggcaagg  
 120  
 atcctgtcag cgcggtggcct ggaccacata ctggaacgga tgcgcaccct ggagtatcag  
 180  
 atggcgaacg gttccgagga cgaccgtgcc gttgcgatgg acaaatacgc gaaggctgaa  
 240  
 gaccgtctcg tcgcggcccg tggctatggc gcctctgcag aggcagcccg aatcgcgtcg  
 300  
 aacttggggc ttgacgaccg cgtcctttcc cagccgttga aaaacctctc ggggtggtcag  
 360  
 cgtcgtcgcg tcgagctggc gcgcatactc ttttccgga  
 399

<210> 2498  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 2498  
 Thr Arg Val Leu Ala Gly Glu Thr Leu Pro Ala Ala Gly Ser Val Arg  
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 Arg Thr Gly Glu Leu Gly Tyr Leu Pro Gln Asp Pro Arg Asp Pro Asp  
 20 25 30  
 Met Glu Met Ile Ala Arg Ala Arg Ile Leu Ser Ala Arg Gly Leu Asp  
 35 40 45  
 His Ile Leu Glu Arg Met Arg Thr Leu Glu Tyr Gln Met Ala Asn Gly  
 50 55 60  
 Ser Glu Asp Asp Arg Ala Val Ala Met Asp Lys Tyr Ala Lys Ala Glu  
 65 70 75 80  
 Asp Arg Leu Val Ala Ala Gly Gly Tyr Gly Ala Ser Ala Glu Ala Ala  
 85 90 95  
 Arg Ile Ala Ser Asn Leu Gly Leu Asp Asp Arg Val Leu Ser Gln Pro  
 100 105 110  
 Leu Lys Asn Leu Ser Gly Gly Gln Arg Arg Arg Val Glu Leu Ala Arg  
 115 120 125  
 Ile Leu Phe Ser Gly  
 130

<210> 2499  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 2499

nggccgggag aagaccggtt ctatatggcc taccacgaca ccgagtgggg cgtgccggaa  
 60  
 tatgacgacc gcgcattgta cgagaagctc attctcgacg gattccaggc cggcctgtcg  
 120  
 tggatcacca tcttgcgcaa gcgcgacaac tttcgcaaag ccttcgacga tttccagccc  
 180  
 gagaagatag cgcggttata tgagaagaag gttcacgcgc tgatgaacga tgccggcatc  
 240  
 gtgcgcaacc gcgccaagat cgaaggcacg atcgccagcg cgaaggcgta tctcgacatc  
 300  
 atggaaaaag gcccgggctt ctccaggctg ctgtgggact tcgtcgac  
 348

&lt;210&gt; 2500

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2500

Xaa	Pro	Gly	Glu	Asp	Pro	Phe	Tyr	Met	Ala	Tyr	His	Asp	Thr	Glu	Trp
1				5					10					15	
Gly	Val	Pro	Glu	Tyr	Asp	Asp	Arg	Ala	Leu	Tyr	Glu	Lys	Leu	Ile	Leu
		20					25						30		
Asp	Gly	Phe	Gln	Ala	Gly	Leu	Ser	Trp	Ile	Thr	Ile	Leu	Arg	Lys	Arg
	35					40					45				
Asp	Asn	Phe	Arg	Lys	Ala	Phe	Asp	Asp	Phe	Gln	Pro	Glu	Lys	Ile	Ala
	50					55				60					
Arg	Tyr	Asn	Glu	Lys	Lys	Val	His	Ala	Leu	Met	Asn	Asp	Ala	Gly	Ile
65				70					75					80	
Val	Arg	Asn	Arg	Ala	Lys	Ile	Glu	Gly	Thr	Ile	Ala	Ser	Ala	Lys	Ala
			85					90					95		
Tyr	Leu	Asp	Ile	Met	Glu	Lys	Gly	Pro	Gly	Phe	Ser	Arg	Leu	Leu	Trp
		100						105					110		
Asp	Phe	Val	Asp												
		115													

&lt;210&gt; 2501

&lt;211&gt; 569

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2501

gaattcgatt catttgtggc aaatgcttac aatttgatga ttgtaacca tcaaatcaca  
 60  
 taatgcccat taagccactc catacacttc tttaaataagg aaaatatatg taaagtacgt  
 120  
 acttagcaca gggcctgacc tatagtaatg gtcaagaatg atagcggggg tgaggtatgg  
 180  
 ctttcaagag tcaaacaatt ttactggtgc atcatttcca tttattcttt ctcttttgca  
 240  
 taataaaaacc actcttaaga ttctaccttg gttagttaga gacaacagtt ctctggaaag  
 300

tagattctat agcttcaact ccctgaagag atgtgtgcta atttacaatca aaaaaatcct  
 360  
 taagggtata aaatatgccca agaactgtca acatcacaga ttaccactgg tagcttctgg  
 420  
 tatattgtta agtttccact taatttttaa gggacactag agaattagta tgactcacct  
 480  
 acactaagtt tatatactgt atttaacagt gtaattttca aatatgacag gaataaccca  
 540  
 gatgtgaaat gctgaatcat taatcacag  
 569

<210> 2502

<211> 100

<212> PRT

<213> Homo sapiens

<400> 2502

Met	Ile	Ala	Gly	Val	Arg	Tyr	Gly	Phe	Gln	Glu	Ser	Asn	Asn	Phe	Thr
1				5					10					15	
Gly	Ala	Ser	Phe	Pro	Phe	Ile	Leu	Ser	Leu	Leu	His	Asn	Lys	Thr	Thr
			20					25					30		
Leu	Lys	Ile	Leu	Pro	Trp	Leu	Val	Arg	Asp	Asn	Ser	Ser	Leu	Glu	Ser
		35				40					45				
Arg	Phe	Tyr	Ser	Phe	Asn	Ser	Leu	Lys	Arg	Cys	Val	Leu	Ile	Tyr	Ile
	50				55				60						
Lys	Lys	Ile	Leu	Lys	Gly	Ile	Lys	Tyr	Ala	Lys	Asn	Cys	Gln	His	His
65				70					75					80	
Arg	Leu	Pro	Leu	Val	Ala	Ser	Gly	Ile	Leu	Leu	Ser	Phe	His	Leu	Ile
			85					90						95	
Phe	Lys	Gly	His												
			100												

<210> 2503

<211> 419

<212> DNA

<213> Homo sapiens

<400> 2503

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 aaggccttgc tacctcagca gtectacagc ttggcccagc cgctgtattc tccagtctgc  
 120  
 accaatgggg agcgctttct ctacctgccg ccacctcact acgtcgggtcc ccacatccca  
 180  
 tcgtccttgg catcaccat gaggtctctg acaccttcgg cctccccagc catccgcct  
 240  
 ctgtccatt gcgcagacaa aagcctcccg tggaagatgg gcgtcagccc tgggaatcct  
 300  
 gttgattccc acgcctatcc tcacatccag aacagtaagc agcccagggt tccctctgcc  
 360  
 aaggcgggtca ccagtggcct gccgggggac acagctctcc tgttgcccc ctcacgcgt  
 419

<210> 2504

<211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 2504  
 Met Tyr Lys Ala Leu Leu Pro Gln Gln Ser Tyr Ser Leu Ala Gln Pro  
 1 5 10 15  
 Leu Tyr Ser Pro Val Cys Thr Asn Gly Glu Arg Phe Leu Tyr Leu Pro  
 20 25 30  
 Pro Pro His Tyr Val Gly Pro His Ile Pro Ser Ser Leu Ala Ser Pro  
 35 40 45  
 Met Arg Leu Ser Thr Pro Ser Ala Ser Pro Ala Ile Pro Pro Leu Val  
 50 55 60  
 His Cys Ala Asp Lys Ser Leu Pro Trp Lys Met Gly Val Ser Pro Gly  
 65 70 75 80  
 Asn Pro Val Asp Ser His Ala Tyr Pro His Ile Gln Asn Ser Lys Gln  
 85 90 95  
 Pro Arg Val Pro Ser Ala Lys Ala Val Thr Ser Gly Leu Pro Gly Asp  
 100 105 110  
 Thr Ala Leu Leu Leu Pro Pro Ser Arg  
 115 120

<210> 2505  
 <211> 540  
 <212> DNA  
 <213> Homo sapiens

<400> 2505  
 tccggagcca atccgactca ggccctcgtc tggagccagg tgctgttgag catggggttg  
 60  
 ccgctcgtgt tgggtgccgtt ggctcgggtc accggcgatc ggcgtctgat gggccaatgg  
 120  
 acgaatgggc gtgtcatggc cgccatcgcg tggatcgteg tggcagcagt ctcggtcttc  
 180  
 aacgtgggtc tcgtcgtcga gacggtcatg ggtgcatgat ccttgagggc agttttctgg  
 240  
 cgacaatcgt gaaaatgagt gacaaactca agcgggtgac gacgccgaac cccgcaccga  
 300  
 cctctgcccc cgagctagcc aacgatttgg ccaactgcatt tcgcgggtac cctgctggag  
 360  
 tggcgatcct cagcagcatg ggagcggctg ggcccagagg cttgacggtc tcctccctgg  
 420  
 cgtcgggtgc agtcgtcccg gctgttgtgt cggtgtcgtt gggtaatggt tcgacgaccc  
 480  
 tggccaccct gacggaggag tcccgcgtca tcgtccacat gcttgatgca gatcgcgcg  
 540

<210> 2506  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<400> 2506  
 Ser Gly Ala Asn Pro Thr Gln Ala Leu Val Trp Ser Gln Val Leu Leu

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      1             5             10             15
Ser Met Gly Leu Pro Leu Val Leu Val Pro Leu Ala Arg Phe Thr Gly
      20             25             30
Asp Arg Arg Leu Met Gly Gln Trp Thr Asn Gly Arg Val Met Ala Ala
      35             40             45
Ile Ala Trp Ile Val Val Ala Ala Val Ser Ala Leu Asn Val Val Leu
      50             55             60
Val Val Glu Thr Val Met Gly Ala
65             70

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&lt;210&gt; 2507

&lt;211&gt; 922

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2507

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nacgcgtgaa gggcagagga gagagaccag tgaaggggga ggaggcggcc aaaaggagac
60
agcttcatgc cccaggaca taaatagccc ggctgctgca ggtacctgaa ggagtccagg
120
acggagcagt gccccctgtt ttcacagcac aagtgcgcgc agcaccggcc gttcacctgc
180
ttccactggc acttctctcaa ccagcggcgc cgcaggcccc tccgcaggcg cgacggcacc
240
ttcaactaca gccccgacgt gtactgtctc aagtacaacg aagccaccgg cgtgtgcccc
300
gacggcgacg agtgtcccta cctgcaccgg acgacggggg acacagaacg caagtaccac
360
ctgcgttact aaaaaacagg aacctgcac cagcagacag acgcacgtgg cactgcgtg
420
aagaatgggc tgcactgtgc ctctcgccac gggcccatg acctccgctc ccctgtctac
480
gacatcaggg agcttcaggc catggaggcc ttgcagaatg gccagaccac ggtagagggg
540
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600
gaggagcctc ggtggcaaga gactgcttat gtgctgggga actataagac ggagccttgc
660
aagaagcccc cgcggctgtg ccgccaaggc tatgcctgtc cctactacca caacagcaag
720
gaccggcggc ggagcccccg gaagcacaaa tacaggctcg ctccatgtcc aaacgtcaag
780
cacggggatg agtggggaga ccctggcaag tgtgagaacg gagacgcctg ccagtactgc
840
cacacccgca ccgagcagca gttccacccc gagatctaca agtccaccaa gtgcaacgga
900
aggggggggg gggtagaggga gg
922

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&lt;210&gt; 2508

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2508

Pro Gly Cys Cys Arg Tyr Leu Lys Glu Phe Arg Thr Glu Gln Cys Pro  
 1 5 10 15  
 Leu Phe Ser Gln His Lys Cys Ala Gln His Arg Pro Phe Thr Cys Phe  
 20 25 30  
 His Trp His Phe Leu Asn Gln Arg Arg Arg Arg Pro Leu Arg Arg Arg  
 35 40 45  
 Asp Gly Thr Phe Asn Tyr Ser Pro Asp Val Tyr Cys Ser Lys Tyr Asn  
 50 55 60  
 Glu Ala Thr Gly Val Cys Pro Asp Gly Asp Glu Cys Pro Tyr Leu His  
 65 70 75 80  
 Arg Thr Thr Gly Asp Thr Glu Arg Lys Tyr His Leu Arg Tyr Tyr Lys  
 85 90 95  
 Thr Gly Thr Cys Ile His Glu Thr Asp Ala Arg Gly His Cys Val Lys  
 100 105 110  
 Asn Gly Leu His Cys Ala Phe Ala His Gly Pro His Asp Leu Arg Ser  
 115 120 125  
 Pro Val Tyr Asp Ile Arg Glu Leu Gln Ala Met Glu Ala Leu Gln Asn  
 130 135 140  
 Gly Gln Thr Thr Val Glu Gly Ser Ile Glu Gly Gln Ser Ala Gly Ala  
 145 150 155 160  
 Ala Ser His Ala Met Ile Glu Lys Ile Leu Ser Glu Glu Pro Arg Trp  
 165 170 175  
 Gln Glu Thr Ala Tyr Val Leu Gly Asn Tyr Lys Thr Glu Pro Cys Lys  
 180 185 190  
 Lys Pro Pro Arg Leu Cys Arg Gln Gly Tyr Ala Cys Pro Tyr Tyr His  
 195 200 205  
 Asn Ser Lys Asp Arg Arg Arg Ser Pro Arg Lys His Lys Tyr Arg Ser  
 210 215 220  
 Ser Pro Cys Pro Asn Val Lys His Gly Asp Glu Trp Gly Asp Pro Gly  
 225 230 235 240  
 Lys Cys Glu Asn Gly Asp Ala Cys Gln Tyr Cys His Thr Arg Thr Glu  
 245 250 255  
 Gln Gln Phe His Pro Glu Ile Tyr Lys Ser Thr Lys Cys Asn Gly Arg  
 260 265 270  
 Gly Gly Gly Val Arg Glu  
 275

&lt;210&gt; 2509

&lt;211&gt; 348

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2509

gccggccttg acctgggccg ggcgatggct ccacggcaag gtccaataact ccgtgcgctt  
 60  
 gtggcgctgg acttcgtcga tgcccgcgag gttttgctgc ccgcgaccat tggactggac  
 120  
 gttcatgaac ggggtggagcc cggcaaaacc gaaactcaac caatccttgg ggatgctgga  
 180  
 cggcaggttg ccgagggcaa acacgttgac cagtttcgca ccgacaccac cgaccacggc  
 240  
 caccgctccc agcggaatct cgtagactta gcgccagggt tggttaaggcg tgtagcggtc  
 300

gtaacgacgg gtgacctga actcggggct tcaaagtctt ctgctgtg  
348

<210> 2510

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2510

Met	Ala	Pro	Arg	Gln	Gly	Pro	Ile	Leu	Arg	Ala	Leu	Val	Ala	Leu	Asp
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Phe	Val	Asp	Ala	Arg	Glu	Val	Leu	Leu	Pro	Ala	Thr	Ile	Gly	Leu	Asp
			20					25					30		
Val	His	Glu	Arg	Val	Glu	Pro	Gly	Lys	Thr	Glu	Thr	Gln	Pro	Ile	Leu
		35					40					45			
Gly	Asp	Ala	Gly	Arg	Gln	Val	Ala	Glu	Gly	Lys	His	Val	Asp	His	Val
	50					55					60				
Arg	Thr	Asp	Thr	Thr	Asp	His	Gly	His	Arg	Ser	Gln	Arg	Asn	Leu	Val
65					70				75					80	
Asp	Leu	Ala	Pro	Gly	Leu	Val	Arg	Arg	Val	Ala	Val	Val	Thr	Thr	Gly
			85					90					95		
Asp	Leu	Glu	Leu	Gly	Ala	Ser	Lys	Ser	Ser	Ala	Val				
			100					105							

<210> 2511

<211> 663

<212> DNA

<213> Homo sapiens

<400> 2511

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120  
cctgtcatcg cacacgtcgg ttatccgcag gccgccgacg agtattacca gttgctttta  
180  
gcattacgcc caggacgcgt tgctggcctg gcggagatcg tcgtcaacgg tcaacctttt  
240  
accgtcactg acgccactga ggatgaacta gctctcactg cttgggctcg tatectctc  
300  
gaggggaactc ccatcgccat ggatggatcg tggcagctgc atcgccgctg agcgggccct  
360  
gagccagttc ggttcgctaa gcgcttcggt ggtgagcaat cgaacacctc gatcatgggtg  
420  
ggcgacgcca tcatcatcaa aatgttccgc cgcttgagc ccggcgacaa ccttgacatc  
480  
accgtgcata gcgccctcaa cgatgccggg atctcatcgg tggccacatt gtacggcttt  
540  
atgtccggac agatccccgc tgaggaacac atcccggctg atctagctat gatcattgag  
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660  
gac  
663

<210> 2512  
 <211> 221  
 <212> PRT  
 <213> Homo sapiens

<400> 2512  
 Xaa Arg Val Trp Asp His Ile Arg Gly Ala Arg Trp Phe Ser Gly Lys  
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 Gly Arg Gly Gly Ser Leu Thr Arg Leu Leu Ser Leu Ala Pro Val Val  
 20 25 30  
 Asn Glu Gln Asp Leu Gln Val Leu Pro Val Ile Ala His Val Gly Tyr  
 35 40 45  
 Pro Gln Ala Ala Asp Glu Tyr Tyr Gln Leu Leu Leu Ala Leu Arg Pro  
 50 55 60  
 Gly Arg Val Ala Gly Leu Ala Glu Ile Val Val Asn Gly Gln Pro Phe  
 65 70 75 80  
 Thr Val Thr Asp Ala Thr Glu Asp Glu Leu Ala Leu Thr Ala Trp Ala  
 85 90 95  
 Arg Ile Leu Leu Glu Gly Thr Pro Ile Ala Met Asp Gly Ser Trp Gln  
 100 105 110  
 Leu His Arg Arg Arg Ala Ala Pro Glu Pro Val Arg Phe Ala Lys Arg  
 115 120 125  
 Phe Gly Gly Glu Gln Ser Asn Thr Ser Ile Met Val Gly Asp Ala Ile  
 130 135 140  
 Ile Ile Lys Met Phe Arg Arg Leu Glu Pro Gly Asp Asn Leu Asp Ile  
 145 150 155 160  
 Thr Val His Ser Ala Leu Asn Asp Ala Gly Ile Ser Ser Val Ala Thr  
 165 170 175  
 Leu Tyr Gly Phe Met Ser Gly Gln Ile Pro Ala Glu Glu His Ile Pro  
 180 185 190  
 Val Asp Leu Ala Met Ile Ile Glu Arg Leu Pro Gln Pro Arg Asp Gly  
 195 200 205  
 Trp Glu Leu Ile Thr Ala Lys Ala Val Asp Leu Val Asp  
 210 215 220

<210> 2513  
 <211> 368  
 <212> DNA  
 <213> Homo sapiens

<400> 2513  
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 60  
 cagcttgacc tggccaagaa ccgcctctat caggccattc agagagctga tgacatcttg  
 120  
 gacctgaagt tctgcatgga tggagttcag actgctttga ggagtgaaga ttatgagcag  
 180  
 gctgcagcac atattcatcg ctacttgtgc ctggacaagt cggtcattga gctcagccga  
 240  
 cagggcaaag agggtcagca tccgaaactg gagcatgatt gatgccaaacc tgaaattgct  
 300  
 gcaggaagct gagcaacgtc tcaaagccat tgtggcagag aagtttgcca ttgccaccaa  
 360



ggaaggtg  
368

<210> 2514  
<211> 93  
<212> PRT  
<213> Homo sapiens

<400> 2514  
Leu Ala Gly Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val Ser  
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Ser Lys Val Arg Gln Leu Asp Leu Ala Lys Asn Arg Leu Tyr Gln Ala  
20 25 30  
Ile Gln Arg Ala Asp Asp Ile Leu Asp Leu Lys Phe Cys Met Asp Gly  
35 40 45  
Val Gln Thr Ala Leu Arg Ser Glu Asp Tyr Glu Gln Ala Ala Ala His  
50 55 60  
Ile His Arg Tyr Leu Cys Leu Asp Lys Ser Val Ile Glu Leu Ser Arg  
65 70 75 80  
Gln Gly Lys Glu Gly Gln His Pro Lys Leu Glu His Asp  
85 90

<210> 2515  
<211> 351  
<212> DNA  
<213> Homo sapiens

<400> 2515  
agatcttaag ggccccagga atttgtttg ttttcctttt taactcccca ggtaattatg  
60  
gtcatcctg gaccagacc ttcctacccc tccaactccc caacaactgg gcaattggaa  
120  
tatcagtcca tccctaaaag ccaaccaggc tctcccgagg gaggcaggaa atcctgctc  
180  
cctccatccc ccaccgggaa tgctgcaggg ggcttgaggg aggcgacaca gtggggagct  
240  
ctgggtgcag gtgggcagac aatgggcca caccaccct cagccccgct ccagtatcag  
300  
cattccagac ccaccacct gggcccttg tcaccgggag acctcacgcg t  
351

<210> 2516  
<211> 98  
<212> PRT  
<213> Homo sapiens

<400> 2516  
Met Ala His Pro Gly Pro Asp Pro Ser Tyr Pro Ser Asn Ser Pro Thr  
1 5 10 15  
Thr Gly Gln Leu Glu Tyr Gln Ser Ile Pro Lys Ser Gln Pro Gly Ser  
20 25 30  
Pro Glu Gly Gly Arg Lys Ser Leu Leu Pro Pro Ser Pro Thr Gly Asn.  
35 40 45  
Ala Ala Gly Gly Leu Arg Glu Ala Thr Gln Trp Gly Ala Leu Gly Ala

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      50              55              60
Gly Gly Gln Thr Met Gly Gln His Thr Pro Ser Ala Pro Leu Gln Tyr
65              70              75              80
Gln His Ser Arg Pro Thr His Leu Gly Pro Trp Ser Pro Gly Asp Leu
      85              90              95
Thr Arg

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&lt;210&gt; 2517

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2517

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60
ggaggtggcc agtgagtcag gaggcggggg ggggggctag ggcttcccca ggggtcagga
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cctgtcacca accaaacccc atgggcctat tcagcagccc caacttggtt ggtctggccg
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aggccacaca ttccctgggg actgagctcc aagggtgctgg gtccttgagc aggaagcggc
240
cagtgttgag tgggcagtgt ctactccag cccctccttc ccaggccagt tcttctcatc
300
tccttcagtc tttcccaagc aggcctcat ctacagggca gacctgactg gctagc
356

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&lt;210&gt; 2518

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2518

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Met Gly Ala Glu Gly Glu Asp Lys Arg Arg Trp Pro Val Ser Gln Glu
1              5              10              15
Ala Gly Gly Gly Ala Arg Ala Ser Pro Gly Val Arg Thr Cys His Gln
      20              25              30
Pro Asn Pro Met Gly Leu Phe Ser Ser Pro Asn Leu Ala Gly Leu Ala
      35              40              45
Glu Ala Thr His Ser Leu Gly Thr Glu Leu Gln Gly Ala Gly Ser Leu
      50              55              60
Ser Arg Lys Arg Pro Val Leu Ser Gly Gln Cys Leu Thr Pro Ala Pro
65              70              75              80
Pro Ser Gln Ala Ser Ser Ser His Leu Pro Gln Ser Phe Pro Ser Arg
      85              90              95
Pro Ser Ser Thr Gly Gln Thr
      100

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&lt;210&gt; 2519

&lt;211&gt; 830

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2519

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 240  
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 420  
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 480  
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 540  
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 660  
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 720  
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 780  
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 830

&lt;210&gt; 2520

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2520

Met	Ser	Pro	Ala	Arg	Arg	Cys	Leu	Gly	Leu	Gly	Pro	Glu	Asn	Phe	Gly
1				5				10					15		
Glu	Glu	Val	Gly	Leu	Leu	Cys	Asn	Cys	Leu	Val	Pro	Phe	Lys	Val	Ile
		20				25				30					
Leu	Pro	Cys	Trp	Gly	Arg	Cys	Ser	Ser	Ser	Phe	Gln	Arg	Arg	Lys	Arg
		35				40				45					
Gly	Trp	Gly	Val	Ala	Gly	Arg	Gly	Ser	Ser	Arg	Pro	Glu	Ser	Gln	Ser
	50				55					60					
Arg	Trp	Arg	Ala	Ala	Ser	Thr	Arg	Phe	Leu	Leu	Val	Gly	Leu	Arg	Gln
65				70				75						80	
Gly	Leu	Ala	Pro	Gly	Leu	Ser	Gly	Lys	Arg	Glu	Glu	Glu	Leu	Arg	Leu
		85					90						95		
Arg	Gly	Ala	Val	Leu	Pro	Arg	Arg	Leu	Thr	Gly					
		100						105							

&lt;210&gt; 2521

&lt;211&gt; 4291

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2521

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420  
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540  
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&lt;210&gt; 2522

&lt;211&gt; 952

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2522

Leu	Ser	Leu	Phe	Arg	Ala	Glu	Ser	Pro	Thr	Thr	Ala	Ser	Pro	Ala	Leu
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Gly	Gly	Pro	Ala	Pro	Gly	Cys	Ser	Arg	Arg	Thr	Pro	Pro	Pro	Pro	Met
				20				25					30		
Ala	Pro	Leu	Ala	Leu	Val	Gly	Val	Thr	Leu	Leu	Leu	Ala	Ala	Pro	Pro
				35				40					45		
Cys	Ser	Gly	Ala	Ala	Thr	Pro	Thr	Pro	Ser	Leu	Pro	Pro	Pro	Pro	Ala
				50				55					60		
Asn	Asp	Ser	Asp	Thr	Ser	Thr	Gly	Gly	Cys	Gln	Gly	Ser	Tyr	Arg	Cys

65					70					75				80
Gln	Pro	Gly	Val	Leu	Leu	Pro	Val	Trp	Glu	Pro	Asp	Asp	Pro	Ser
				85					90					95
Gly	Asp	Lys	Ala	Ala	Arg	Ala	Val	Val	Tyr	Phe	Val	Ala	Met	Val
			100					105					110	
Met	Phe	Leu	Gly	Val	Ser	Ile	Ile	Ala	Asp	Arg	Phe	Met	Ala	Ala
	115					120						125		
Glu	Val	Ile	Thr	Ser	Lys	Glu	Lys	Glu	Ile	Thr	Ile	Thr	Lys	Ala
	130					135					140			
Gly	Glu	Thr	Ser	Val	Gly	Thr	Val	Arg	Ile	Trp	Asn	Glu	Thr	Val
145					150					155				160
Asn	Leu	Thr	Leu	Met	Ala	Leu	Gly	Ser	Ser	Ala	Pro	Glu	Ile	Leu
			165						170					175
Ser	Val	Ile	Glu	Val	Cys	Gly	His	Asn	Phe	Gln	Ala	Gly	Glu	Leu
			180					185					190	
Pro	Gly	Thr	Ile	Val	Gly	Ser	Ala	Ala	Phe	Asn	Met	Phe	Val	Val
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Ala	Val	Cys	Ile	Tyr	Val	Ile	Pro	Ala	Gly	Glu	Ser	Arg	Lys	Ile
	210				215						220			
His	Leu	Arg	Val	Phe	Phe	Val	Thr	Ala	Ser	Trp	Ser	Ile	Phe	Ala
225					230					235				240
Val	Trp	Leu	Tyr	Leu	Ile	Leu	Ala	Val	Phe	Ser	Pro	Gly	Val	Val
			245						250					255
Val	Trp	Glu	Ala	Leu	Leu	Thr	Leu	Val	Phe	Phe	Pro	Val	Cys	Val
		260					265					270		
Phe	Ala	Trp	Met	Ala	Asp	Lys	Arg	Leu	Leu	Phe	Tyr	Lys	Tyr	Val
	275					280						285		
Lys	Arg	Tyr	Arg	Thr	Asp	Pro	Arg	Ser	Gly	Ile	Ile	Ile	Gly	Ala
	290				295					300				
Gly	Asp	Pro	Pro	Lys	Ser	Ile	Glu	Leu	Asp	Gly	Thr	Phe	Val	Gly
305				310						315				320
Glu	Ala	Pro	Gly	Glu	Leu	Gly	Gly	Leu	Gly	Pro	Gly	Pro	Ala	Glu
			325						330					335
Arg	Glu	Leu	Asp	Ala	Ser	Arg	Arg	Glu	Val	Ile	Gln	Ile	Leu	Lys
			340					345					350	
Leu	Lys	Gln	Lys	His	Pro	Asp	Lys	Asp	Leu	Glu	Gln	Leu	Val	Gly
	355					360						365		
Ala	Asn	Tyr	Tyr	Ala	Leu	Leu	His	Gln	Gln	Lys	Ser	Arg	Ala	Phe
	370				375					380				
Arg	Ile	Gln	Ala	Thr	Arg	Leu	Met	Thr	Gly	Ala	Gly	Asn	Val	Leu
385				390						395				400
Arg	His	Ala	Ala	Asp	Ala	Ser	Arg	Arg	Ala	Ala	Pro	Ala	Glu	Gly
			405						410				415	
Gly	Glu	Asp	Glu	Asp	Asp	Gly	Ala	Ser	Arg	Ile	Phe	Phe	Glu	Pro
		420						425					430	
Leu	Tyr	His	Cys	Leu	Glu	Asn	Cys	Gly	Ser	Val	Leu	Leu	Ser	Val
	435					440						445		
Cys	Gln	Gly	Gly	Glu	Gly	Asn	Ser	Thr	Phe	Tyr	Val	Asp	Tyr	Arg
	450					455				460				
Glu	Asp	Gly	Ser	Ala	Lys	Ala	Gly	Ser	Asp	Tyr	Glu	Tyr	Ser	Glu
465				470						475				480
Thr	Leu	Val	Phe	Lys	Pro	Gly	Glu	Thr	Gln	Lys	Glu	Leu	Arg	Ile
			485						490					495
Ile	Ile	Asp	Asp	Asp	Ile	Phe	Glu	Glu	Asp	Glu	His	Phe	Phe	Val

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Leu	Leu	Asn	Leu	Arg	Val	Gly	Asp	Ala	Gln	Gly	Met	Phe	Glu	Pro	Asp				
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Val	Thr	Ile	Leu	Asp	Asp	Asp	His	Ala	Gly	Ile	Phe	Ser	Phe	Gln	Asp				
545					550					555					560				
Arg	Leu	Leu	His	Val	Ser	Glu	Cys	Met	Gly	Thr	Val	Asp	Val	Arg	Val				
				565					570						575				
Val	Arg	Ser	Ser	Gly	Ala	Arg	Gly	Thr	Val	Arg	Leu	Pro	Tyr	Arg	Thr				
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Val	Asp	Gly	Thr	Ala	Arg	Gly	Gly	Gly	Val	His	Tyr	Glu	Asp	Ala	Cys				
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Lys	Ile	Val	Asp	Asp	Glu	Glu	Tyr	Glu	Lys	Lys	Asp	Asn	Phe	Phe	Ile				
625					630					635					640				
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Leu	Asn	Gln	Gly	Asp	Gly	Asp	Arg	Lys	Leu	Thr	Ala	Glu	Glu	Glu	Glu				
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Ala	Arg	Arg	Ile	Ala	Glu	Met	Gly	Lys	Pro	Val	Leu	Gly	Glu	Asn	Cys				
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Asp	Lys	Leu	Ile	Lys	Lys	Thr	Asn	Leu	Ala	Leu	Val	Ile	Gly	Thr	His				
705					710					715					720				
Ser	Trp	Arg	Glu	Gln	Phe	Leu	Glu	Ala	Ile	Thr	Val	Ser	Ala	Gly	Asp				
				725					730						735				
Glu	Glu	Glu	Glu	Glu	Asp	Gly	Ser	Arg	Glu	Glu	Arg	Leu	Pro	Ser	Cys				
				740				745							750				
Phe	Asp	Tyr	Val	Met	His	Phe	Leu	Thr	Val	Phe	Trp	Lys	Val	Leu	Phe				
		755					760					765							
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Val	Ser	Ile	Leu	Val	Ile	Gly	Leu	Leu	Thr	Ala	Leu	Ile	Gly	Asp	Leu				
785					790					795					800				
Ala	Ser	His	Phe	Gly	Cys	Thr	Val	Gly	Leu	Lys	Asp	Ser	Val	Asn	Ala				
				805					810						815				
Val	Val	Phe	Val	Ala	Leu	Gly	Thr	Ser	Ile	Pro	Asp	Thr	Phe	Ala	Ser				
				820				825							830				
Lys	Val	Ala	Ala	Leu	Gln	Asp	Gln	Cys	Ala	Asp	Ala	Ser	Ile	Gly	Asn				
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Val</																			



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945 950

940

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<211> 392  
<212> DNA  
<213> Homo sapiens

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120  
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392

<210> 2524  
<211> 130  
<212> PRT  
<213> Homo sapiens

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Val Val Asp Val Phe Ser Arg Lys Ile Val Gly Val Ala Thr Arg Ser  
20 25 30  
Thr Met Arg Thr Asp Ala Leu Pro Met Glu Ala Leu Glu His Ala Leu  
35 40 45  
Thr Thr Ala Gly Arg Ile His Gly Asn Gln Leu Ile His His Ser Asp  
50 55 60  
Arg Gly Ser Gln Tyr Val Ser Leu Lys Tyr Ser Thr Ala Leu Ala Glu  
65 70 75 80  
Ser Gly Ile Arg Pro Ser Val Gly Thr Val Gly Asp Ser Tyr Asp Asn  
85 90 95  
Ala Leu Ala Glu Thr Val Asn Gly Leu Tyr Lys Ala Glu Leu Ile His  
100 105 110  
Ala Gln Gly Pro Trp Thr Ser Val Gly Glu Val Glu Leu Ala Thr Leu  
115 120 125  
Arg Xaa  
130

<210> 2525  
<211> 378  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 2525

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180  
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240  
gaagtcagcg gtgcgcccgc acgcctgcga ttctgggtga agacgcgcga ctaccattca  
300  
gaactggtgg ccgcaacact cattcgcagc gagaagcccg ccgatttgcc caacacctat  
360  
caatacggcg tggaattc  
378

&lt;210&gt; 2526

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2526

Met	Ala	Val	Cys	Arg	Ile	Pro	Phe	Glu	Tyr	Val	Val	Leu	Ser	Pro	Pro
1			5					10					15		
Arg	Glu	Ser	Arg	Thr	Ala	Arg	Cys	Ala	Asn	Arg	Cys	Ala	Thr	His	Gln
		20					25					30			
Arg	Gly	Arg	Gln	Asp	Val	Gly	Gln	Arg	Arg	Ala	Pro	Xaa	Met	Ile	His
	35					40					45				
Ile	Ser	Asp	Ile	Ser	Thr	Thr	Gly	Ala	Ser	Phe	Arg	Ser	Ala	His	Arg
	50				55				60						
Leu	Gly	Ser	Gln	Arg	Cys	Ala	Arg	Thr	Pro	Ala	Ile	Ser	Gly	Glu	Asp
65				70					75					80	
Ala	Arg	Leu	Pro	Phe	Arg	Thr	Gly	Gly	Arg	Asn	Thr	His	Ser	Gln	Arg
		85					90						95		
Glu	Ala	Arg	Arg	Phe	Ala	Gln	His	Leu	Ser	Ile	Arg	Arg	Gly	Ile	
		100					105						110		

&lt;210&gt; 2527

&lt;211&gt; 305

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2527

ntggtcacct tccgaatggg acggcggccc aaacccgaga tcatggccag caaagagcag  
60  
cagatccaga gagacgacct tggagccagt ccccagagca gcagccagcc agaccacggc  
120  
cgcctctccc cccagaagc tcccagacag cccaccatct ccacggcctc cgagacctca  
180  
gtgtacgtga cctggattcc ccgtgggaat ggtgggttcc caatccagtc cttccgtgtg  
240  
gagtacaaga agctaaagaa agtgggagac tggattctgg ccaccagcgc catcccccca  
300

cgcgct

305

&lt;210&gt; 2528

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2528

```

Xaa Val Thr Phe Arg Met Gly Arg Arg Pro Lys Pro Glu Ile Met Ala
 1           5           10           15
Ser Lys Glu Gln Gln Ile Gln Arg Asp Asp Leu Gly Ala Ser Pro Gln
      20           25           30
Ser Ser Ser Gln Pro Asp His Gly Arg Leu Ser Pro Pro Glu Ala Pro
      35           40           45
Asp Arg Pro Thr Ile Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr
      50           55           60
Trp Ile Pro Arg Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val
      65           70           75           80
Glu Tyr Lys Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser
      85           90           95
Ala Ile Pro Pro Arg
      100

```

&lt;210&gt; 2529

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2529

```

acgcgtctcc ccgtggtggg tcccgatccc ccggccggct ctgccactga agcctctccc
60
tgtgtcctcc gtgccccccg agtggcctgc tagcccgctc tcccacacag tctccttgat
120
gtgaagtgtc acccggttg ctgcggcggtg tctccgccgt aacacgtgta taccgggtca
180
gccatggcgg cggctgctgg gaaggctcct gcgtatggct ttgccatccg ggacccgggc
240
tttgctctgc aggggtgggc ttctgagcag aggaaggcca gaggtaacca ggtccatgca
300
cgtttgtgtc tttccacaat gtcgggcttt tatggatgct ttagtgtctca gtcacaaaag
360
ccatgagctc cacaggttcc tgaggga
387

```

&lt;210&gt; 2530

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2530

```

Met Ala Phe Val Thr Glu Thr Lys Ser Ile His Lys Ser Pro Thr Leu
 1           5           10           15
Trp Lys Asp Thr Asn Val His Gly Pro Gly Tyr Leu Trp Pro Ser Ser

```

```

                20                25                30
Ala Gln Lys Pro Thr Pro Ala Glu Gln Ser Pro Gly Pro Gly Trp Gln
                35                40                45
Ser His Thr Gln Glu Pro Ser Gln Gln Pro Pro Pro Trp Leu Ser Arg
                50                55                60
Tyr Thr Arg Val Thr Ala Glu Thr Arg Arg Ser Lys Pro Gly Asp Thr
65                70                75                80
Ser His Gln Gly Asp Cys Val Gly Glu Arg Ala Ser Arg Pro Leu Gly
                85                90                95
Gly His Gly Gly His Arg Glu Arg Leu Gln Trp Gln Ser Arg Pro Gly
                100                105                110
Asp Arg Asp Pro Pro Arg Gly Asp Ala
                115                120

```

&lt;210&gt; 2531

&lt;211&gt; 396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2531

```

tctagagata caaaaagtac tctatacact gagagacatc tggataaata caaaggttga
60
gctttccaac cagctgaaga tgacaagact aaacccaag tcgctgcagc tctgtgtcat
120
ctcatcagca gccctggaga tgacaaagat agtgctgagg gggaacagac cttcgtcatc
180
agttaaagat atgctagctt ttctttttct tccagacatt cctgaatcca gagaactttc
240
ctgtaatgcy tcaaatcctt taggtctcaa ttctttccct agagagacaa ggagcacagt
300
tcgttcccaa ggccccccat gcttggcgag ggcgtctctg ctttccaggc agggctcctgc
360
tgccctccacc cacgtgcagg gaaaggaagg acgcgt
396

```

&lt;210&gt; 2532

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2532

```

Met Thr Arg Leu Asn Pro Lys Ser Leu Gln Leu Cys Val Ile Ser Ser
1                5                10                15
Ala Ala Leu Glu Met Thr Lys Ile Val Leu Arg Gly Asn Arg Pro Ser
                20                25                30
Ser Ser Val Lys Asp Met Leu Ala Phe Leu Phe Leu Pro Asp Ile Pro
35                40                45
Glu Ser Arg Glu Leu Ser Cys Asn Ala Ser Asn Pro Leu Gly Leu Asn
50                55                60
Ser Phe Pro Arg Glu Thr Arg Ser Thr Val Arg Ser Gln Gly Pro Pro
65                70                75                80
Cys Leu Ala Arg Ala Ser Leu Leu Ser Arg Gln Gly Pro Ala Ala Ser
85                90                95
Thr His Val Gln Gly Lys Glu Gly Arg

```

100

105

<210> 2533  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<400> 2533  
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 60  
 gctgtggcan ccccatgga cgtgatcaag tcgagactgc aggcagacgg gcagggccag  
 120  
 aggcgctacc ggggtctcct gcactgtatg gtgaccagcg ttcgagagga gggaccccg  
 180  
 gtccttttca aggggctggt actcaattgc tgccgcgct tccctgtcaa catggtggtc  
 240  
 ttcgtcgct atgaggcagt gctgaggctc gcccggggtc tgctcacata gccggtcctc  
 300  
 acgcccagcg gccacccac cagcagctgc tggaggctcgt agtggttgga ggaggcaagg  
 360  
 ggtagtgtgg ctgggttcgg gacccacag gccattgcc caggagaatg aggagcctcc  
 420  
 ctgcagtgtt gtcggccgag gcctgagctc gcctgcca gctactgacc tcaggctcag  
 480  
 gggcccgcga gccat  
 495

<210> 2534  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 2534  
 Xaa Arg Pro Asp Val Pro Gly Val Leu Val Ala Gly Gly Cys Ala Gly  
 1 5 10 15  
 Val Leu Ala Trp Ala Val Ala Xaa Pro Met Asp Val Ile Lys Ser Arg  
 20 25 30  
 Leu Gln Ala Asp Gly Gln Gly Gln Arg Arg Tyr Arg Gly Leu Leu His  
 35 40 45  
 Cys Met Val Thr Ser Val Arg Glu Glu Gly Pro Arg Val Leu Phe Lys  
 50 55 60  
 Gly Leu Val Leu Asn Cys Cys Arg Ala Phe Pro Val Asn Met Val Val  
 65 70 75 80  
 Phe Val Ala Tyr Glu Ala Val Leu Arg Leu Ala Arg Gly Leu Leu Thr  
 85 90 95

<210> 2535  
 <211> 1904  
 <212> DNA  
 <213> Homo sapiens

<400> 2535  
 ncggccccggg aacgtggctg gttggaggag gtagatcacc ctttctgcgg gggacgattt  
 60

cgctcgggtgtt aggcctgctac catgaggttg aatcagaaca ccttgctgct ggggaagaag  
120  
gtggctccttg taccctacac ctccgagcat gtgcccagca ggtaccacga gtggatgaaa  
180  
tcagaggagc tgcagcgttt gacagcctcg gagccgctga ccctggagca ggagtatgcc  
240  
atgcagtga gctggcagga agatgcagac aagtgtacct tcattgtgct ggatgccgag  
300  
aagtggcagg ccagccagg cgccaccgaa gagagctgca tgggtgggaga cgtgaacctc  
360  
ttcctcacag atctagaaga cccaccttg ggggagatcg aggtcatgat tgcagagccc  
420  
agctgcaggg gtaagggcct tggcactgag gccgttctcg cgatgctgtc ttacggagtg  
480  
accacgctag gtctgaccaa gtttgaggct aaaattgggc aaggaaatga accaagcatc  
540  
cggatgttcc agaaacttca ctttgagcag gtggctacga gcagtgtttt tcaggagggtg  
600  
accctcagac tgacagtga tgagtccgag catcagtggc ttctggagca gaccagccac  
660  
gtggaagaga agccttacag agatgggtcg gcagagccct gctgatggct gggccttggtg  
720  
ggcagccact ctgtgtgagc aggggtgttg gccatacac ttcaaagacc agagccctgc  
780  
actgggagag tgctcctggc ccaggctggg aatcaccttt cgaggccctt cagactctgg  
840  
cggggcttgc tgtggcctcc ctccagctag tgggtgtggc gagcagactc cagggccagg  
900  
gccagttccc ttctcccctc ccggccaaac ccagaccag actctaggaa gctggaatgg  
960  
agggcagggg tccatgggag atgtcgggat gaaggtggga gctggagggtg cagggggacc  
1020  
tggaacatgg atgggagtg acaggccttt ctcccttagag gccagagggtg ctgccctggc  
1080  
tgggagtga gctccaggca ctaccagctt tctgatttt cccgtttggc ccatgtgaag  
1140  
agctaccag agccccagcc tcacagtgtc cactcaaggg cagcttggtc ctctgtcct  
1200  
gcagaggcag gctggtgtga ccctgggaac ttgaccggg aacaacaggt ggtccagagt  
1260  
gagtgtggc tggccctca acctagtgtc cgtcctcctc tctcctggag ccagtcttga  
1320  
gtttaaggc attagtgtta gatacagctc cttgtggctg gaaaacaccc ctctgtgat  
1380  
aaagctcagg gggcactgag gaagcagagg ccccttggg gtgccctcct gaagagagcg  
1440  
tcaggccatc agctctgtcc ctctggtgct cccagctctg ttccctaccc tccatctctg  
1500  
ggagcagctg cacctgactg gccacgcggg ggcagtggag gcacaggctc aggggtggcg  
1560  
ggctacctg caccctatgg cttacaaagt agagtggcc cagtttcctt ccacctgagg  
1620  
ggagcactct gactcctaac agtcttcctt gcctgccaat catctggggg ggctggctgt  
1680

caagaaaggc cgggcatgct ttctaaacac agccacagga ggcttgtagg gcattctcca  
 1740  
 ggtggggaaa cagtcttaga taagtaaggt gacttgccca aggcctccca gcacccttga  
 1800  
 tcttgagtc tcacagcaga ctgcatgtga acaactggaa ccgaaaacat gcctcagtat  
 1860  
 aaaacaaaca ttataaaacg aaaaaaaaaa aaaaaaaaaa tact  
 1904

<210> 2536

<211> 207

<212> PRT

<213> Homo sapiens

<400> 2536

Met	Arg	Leu	Asn	Gln	Asn	Thr	Leu	Leu	Leu	Gly	Lys	Lys	Val	Val	Leu
1			5					10					15		
Val	Pro	Tyr	Thr	Ser	Glu	His	Val	Pro	Ser	Arg	Tyr	His	Glu	Trp	Met
			20					25					30		
Lys	Ser	Glu	Glu	Leu	Gln	Arg	Leu	Thr	Ala	Ser	Glu	Pro	Leu	Thr	Leu
			35				40					45			
Glu	Gln	Glu	Tyr	Ala	Met	Gln	Cys	Ser	Trp	Gln	Glu	Asp	Ala	Asp	Lys
			50			55				60					
Cys	Thr	Phe	Ile	Val	Leu	Asp	Ala	Glu	Lys	Trp	Gln	Ala	Gln	Pro	Gly
65					70					75				80	
Ala	Thr	Glu	Glu	Ser	Cys	Met	Val	Gly	Asp	Val	Asn	Leu	Phe	Leu	Thr
				85				90					95		
Asp	Leu	Glu	Asp	Pro	Thr	Leu	Gly	Glu	Ile	Glu	Val	Met	Ile	Ala	Glu
			100					105					110		
Pro	Ser	Cys	Arg	Gly	Lys	Gly	Leu	Gly	Thr	Glu	Ala	Val	Leu	Ala	Met
			115				120					125			
Leu	Ser	Tyr	Gly	Val	Thr	Thr	Leu	Gly	Leu	Thr	Lys	Phe	Glu	Ala	Lys
			130				135					140			
Ile	Gly	Gln	Gly	Asn	Glu	Pro	Ser	Ile	Arg	Met	Phe	Gln	Lys	Leu	His
145					150					155				160	
Phe	Glu	Gln	Val	Ala	Thr	Ser	Ser	Val	Phe	Gln	Glu	Val	Thr	Leu	Arg
				165				170					175		
Leu	Thr	Val	Ser	Glu	Ser	Glu	His	Gln	Trp	Leu	Leu	Glu	Gln	Thr	Ser
			180					185					190		
His	Val	Glu	Glu	Lys	Pro	Tyr	Arg	Asp	Gly	Ser	Ala	Glu	Pro	Cys	
			195				200					205			

<210> 2537

<211> 509

<212> DNA

<213> Homo sapiens

<400> 2537

acgcgttctc gtaaggacaa gcttgacgcc gaggtgcatg ccggtgaagg caccctcggg  
 60  
 gatgtcatcg tgctgcggtt ttccggagcc atggcgaagc gtctgcctc agttatcctt  
 120  
 ccgctgctac tgctggactc ccccgctcatt gcgtggtggc ccttctccgg ccctgacaac  
 180

WO 00/58473

ggggtcccga tgaacgtcga cctcacgtca acagacgggc taggcactcc tctgcccctc  
 240  
 gtagtggcca atatgaccgc aatttcggga cgtcgcatgg cagagaccat cgccaggcgc  
 300  
 ggaggcattg ctgttctgcc ccaagatatc ccggcggatt tcgtcgcccg gtccattcgg  
 360  
 cgcgtcaaag atgcgcatac tcgattcgac accccagtca ccgtcaaccc gacaacgact  
 420  
 gtcggtgagg ccatgaactt gctcaacaag cgc  
 453

<210> 2540  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 2540  
 Phe Ala Ala Ser Arg His Asp Pro Arg Ile Val Thr Trp Asp Asn Gly  
 1 5 10 15  
 Tyr Val Arg Phe Leu Asn Glu Gln Pro Asn Tyr Asp Leu Thr Tyr Asp  
 20 25 30  
 Asp Val Phe Met Ala Pro Asn Arg Ser Ser Val Gly Ser Arg Met Asn  
 35 40 45  
 Val Asp Leu Thr Ser Thr Asp Gly Leu Gly Thr Pro Leu Pro Leu Val  
 50 55 60  
 Val Ala Asn Met Thr Ala Ile Ser Gly Arg Arg Met Ala Glu Thr Ile  
 65 70 75 80  
 Ala Arg Arg Gly Gly Ile Ala Val Leu Pro Gln Asp Ile Pro Ala Asp  
 85 90 95  
 Phe Val Ala Arg Ser Ile Arg Arg Val Lys Asp Ala His Thr Arg Phe  
 100 105 110  
 Asp Thr Pro Val Thr Val Asn Pro Thr Thr Thr Val Gly Glu Ala Met  
 115 120 125  
 Asn Leu Leu Asn Lys Arg  
 130

<210> 2541  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<400> 2541  
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 60  
 ccttgcattg aaccattgc agggcacacg cagtctacat gtatcccagg ttttatgctc  
 120  
 acagagcctg caatactccg tgtctggaat acgttatttg ctgcacacct cccagaggaa  
 180  
 catgtaacgt ctgtgtaaca tgctatcctg cacacatctg aaagaatctg tgtacacaac  
 240  
 actattatgc tgtgcacaca tttcctcata ttctgtgtag agagcacctc attttgact  
 300  
 caaatattcg gcttcataa caagttacat tgctcacatc ttaaaatatt cattacacgt  
 360



ctcgctcgg accccatcgg agcccttgcg gaccgcccga tcaccgactc ggcagctgac  
 240  
 aaagatccgt gcaaagccct catacgccgt gcgggtcacc taaccgaggg tgactccgac  
 300  
 ctgtgttggg ctgcaccac cagctggaga gccctagctg cagcagcttt ggatcaacat  
 360  
 ccagcgaccg tcaagttcgc tcgggtagag tcagccgccg gtaatgcgcc ggcgatgctg  
 420  
 ctggcagcct ggctaggatt gcgtctcggc gtcccggctg agcgggtgac aaccgacgcg  
 480  
 cccggcatct ccgcgatcgt catgtcgac  
 509

<210> 2538  
 <211> 169  
 <212> PRT  
 <213> Homo sapiens

<400> 2538  
 Thr Arg Ser Arg Lys Asp Lys Leu Asp Ala Glu Val His Ala Gly Glu  
 1 5 10 15  
 Gly Thr Pro Gly Asp Val Ile Val Leu Arg Phe Ser Gly Ala Met Ala  
 20 25 30  
 Lys Arg Pro Ala Ser Val Ile Leu Pro Leu Leu Ser Asp Ser Pro  
 35 40 45  
 Val Ile Ala Trp Trp Pro Phe Ser Gly Pro Asp Asn Leu Ala Ser Asp  
 50 55 60  
 Pro Ile Gly Ala Leu Ala Asp Arg Arg Ile Thr Asp Ser Ala Ala Asp  
 65 70 75 80  
 Lys Asp Pro Cys Lys Ala Leu Ile Arg Arg Ala Ala His Leu Thr Glu  
 85 90 95  
 Gly Asp Ser Asp Leu Cys Trp Ala Arg Thr Thr Ser Trp Arg Ala Leu  
 100 105 110  
 Ala Ala Ala Ala Leu Asp Gln His Pro Ala Thr Val Lys Phe Ala Arg  
 115 120 125  
 Val Glu Ser Ala Ala Gly Asn Ala Pro Ala Met Leu Leu Ala Ala Trp  
 130 135 140  
 Leu Gly Leu Arg Leu Gly Val Pro Val Glu Arg Val Thr Thr Asp Ala  
 145 150 155 160  
 Pro Gly Ile Ser Ala Ile Val Met Ser  
 165

<210> 2539  
 <211> 453  
 <212> DNA  
 <213> Homo sapiens

<400> 2539  
 aagcttctac tgccgcgagc acgtcgtcca ccgtcgaggt catggttcta gtttgccgcg  
 60  
 tcgcggcatg acccgaggat agtgacgtgg gacaatggct acgtgcgttt tctcaacgag  
 120  
 cagccgaact acgacctgac gtatgacgac gtcttcatgg caccaaaccg ttctcgggtg  
 180

WO 00/58473

&lt;213&gt; Homo sapiens

<400> 2544  
 Met Glu Trp Gly Gly Arg Ala Arg Val Gly Thr Cys Trp Asn Val Pro  
 1 5 10 15  
 Met Leu Ser Ala Pro His Trp Met Thr Glu Gly Glu Gly Thr Ser Val  
 20 25 30  
 Leu Pro Leu Leu Met Arg Phe Leu Phe Leu Pro Asn Lys Glu Met Cys  
 35 40 45  
 Met Asn Ala Arg Leu Phe Ala Gly Ala Gly Arg Arg Arg Val Leu Gly  
 50 55 60  
 Ile Ala Ala Asp Asn Ser Trp Asn Ser Cys Leu Gly Pro Pro Ala Gly  
 65 70 75 80  
 Leu Glu Arg Ala Val Ile Ile Cys Pro Leu Asp Arg Lys Val Cys Lys  
 85 90 95  
 Gly Leu Phe Ala Tyr Trp Val Pro Ile Phe Ser Leu Leu Lys Pro Leu  
 100 105 110  
 Ser Asn Gly Ala Gln Gln Ala Ala Val Leu  
 115 120

&lt;210&gt; 2545

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 2545  
 gcgattatatt tcgtgctgcc cggacttatc atggtcggct ggtggtcagg tttcccgta  
 60  
 tggaccaccc tcgctatctg tctagtcggc ggcacccctcg gcgttatgta ctcgattccg  
 120  
 ctgcgtcggg ccctcgtgac aggctcggat ctccctacc cggagggcgt cgcaggagct  
 180  
 gaggtgctca aagtaggcga ttccgctggt gccgcccagg ctaacaaggt gggctcgcga  
 240  
 gtcacatcg tcggttctgt ggtctctgca gcgtacgccc tgttgctgga tcttaagctt  
 300  
 gtgaagtcgg cgctgaccaa gcctttcaag acgggc  
 336

&lt;210&gt; 2546

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<400> 2546  
 Ala Ile Ile Phe Val Leu Pro Gly Leu Ile Met Val Gly Trp Trp Ser  
 1 5 10 15  
 Gly Phe Pro Tyr Trp Thr Thr Leu Ala Ile Cys Leu Val Gly Gly Ile  
 20 25 30  
 Leu Gly Val Met Tyr Ser Ile Pro Leu Arg Arg Ala Leu Val Thr Gly  
 35 40 45  
 Ser Asp Leu Pro Tyr Pro Glu Gly Val Ala Gly Ala Glu Val Leu Lys  
 50 55 60  
 Val Gly Asp Ser Ala Gly Ala Ala Glu Ala Asn Lys Val Gly Leu Arg

gaaaccaccg catggtaccg acatccttct ggaatgtccc gcacagaggc tgatatatgt  
 420  
 gcacagttct cactgttctg cgtgcccagc cctcacact ggacgcccac ctcacactct  
 480  
 tctgccaaagg gagactttgg ttctcccctt cctgtgctg gctgtgctgg ccacagtctt  
 540  
 ctgcacgcca gcagcatgac gcgt  
 564

<210> 2542  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 2542  
 Met Leu Cys Thr His Phe Leu Ile Phe Cys Val Glu Ser Thr Ser Phe  
 1 5 10 15  
 Cys Thr Gln Ile Phe Gly Phe His Asn Lys Leu His Cys Ser His Leu  
 20 25 30  
 Lys Ile Phe Ile Thr Arg Glu Thr Thr Ala Trp Tyr Arg His Pro Ser  
 35 40 45  
 Gly Met Ser Arg Thr Glu Ala Asp Ile Cys Ala Gln Phe Ser Leu Phe  
 50 55 60  
 Cys Val Pro Ser Pro Ser His Trp Thr Pro Thr Ser His Ser Ser Ala  
 65 70 75 80  
 Lys Gly Asp Phe Gly Ser Pro Leu Pro Cys Ala Gly Cys Ala Gly His  
 85 90 95  
 Ser Pro Leu His Ala Ser Ser Met Thr Arg  
 100 105

<210> 2543  
 <211> 387  
 <212> DNA  
 <213> Homo sapiens

<400> 2543  
 cgcttgaagg gggcggggaa aatggaatgg gggggaaggg cgcggtggg gacatgctgg  
 60  
 aacgtgccca tgctttctgc accacactgg atgactgaag gggaaggaac gagcgtctta  
 120  
 ccgctcctga tgagattttt gtttttgcct aacaaagaaa tgtgtatgaa tgcacgtctg  
 180  
 ttgcagggg caggaggag gagggctctt ggaatagctg ccgacaacag ctggaactcc  
 240  
 tgtctgggtc cccagctgg gctagagagg gcagtgatca tctgtccact ggacaggaag  
 300  
 gtttgcaaag ggctgtttgc ttactgggtc ccaattttta gccttctgaa gcccctgtcc  
 360  
 aatggggccc agcaggcagc agtgctg  
 387

<210> 2544  
 <211> 122  
 <212> PRT